References

Aktuell

Bendavid 2020

Eran Bendavid et al., *COVID-19 Antibody Seroprevalence in Santa Clara County, California.* medRxiv **2020**, 20062463, 1–17. DOI:10.1101/2020.04.14.20062463.

medRxiv2020-a20062463-Supplement.pdf

Background: Addressing COVID-19 is a pressing health and social concern. To date, many epidemic projections and policies addressing COVID-19 have been designed without seroprevalence data to inform epidemic parameters. We measured the seroprevalence of antibodies to SARS-CoV-2 in Santa Clara County.

Methods: On 4/3-4/4, 2020, we tested county residents for antibodies to SARS-CoV-2 using a lateral flow immunoassay. Participants were recruited using Facebook ads targeting a representative sample of the county by demographic and geographic characteristics. We report the prevalence of antibodies to SARSCoV2 in a sample of 3,330 people, adjusting for zip code, sex, and race/ethnicity. We also adjust for test performance characteristics using 3 different estimates: (i) the test manufacturer's data, (ii) a sample of 37 positive and 30 negative controls tested at Stanford, and (iii) a combination of both.

Results: The unadjusted prevalence of antibodies to SARS-CoV-2 in Santa Clara County was 1.5 % (exact binomial 95CI 1.11-1.97 %), and the population-weighted prevalence was 2.81 % (95CI 2.24-3.37 %). Under the three scenarios for test performance characteristics, the population prevalence of COVID-19 in Santa Clara ranged from 2.49 % (95CI 1.80-3.17 %) to 4.16 % (2.58-5.70 %). These prevalence estimates represent a range between 48,000 and 81,000 people infected in Santa Clara County by early April, 5085-fold more than the number of confirmed cases.

Conclusions: The population prevalence of SARS-CoV-2 antibodies in Santa Clara County implies that the infection is much more widespread than indicated by the number of confirmed cases. Population prevalence estimates can now be used to calibrate epidemic and mortality projections.

Bi 2020

Qifang Bi et al., *Epidemiology and Transmission of COVID-19 in Shenzhen China: Analysis of 391 cases and 1,286 of their close contacts.* medRxiv **2020**, 20028423, 1–22. DOI:10.1101/2020.03.03.20028423.

Background: Rapid spread of SARS-CoV-2 in Wuhan prompted heightened surveillance in Shenzhen and elsewhere in China. The resulting data provide a rare opportunity to measure key metrics of disease course, transmission, and the impact of control.

Methods: The Shenzhen CDC identified 391 SARS-CoV-2 cases from January 14 to February 12, 2020 and 1286 close contacts. We compare cases identified through symptomatic surveillance and contact tracing, and estimate the time from symptom onset to confirmation, isolation, and hospitalization. We estimate metrics of disease transmission and analyze factors influencing transmission risk.

Findings Cases were older than the general population (mean age 45) and balanced between males (187) and females (204). Ninety-one percent had mild or

moderate clinical severity at initial assessment. Three have died, 225 have recovered (median time to recovery is 21 days). Cases were isolated on average 4.6 days after developing symptoms; contact tracing reduced this by 1.9 days. Household contacts and those travelling with a case where at higher risk of infection (ORs 6 and 7) than other close contacts. The household secondary attack rate was 15 %, and children were as likely to be infected as adults. The observed reproductive number was 0.4, with a mean serial interval of 6.3 days.

Interpretation Our data on cases as well as their infected and uninfected close contacts provide key insights into SARS-CoV-2 epidemiology. This work shows that heightened surveillance and isolation, particularly contact tracing, reduces the time cases are infectious in the community, thereby reducing R. Its overall impact, however, is uncertain and highly dependent on the number of asymptomatic cases. We further show that children are at similar risk of infection as the general population, though less likely to have severe symptoms; hence should be considered in analyses of transmission and control.

CIUFOLINI 2020

Ignazio Ciufolini & Antonio Paolozzi, *Mathematical prediction of the time evolution of the COVID-19 pandemic in Italy by a Gauss error function and Monte Carlo simulations.* European Physical Journal Plus **135** (2020), 355, 1–8. DOI:10.1140/epjp/s13360-020-00383-y.

In this paper are presentedmathematical predictions on the evolution in time of the number of positive cases in Italy of the COVID-19 pandemic based on official data and on the use of a function of the type of a Gauss error function, with four parameters, as a cumulative distribution function. We have analyzed the available data for China and Italy. The evolution in time of the number of cumulative diagnosed positive cases ofCOVID-19 in China verywell approximates a distribution of the type of the error function, that is, the integral of a normal, Gaussian distribution. We have then used such a function to study the potential evolution in time of the number of positive cases in Italy by performing a number of fits of the official data so far available. We then found a statistical prediction for the day in which the peak of the number of daily positive cases in Italy occurs, corresponding to the flex of the fit, that is, to the change in sign of its second derivative (i.e., the change from acceleration to deceleration), as well as of the day in which a substantial attenuation of such number of daily cases is reached. We have also analyzed the predictions of the cumulative number of fatalities in both China and Italy, obtaining consistent results. We have then performed 150 Monte Carlo simulations to have a more robust prediction of the day of the above-mentioned peak and of the day of the substantial decrease in the number of daily positive cases and fatalities. Although official data have been used, those predictions are obtained with a heuristic approach since they are based on a statistical approach and do not take into account either a number of relevant issues (such as number of daily nasopharyngeal swabs, medical, social distancing, virological and epidemiological) or models of contamination diffusion.

GRONENBORN 2020

Detlef Gronenborn, *Die COVID-19-Pandemie, Teil 3: Die möglichen Konsequenzen der Krise für Deutschland.* Online **2020**, Apr. 16. <http://archaeologik.blogspot.com/2020/04/> (2020-04-21).

Gudbjartsson 2020

D. F. Gudbjartsson et al., *Spread of SARS-CoV-2 in the Icelandic Population.* New England Journal of Medicine (2020), preprint, 1–14. DOI:10.1056/NEJMoa2006100.

BACKGROUND: During the current worldwide pandemic, coronavirus disease 2019 (Covid-19) was first diagnosed in Iceland at the end of February. However, data are limited on how SARS-CoV-2, the virus that causes Covid-19, enters and spreads in a population.

Methods: We targeted testing to persons living in Iceland who were at high risk for infection (mainly those who were symptomatic, had recently traveled to high-risk countries, or had contact with infected persons). We also carried out population screening using two strategies: issuing an open invitation to 10,797 persons and sending random invitations to 2283 persons. We sequenced SARS-CoV-2 from 643 samples.

Results: As of April 4, a total of 1221 of 9199 persons (13.3 %) who were recruited for targeted testing had positive results for infection with SARS-CoV-2. Of those tested in the general population, 87 (0.8 %) in the open-invitation screening and 13 (0.6 %) in the random-population screening tested positive for the virus. In total, 6 % of the population was screened. Most persons in the targeted-testing group who received positive tests early in the study had recently traveled internationally, in contrast to those who tested positive later in the study. Children under 10 years of age were less likely to receive a positive result than were persons 10 years of age or older, with percentages of 6.7 % and 13.7 %, respectively, for targeted testing; in the population screening, no child under 10 years of age had a positive result, as compared with 0.8 % of those 10 years of age or older. Fewer females than males received positive Results both in targeted testing (11.0 % vs. 16.7 %) and in population screening (0.6 % vs. 0.9 %). The haplotypes of the sequenced SARS-CoV-2 viruses were diverse and changed over time. The percentage of infected participants that was determined through population screening remained stable for the 20-day duration of screening.

Conclusions: In a population-based study in Iceland, children under 10 years of age and females had a lower incidence of SARS-CoV-2 infection than adolescents or adults and males. The proportion of infected persons identified through population screening did not change substantially during the screening period, which was consistent with a beneficial effect of containment efforts. (Funded by deCODE Genetics–Amgen.)

Kupferschmidt 2020

Kai Kupferschmidt, *The lockdowns worked—but what comes next?* science **368** (2020), 218–219. DOI:10.1126/science.368.6488.218.

Easing the rules while keeping the virus at bay will be a process of trial and error.

But what is the exit strategy? "We've managed to get to the life raft," says epidemiologist Marc Lipsitch of the Harvard T.H. Chan School of Public Health (HSPH). "But I'm really unclear how we will get to the shore."

Lavezzo 2020

Enrico Lavezzo et al., *Suppression of COVID-19 outbreak in the municipality of Vò, Italy.* medRxiv **2020**, 20053157, 1–23. DOI:10.1101/2020.04.17.20053157.

medRxiv2020-a20053157-Supplement1.pdf, medRxiv2020-a20053157-Supplement2.xlsx

On the 21st of February 2020 a resident of the municipality of Vo', a small town near Padua, died of pneumonia due to SARS-CoV-2 infection1. This was the first COVID-19 death detected in Italy since the emergence of SARS-CoV-2 in the Chinese city of Wuhan, Hubei province2. In response, the regional authorities imposed the lockdown of the whole municipality for 14 days3. We collected information on the demography, clinical presentation, hospitalization, contact network and presence of SARS-CoV-2 infection in nasopharyngeal swabs for 85.9 % and 71.5 % of the population of Vo' at two consecutive time points. On the first survey, which was conducted around the time the town lockdown started, we found a prevalence of infection of 2.6 % (95 % confidence interval (CI) 2.13.3 %). On the second survey, which was conducted at the end of the lockdown, we found a prevalence of 1.2 % (95 % CI 0.8-1.8 %). Notably, 43.2 % (95 % CI 32.2-54.7 %) of the confirmed SARSCoV2 infections detected across the two surveys were asymptomatic. The mean serial interval was 6.9 days (95 % CI 2.6-13.4). We found no statistically significant difference in the viral load (as measured by genome equivalents inferred from cycle threshold data) of symptomatic versus asymptomatic infections (p-values 0.6 and 0.2 for E and RdRp genes, respectively, Exact WilcoxonMann-Whitney test). Contact tracing of the newly infected cases and transmission chain reconstruction revealed that most new infections in the second survey were infected in the community before the lockdown or from asymptomatic infections living in the same household. This study sheds new light on the frequency of asymptomatic SARS-CoV-2 infection and their infectivity (as measured by the viral load) and provides new insights into its transmission dynamics, the duration of viral load detectability and the efficacy of the implemented control measures.

Wadman 2020

Meredith Wadman, Jennifer Couzin-Frankel, Jocelyn Kaiser & Catherine Matacic, *How does coronavirus kill? Clinicians trace a ferocious rampage through the body, from brain to toes.* science **2020**, abc3208. DOI:10.1126/science.abc3208.

Ziegler 2020

Carly G. K. Ziegler et al., *SARS-CoV-2 receptor ACE2 is an interferon-stimulated gene in human airway epithelial cells and is detected in specific cell subsets across tissues.* Cell (2020), preprint, 1–76. DOI:10.1016/j.cell.2020.04.035.

There is pressing urgency to understand the pathogenesis of the severe acute respiratory syndrome coronavirus clade 2 (SARS-CoV-2) which causes the disease COVID-19. SARS-CoV2 spike (S)-protein binds ACE2, and in concert with host proteases, principally TMPRSS2, promotes cellular entry. The cell subsets targeted by SARS-CoV-2 in host tissues, and the factors that regulate ACE2 expression, remain unknown. Here, we leverage human, non-human primate, and mouse single-cell RNA-sequencing (scRNA-seq) datasets across health and disease to uncover putative targets of SARS-CoV-2 amongst tissue-resident cell subsets. We identify ACE2 and TMPRSS2 co-expressing cells within lung type II pneumocytes, ileal absorptive enterocytes, and nasal goblet secretory cells. Strikingly, we discover that ACE2 is a human interferonstimulated gene (ISG) in vitro using airway epithelial cells, and extend our findings to in vivo viral infections. Our data suggest that SARS-CoV-2 could exploit species-specific interferon-driven upregulation of ACE2, a tissue-protective mediator during lung injury, to enhance infection.

Altpaläolithikum

BUNN 2010

Henry T. Bunn & Travis Rayne Pickering, *Bovid mortality profiles in paleoecological context falsify hypotheses of endurance running–hunting and passive scavenging by early Pleistocene hominins.* Quaternary Research **74** (2010), 395–404.

The world's first archaeological traces from 2.6 million years ago (Ma) at Gona, in Ethiopia, include sharpedged cutting tools and cut-marked animal bones, which indicate consumption of skeletal muscle by early hominin butchers. From that point, evidence of hominin meat-eating becomes increasingly more common throughout the Pleistocene archaeological record. Thus, the substantive debate about hominin meat-eating now centers on mode(s) of carcass resource acquisition. Two prominent hypotheses suggest, alternatively, (1) that early Homo hunted ungulate prey by running them to physiological failure and then dispatching them, or (2) that early Homo was relegated to passively scavenging carcass residues abandoned by carnivore predators. Various paleontologically testable predictions can be formulated for both hypotheses. Here we test four predictions concerning age-frequency distributions for bovids that contributed carcass remains to the 1.8 Ma old FLK 22 Zinjanthropus (FLK Zinj, Olduvai Gorge, Tanzania) fauna, which zooarchaeological and taphonomic data indicate was formed predominantly by early Homo. In all but one case, the bovid mortality data from FLK Zinj violate test predictions of the endurance running-hunting and passive scavenging hypotheses. When combined with other taphonomic data, these results falsify both hypotheses, and lead to the hypothesis that early Homo operated successfully as an ambush predator.

Keywords: Uniformitarianism | Bovid mortality profiles | Carcass foraging | Early Homo | FLK 22 Zinjanthropus

Anthropologie

ANTÓN 2020

Susan C. Antón, *All who wander are not lost.* science **368** (2020), 34–35.

New hominin cranial fossils highlight the early exploits of Homo erectus.

Scientists have hypothesized that Homo as a genus relied more heavily on technological extraction of food resources (meat, marrow, and plants) and was behaviorally more flexible than Paranthropus or Australopithecus. Even in light of the diversity among Homo species, H. erectus seems to be the beginning of something new. In the ≈7-million-year history of the human lineage, H. erectus was the first species to leave the African continent (see the figure). In fact, almost as soon as they arose, H. erectus appeared outside of Africa at the site of Dmanisi in the Republic of Georgia. Over the next nearly 2 million years, H. erectus occupied a variety of different habitats and contexts before going extinct well after 0.5 million years ago on presentday Java.

RACIMO 2020

Fernando Racimo, Jessie Woodbridge, Ralph M. Fyfe, Karl-Göran Sjögren, Kristian Kristiansen & Marc Vander Linden et al., *The spatiotemporal spread of human migrations during the European Holocene.* PNAS **117** (2020), 8989–9000.

pnas117-08989-Supplement1.pdf, pnas117-08989-Supplement2.xlsx, pnas117-08989-Supplement3.gif, pnas117-08989-Supplement4.gif, pnas117-08989-Supplement5.gif

The European continent was subject to two major migrations of peoples during the Holocene: the northwestward movement of Anatolian farmer populations during the Neolithic and the westward movement of Yamnaya steppe peoples during the Bronze Age. These movements changed the genetic composition of the continent's inhabitants. The Holocene was also characterized by major changes in vegetation composition, which altered the environment occupied by the original hunter-gatherer populations. We aim to test to what extent vegetation change through time is associated with changes in population composition as a consequence of these migrations, or with changes in climate. Using ancient DNA in combination with geostatistical techniques, we produce detailed maps of ancient population movements, which allow us to visualize how these migrations unfolded through time and space. We find that the spread of Neolithic farmer ancestry had a two-pronged wavefront, in agreement with similar findings on the cultural spread of farming from radiocarbon-dated archaeological sites. This movement, however, did not have a strong association with changes in the vegetational landscape. In contrast, the Yamnaya migration speed was at least twice as fast and coincided with a reduction in the amount of broad-leaf forest and an increase in the amount of pasture and natural grasslands in the continent. We demonstrate the utility of integrating ancient genomes with archaeometric datasets in a spatiotemporal statistical framework, which we foresee will enable future studies of ancient populations' movements, and their putative effects on local fauna and flora.

Keywords: migrations | ancient DNA | Neolithic | Bronze Age | land cover

Fernando Racimo, Jessie Woodbridge, Ralph M. Fyfe, Martin Sikora, Karl-Göran Sjögren, Kristian Kristiansen & Marc Vander Linden

Significance: We present a study to model the spread of ancestry in ancient genomes through time and space and a geostatistical framework for comparing human migrations and land-cover changes, while accounting for changes in climate. We show that the two major migrations during the European Holocene had different spatiotemporal structures and expansion rates. In addition, we find that the Yamnaya expansion had a stronger association with vegetational landscape changes than the earlier Neolithic farmer expansion. Our approach paves the way for future work linking paleogenomics with other archaeometric datasets in the study of the past.

Bibel

G ARFINKEL 2020

Yosef Garfinkel & Anat Mendel-Geberovich, *Hierarchy, Geography and Epigraphy*, *Administration in the Kingdom of Judah.* Oxford Journal of Archaeology **39** (2020), 159–176.

Hundreds of epigraphic finds have been uncovered in excavations conducted in the ancient Kingdom of Judah, located in the south Levant and dated to the Iron Age (c.1000–586 BCE). These finds are usually studied from the linguistic and historical points of view, in a basic, descriptive manner. Here we present a new approach, analysing aspects relating to spatial distribution of epigraphic finds, spatial hierarchy of sites, bureaucratic hierarchy of officials, core and periphery, and ecological diversity of various regions of the kingdom.

In Memoriam Joseph Naveh

Biologie

XIE 2020

Fei Xie, Alan J. Drew & David J. Dunstan et al., *Explanation of the Colour Change in Alexandrites.* Scientific Reports **10** (2020), 6130. DOI:10.1038/s41598-020-62707-3.

Alexandrites are remarkable and rare gemstones. They display an extraordinary colour change according to the ambient lighting, from emerald green in daylight to ruby red in incandescent light from tungsten lamps or candles. While this colour change has been correctly attributed to chromium impurities and their absorption band in the yellow region of the visible light spectrum, no adequate explanation of the mechanism has been given. Here, the alexandrite effect is fully explained by considering the von Kries model of the human colour constancy mechanism. This implies that our colour constancy mechanism is real (objective) and primarily attuned to correct for the colour temperature of black-body illuminants.

Fei Xie, Yu Cao, Cindy Ranchon, Alan Hart, Robin Hansen, Jeffrey E. Post, Coralyn W. Whitney, Emma Dawson-Tarr, Alan J. Drew & David J. Dunstan

Datierung

CASANOVA 2020

Emmanuelle Casanova et al., *Accurate compound-specific ^{14}C dating of archaeological pottery vessels.* nature **580** (2020), 506–510.

n580-0506-Supplement.pdf

Pottery is one of the most commonly recovered artefacts from archaeological sites. Despite more than a century of relative dating based on typology and seriation1, accurate dating of pottery using the radiocarbon dating method has proven extremely challenging owing to the limited survival of organic temper and unreliability of visible residues2–4. Here we report a method to directly date archaeological pottery based on accelerator mass spectrometry analysis of 14C in absorbed food residues using palmitic (C16:0) and stearic (C18:0) fatty acids purified by preparative gas chromatography5–8. We present accurate compound-specific radiocarbon determinations of lipids extracted from pottery vessels, which were rigorously evaluated by comparison with dendrochronological dates9,10 and inclusion in site and regional chronologies that contained previously determined radiocarbon dates on other materials11–15. Notably, the compound-specific dates from each of the C16:0 and C18:0 fatty acids in pottery vessels provide an internal quality control of the Results6 and are entirely compatible with dates for other commonly dated materials. Accurate radiocarbon dating of pottery vessels can reveal: (1) the period of use of pottery; (2) the antiquity of organic residues, including when specific foodstuffs were exploited; (3) the chronology of sites in the absence of traditionally datable materials; and (4) direct verification of pottery typochronologies. Here we used the method to date the exploitation of dairy and carcass products in Neolithic vessels from Britain, Anatolia, central and western Europe, and Saharan Africa.

Emmanuelle Casanova, Timothy D. J. Knowles, Alex Bayliss, Julie Dunne, Marek Z. Barañski, Anthony Denaire, Philippe Lefranc, Savino di Lernia, Mélanie Roffet-Salque, Jessica Smyth, Alistair Barclay, Toby Gillard, Erich Claßen, Bryony Coles, Michael Ilett, Christian Jeunesse, Marta Krueger, Arkadiusz Marciniak, Steve Minnitt, Rocco Rotunno, Pieter van de Velde, Ivo van Wijk, Jonathan Cotton, Andy Daykin & Richard P. Evershed

K U T S C H E R A 2020

Walter Kutschera, *On the enigma of dating the Minoan eruption of Santorini.* PNAS **117** (2020), 8677–8679.

The publication of Pearson et al. in PNAS (13) goes a step farther by synchronizing a "floating" tree-ring series of the Mediterranean juniper, measured with annual 14C resolution, to the also annually 14C-measured absolute tree-ring series of the North American bristle cone pine and Irish oak (10). This in itself does not solve the radiocarbon dating dilemma and still has to await a generally accepted new 14C calibration curve after IntCal13 (9), but it provides now a Mediterranean tree-ring series with yearly resolution in the critical time period of the Santorini eruption. Pearson et al. (13) performed an X-ray resonance fluorescence analysis of the juniper tree-ring series, which revealed a significant depletion of calcium around 1560 BCE. As the authors point out (13), this was possibly caused by the Santorini eruption.

W E N I N G E R 2020

Bernhard Weninger, *Barcode Seriation and Concepts of Gauge Theory, The ^{14}C-Chronology of Starčevo, LBK, and early Vinča.* Quaternary International (2020), preprint, 1–41.

A new method for automated construction of 14C-based archaeological chronologies, called Barcode Seriation (BS), is introduced. The application of BS is demonstrated for mediumsized (N≈50 sites) datasets of the early Neolithic cultures Starèevo/Körös/Cris, LBK-I, and Vinèa A. The BS-method is easy to apply, but nevertheless allows construction of 14C-chronologies at comparatively high dating precision. The key to BS is a new timing discriminator (TD), designed for leading/trailing edge shape-analysis of summed probability distributions of 14C-ages (SPDs). In functional terms, the TD works as an Analog-to-Digital Converter. The SPD signal digitisation, in turn, supports large-scale 14C-database analysis on different levels of data confinement (e.g. by sites, periods, periods, cultures, phases) as well as on large geographic scales (regional-continental). Due to the compactness of the chosen graphic-output topology, the combined BS/TD-technology supports ordination and plotting of very large 14C-datasets, but leaving room in graphic representation for the chronology to be shown in context with other records e.g. from palaeoenvironmental, archaeobiological, and palaeaoclimatological studies. The feasibility of routine application of the new method is demonstrated by case-comparisons at high dating-resolution for the sites of Pityerdomb (Hungary), Vráble (Slowakia), Versend-Gilencsa (Hungary), Vinèa-Belo-Brdo (Serbia), and at two LBK-sites ('Lüsse' and 'Unteres Feld') both located in the Ammer Valley near Tübingen (Germany). The new methodology is complemented with studies towards the application of Gauge Theory in support of archaeological 14C-analysis.

Keywords: Chronology | Neolithic | Radiocarbon Calibration | Starcevo | Linearbandkeramik | Vinca

Klima

S T A H L E 2020

David W. Stahle, *Anthropogenic megadrought, Human-driven climate warming worsens an otherwise moderate drought.* science **368** (2020), 238–239.

Trisos 2020

> Christopher H. Trisos, Cory Merow & Alex L. Pigot, *The projected timing of abrupt ecological disruption from climate change.* nature **580** (2020), 496–501.
>
>> n580-0496-Supplement.pdf
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>> As anthropogenic climate change continues the risks to biodiversity will increase over time, with future projections indicating that a potentially catastrophic loss of global biodiversity is on the horizon1–3. However, our understanding of when and how abruptly this climate-driven disruption of biodiversity will occur is limited because biodiversity forecasts typically focus on individual snapshots of the future. Here we use annual projections (from 1850 to 2100) of temperature and precipitation across the ranges of more than 30,000 marine and terrestrial species to estimate the timing of their exposure to potentially dangerous climate conditions. We project that future disruption of ecological assemblages as a result of climate change will be abrupt, because within any given ecological assemblage the exposure of most species to climate conditions beyond their realized niche limits occurs almost simultaneously. Under a high-emissions scenario (representative concentration pathway (RCP) 8.5), such abrupt exposure events begin before 2030 in tropical oceans and spread to tropical forests and higher latitudes by 2050. If global warming is kept below 2 °C, less than 2 % of assemblages globally are projected to undergo abrupt exposure events of more than 20 % of their constituent species; however, the risk accelerates with the magnitude of warming, threatening 15 % of assemblages at 4 °C, with similar levels of risk in protected and unprotected areas. These results highlight the impending risk of sudden and severe biodiversity losses from climate change and provide a framework for predicting both when and where these events may occur.

Williams 2020

> A. Park Williams et al., *Large contribution from anthropogenic warming to an emerging North American megadrought.* science **368** (2020), 314–318.
>
>> s368-0314-Supplement.pdf
>
>> Severe and persistent 21st-century drought in southwestern North America (SWNA) motivates comparisons to medieval megadroughts and questions about the role of anthropogenic climate change. We use hydrological modeling and new 1200-year tree-ring reconstructions of summer soil moisture to demonstrate that the 2000–2018 SWNA drought was the second driest 19-year period since 800 CE, exceeded only by a late-1500s megadrought. The megadrought-like trajectory of 2000–2018 soil moisture was driven by natural variability superimposed on drying due to anthropogenic warming. Anthropogenic trends in temperature, relative humidity, and precipitation estimated from 31 climate models account for 47 % (model interquartiles of 35 to 105 %) of the 2000–2018 drought severity, pushing an otherwise moderate drought onto a trajectory comparable to the worst SWNA megadroughts since 800 CE.
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>> A. Park Williams, Edward R. Cook, Jason E. Smerdon, Benjamin I. Cook, John T. Abatzoglou, Kasey Bolles, Seung H. Baek, Andrew M. Badger & Ben Livneh

Ozeanien

Sear 2020

> David A. Sear et al., *Human settlement of East Polynesia earlier,*

incremental, and coincident with prolonged South Pacific drought.

pnas117-08813-Supplement1.pdf, pnas117-08813-Supplement2.xls

The timing of human colonization of East Polynesia, a vast area lying between Hawai'i, Rapa Nui, and New Zealand, is much debated and the underlying causes of this great migration have been enigmatic. Our study generates evidence for human dispersal into eastern Polynesia from islands to the west from around AD 900 and contemporaneous paleoclimate data from the likely source region. Lake cores from Atiu, Southern Cook Islands (SCIs) register evidence of pig and/or human occupation on a virgin landscape at this time, followed by changes in lake carbon around AD 1000 and significant anthropogenic disturbance from c. AD 1100. The broader paleoclimate context of these early voyages of exploration are derived from the Atiu lake core and complemented by additional lake cores from Samoa (directly west) and Vanuatu (southwest) and published hydroclimate proxies from the Society Islands (northeast) and Kiribati (north). Algal lipid and leaf wax biomarkers allow for comparisons of changing hydroclimate conditions across the region before, during, and after human arrival in the SCIs. The evidence indicates a prolonged drought in the likely western source region for these colonists, lasting c. 200 to 400 y, contemporaneous with the phasing of human dispersal into the Pacific. We propose that drying climate, coupled with documented social pressures and societal developments, instigated initial eastward exploration, resulting in SCI landfall(s) and return voyaging, with colonization a century or two later. This incremental settlement process likely involved the accumulation of critical maritime knowledge over several generations.

David A. Sear, Melinda S. Allen, Jonathan D. Hassall, Ashley E. Maloney, Peter G. Langdon, Alex E. Morrison, Andrew C. G. Henderson, Helen Mackay, Ian W. Croudace, Charlotte Clarke, Julian P. Sachs, Georgiana Macdonald, Richard C. Chiverrell, Melanie J. Leng, L. M. Cisneros-Dozal & Thierry Fonville

Significance: We combine indicators from lake sediments with archaeological records that identify an earlier and incremental arrival of humans in East Polynesia than indicated by current models. We use lake sediments to reconstruct a quantitative, multiproxy hydroclimate sequences from Vanuatu, Samoa, and the Southern Cook Islands and combine these with published data to show that the timing of human migration into East Polynesia coincided with a prolonged drought. We postulate this regional drought was a significant contributory factor in eastward exploration and subsequent colonization of the Southern Cook Islands and beyond. The return of wetter conditions in East Polynesia after c. AD 1150 supported subsequent colonization of other central islands and, eventually, migration into far eastern and South Polynesia.

Story or Book

D aniels 2020

Lori Daniels, *What tree rings can tell us.* science **368** (2020), 250.

From ancient timbers to mountaintop forests, trees hold important climate clues.
Tree Story: The History of the World Written in Rings. Valerie Trouet. Johns Hopkins University Press, 2020. 256 pp.