

References

Aktuell

CALY 2020

Leon Caly, Julian D. Druce, Mike G. Catton, David A. Jans & Kylie M. Wagstaff, *The FDA-approved drug ivermectin inhibits the replication of SARS-CoV-2 in vitro*. [Antiviral Research](#) **178** (2020), 104787, 1–4. DOI:10.1016/j.antiviral.2020.104787.

Although several clinical trials are now underway to test possible therapies, the worldwide response to the COVID-19 outbreak has been largely limited to monitoring/containment. We report here that Ivermectin, an FDA-approved anti-parasitic previously shown to have broad-spectrum anti-viral activity in vitro, is an inhibitor of the causative virus (SARS-CoV-2), with a single addition to Vero-hSLAM cells 2 h post infection with SARS-CoV-2 able to effect ≈ 5000 -fold reduction in viral RNA at 48 h. Ivermectin therefore warrants further investigation for possible benefits in humans.

DAVIES 2021

Nicholas G. Davies et al., *Estimated transmissibility and impact of SARS-CoV-2 lineage B.1.1.7 in England*. [science](#) **372** (2021), eabg3055. DOI:10.1126/science.abg3055.

s372-eabg3055-Supplement.pdf

A severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variant, VOC 202012/01 (lineage B.1.1.7), emerged in southeast England in September 2020 and is rapidly spreading toward fixation. Using a variety of statistical and dynamic modeling approaches, we estimate that this variant has a 43 to 90 % (range of 95 % credible intervals, 38 to 130 %) higher reproduction number than preexisting variants. A fitted two-strain dynamic transmission model shows that VOC 202012/01 will lead to large resurgences of COVID-19 cases. Without stringent control measures, including limited closure of educational institutions and a greatly accelerated vaccine rollout, COVID-19 hospitalizations and deaths across England in the first 6 months of 2021 were projected to exceed those in 2020. VOC 202012/01 has spread globally and exhibits a similar transmission increase (59 to 74 %) in Denmark, Switzerland, and the United States.

Nicholas G. Davies, Sam Abbott, Rosanna C. Barnard, Christopher I. Jarvis, Adam J. Kucharski, James D. Munday, Carl A. B. Pearson, Timothy W. Russell, Damien C. Tully, Alex D. Washburne, Tom Wenseleers, Amy Gimma, William Waites, Kerry L. M. Wong, Kevin van Zandvoort, Justin D. Silverman, C. M. M. COV-Working Group, COV-Genomics U. K. Consortium, Karla Diaz-Ordaz, Ruth Keogh, Rosalind M. Eggo, Sebastian Funk, Mark Jit, Katherine E. Atkins & W. John Edmunds

KEMP 2021

Steven A. Kemp et al., *SARS-CoV-2 evolution during treatment of chronic infection*. [nature](#) **592** (2021), 277–282. DOI:10.1038/s41586-021-03291-y.

n592-0277-Supplement.docx

The spike protein of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is critical for virus infection through the engagement of the human ACE2 protein¹ and is a major antibody target. Here we show that chronic infection with SARS-CoV-2 leads to viral evolution and reduced sensitivity to neutralizing antibodies in an immunosuppressed individual treated with convalescent plasma, by generating whole-genome ultra-deep sequences for 23 time points that span 101 days and using in vitro techniques to characterize the mutations revealed by sequencing. There was little change in the overall structure of the viral population after two courses of remdesivir during the first 57 days. However, after convalescent plasma therapy, we observed large, dynamic shifts in the viral population, with the emergence of a dominant viral strain that contained a substitution (D796H) in the S2 subunit and a deletion (DH69/DV70) in the S1 N-terminal domain of the spike protein. As passively transferred serum antibodies diminished, viruses with the escape genotype were reduced in frequency, before returning during a final, unsuccessful course of convalescent plasma treatment. In vitro, the spike double mutant bearing both DH69/DV70 and D796H conferred modestly decreased sensitivity to convalescent plasma, while maintaining infectivity levels that were similar to the wild-type virus. The spike substitution mutant D796H appeared to be the main contributor to the decreased susceptibility to neutralizing antibodies, but this mutation resulted in an infectivity defect. The spike deletion mutant DH69/DV70 had a twofold higher level of infectivity than wild-type SARS-CoV-2, possibly compensating for the reduced infectivity of the D796H mutation. These data reveal strong selection on SARS-CoV-2 during convalescent plasma therapy, which is associated with the emergence of viral variants that show evidence of reduced susceptibility to neutralizing antibodies in immunosuppressed individuals.

Steven A. Kemp, Dami A. Collier, Rawlings P. Datir, Isabella A. T. M. Ferreira, Salma Gayed, Aminu Jahun, Myra Hosmillo, Chloe Rees-Spear, Petra Mlcochova, Ines Ushiro Lumb, David J. Roberts, Anita Chandra, Nigel Temperton, The CITI-N. I. H. R. BioResource COV- Collaboratio, The COV- Genomics U. K. Consortiu, Katherine Sharrocks, Elizabeth Blane, Yorgo Modis, Kendra E. Leigh, John A. G. Briggs, Marit J. van Gils, Kenneth G. C. Smith, John R. Bradley, Chris Smith, Rainer Doffinger, Lourdes Ceron-Gutierrez, Gabriela Barcenas-Morales, David D. Pollock, Richard A. Goldstein, Anna Smielewska, Jordan P. Skittrall, Theodore Gouliouris, Ian G. Goodfellow, Effrossyni Gkrania-Klotsas, Christopher J. R. Illingworth, Laura E. McCoy & Ravindra K. Gupta

SNEPPEN 2021

Kim Sneppen, Bjarke Frost Nielsen, Robert J. Taylor & Lone Simonsen, *Overdispersion in COVID-19 increases the effectiveness of limiting nonrepetitive contacts for transmission control*. *PNAS* **118** (2021), [e2016623118](https://doi.org/10.1073/pnas.2016623118). DOI:10.1073/pnas.2016623118.

[pnas118-e2016623118-Supplement.pdf](#)

Increasing evidence indicates that superspreading plays a dominant role in COVID-19 transmission. Recent estimates suggest that the dispersion parameter k for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is on the order of 0.1, which corresponds to about 10% of cases being the source of 80% of infections. To investigate how overdispersion might affect the outcome of various mitigation strategies, we developed an agent-based model with a social network that allows transmission through contact in three sectors: “close” (a small, unchanging group of mutual contacts as might be found in a household), “regular” (a larger, unchanging group as might be found in a workplace or school), and “random” (drawn from the entire model population and not repeated regularly). We assigned individual infectivity from a gamma distribution with dispersion

parameter k . We found that when k was low (i.e., greater heterogeneity, more superspreading events), reducing random sector contacts had a far greater impact on the epidemic trajectory than did reducing regular contacts; when k was high (i.e., less heterogeneity, no superspreading events), that difference disappeared. These results suggest that overdispersion of COVID-19 transmission gives the virus an Achilles' heel: Reducing contacts between people who do not regularly meet would substantially reduce the pandemic, while reducing repeated contacts in defined social groups would be less effective.

Keywords: pandemic | overdispersion | mitigation strategies | superspreading | social networks

Significance: Evidence indicates that superspreading plays a dominant role in COVID-19 transmission, so that a small fraction of infected people causes a large proportion of new COVID-19 cases. We developed an agent-based model that simulates a superspreading disease moving through a society with networks of both repeated contacts and nonrepeated, random contacts. The results indicate that superspreading is the virus' Achilles' heel: Reducing random contacts—such as those that occur at sporting events, restaurants, bars, and the like—can control the outbreak at population scales.

VOGEL 2021

Annette B. Vogel & Ugur Sahin et al., *BNT162b vaccines protect rhesus macaques from SARS-CoV-2*. *nature* **592** (2021), 283–289.

[DOI:10.1038/s41586-021-03275-y](https://doi.org/10.1038/s41586-021-03275-y).

[n592-0283-Supplement.pdf](#)

A safe and effective vaccine against COVID-19 is urgently needed in quantities that are sufficient to immunize large populations. Here we report the preclinical development of two vaccine candidates (BNT162b1 and BNT162b2) that contain nucleoside-modified messenger RNA that encodes immunogens derived from the spike glycoprotein (S) of SARS-CoV-2, formulated in lipid nanoparticles. BNT162b1 encodes a soluble, secreted trimerized receptor-binding domain (known as the RBD–foldon). BNT162b2 encodes the full-length transmembrane S glycoprotein, locked in its prefusion conformation by the substitution of two residues with proline (S(K986P/V987P); hereafter, S(P2) (also known as P2 S)). The flexibly tethered RBDs of the RBD–foldon bind to human ACE2 with high avidity. Approximately 20% of the S(P2) trimers are in the two-RBD ‘down’, one-RBD ‘up’ state. In mice, one intramuscular dose of either candidate vaccine elicits a dose-dependent antibody response with high virus-entry inhibition titres and strong T-helper-1 CD4+ and IFN α +CD8+ T cell responses. Prime–boost vaccination of rhesus macaques (*Macaca mulatta*) with the BNT162b candidates elicits SARS-CoV-2-neutralizing geometric mean titres that are 8.2–18.2| that of a panel of SARS-CoV-2-convalescent human sera. The vaccine candidates protect macaques against challenge with SARS-CoV-2; in particular, BNT162b2 protects the lower respiratory tract against the presence of viral RNA and shows no evidence of disease enhancement. Both candidates are being evaluated in phase I trials in Germany and the USA1–3, and BNT162b2 is being evaluated in an ongoing global phase II/III trial (NCT04380701 and NCT04368728).

Altpaläolithikum

HOVERS 2009

Erella Hovers, *Learning from Mistakes, Flaking Accidents and Knapping Skills in the Assemblage of A.L. 894 (Hadar, Ethiopia)*. In: KATHY

SCHICK & NICHOLAS TOTH (Hrsg.), *The Cutting Edge, New Approaches to the Archaeology of Human Origins*. Stone Age Institute Publication Series 3 (Gosport 2009), 137–150.

Researchers have focused on broken, hinge and step flakes as proxies for knapping skills. Some basic measures such as frequencies of accidents (expressed by a number of assemblage composition variables and/or flake traits) have been applied as a coarse measure for the level of knapping skills.

In the assemblage of A.L. 894 artifacts conventionally defined as “accidents” reveal knappers’ ability to extend the knapping process after accidents had occurred, indicating high skill levels and at least short-term technological foresight. These interpretations are consistent with the notion that very early tool-makers were cognizant of flaking mechanics.

WILKINS 2021

Jayne Wilkins et al., *Innovative Homo sapiens behaviours 105,000 years ago in a wetter Kalahari*. *nature* **592** (2021), 248–252.

n592-0248-Supplement.pdf

The archaeological record of Africa provides the earliest evidence for the emergence of the complex symbolic and technological behaviours that characterize *Homo sapiens* 1–7. The coastal setting of many archaeological sites of the Late Pleistocene epoch, and the abundant shellfish remains recovered from them, has led to a dominant narrative in which modern human origins in southern Africa are intrinsically tied to the coast and marine resources 8–12, and behavioural innovations in the interior lag behind. However, stratified Late Pleistocene sites with good preservation and robust chronologies are rare in the interior of southern Africa, and the coastal hypothesis therefore remains untested. Here we show that early human innovations that are similar to those dated to around 105 thousand years ago (ka) in coastal southern Africa existed at around the same time among humans who lived over 600 km inland. We report evidence for the intentional collection of non-utilitarian objects (calcite crystals) and ostrich eggshell from excavations of a stratified rockshelter deposit in the southern Kalahari Basin, which we date by optically stimulated luminescence to around 105 ka. Uranium–thorium dating of relict tufa deposits indicates sporadic periods of substantial volumes of fresh, flowing water; the oldest of these episodes is dated to between 110 and 100 ka and is coeval with the archaeological deposit. Our results suggest that behavioural innovations among humans in the interior of southern Africa did not lag behind those of populations near the coast, and that these innovations may have developed within a wet savannah environment. Models that tie the emergence of behavioural innovations to the exploitation of coastal resources by our species may therefore require revision.

Jayne Wilkins, Benjamin J. Schoville, Robyn Pickering, Luke Gliganic, Benjamin Collins, Kyle S. Brown, Jessica von der Meden, Wendy Khumalo, Michael C. Meyer, Sechaba Maape, Alexander F. Blackwood & Amy Hatton

WILLOUGHBY 2021

Pamela R. Willoughby, *Early Africans living inland collected unusual objects*. *nature* **592** (2021), 193–194.

Ostrich eggshells and crystals gathered more than 100,000 years ago shed light on the cultural evolution of early humans. Found in South Africa’s interior, they reveal that technological innovations occurred beyond its coast.

Amerika

CASTRO E SILVA 2021

Marcos Araújo Castro e Silva, Tiago Ferraz, Maria Cátira Bortolini, David Comas & Tábita Hünemeier, *Deep genetic affinity between coastal Pacific and Amazonian natives evidenced by Australasian ancestry*. [PNAS 118 \(2021\), e2025739118](#).

[pnas118-e2025739118-Supplement.pdf](#)

Different models have been proposed to elucidate the origins of the founding populations of America, along with the number of migratory waves and routes used by these first explorers. Settlements, both along the Pacific coast and on land, have been evidenced in genetic and archeological studies. However, the number of migratory waves and the origin of immigrants are still controversial topics. Here, we show the Australasian genetic signal is present in the Pacific coast region, indicating a more widespread signal distribution within South America and implicating an ancient contact between Pacific and Amazonian dwellers. We demonstrate that the Australasian population contribution was introduced in South America through the Pacific coastal route before the formation of the Amazonian branch, likely in the ancient coastal Pacific/Amazonian population. In addition, we detected a significant amount of interpopulation and intrapopulation variation in this genetic signal in South America. This study elucidates the genetic relationships of different ancestral components in the initial settlement of South America and proposes that the migratory route used by migrants who carried the Australasian ancestry led to the absence of this signal in the populations of Central and North America.

Keywords: settlement of South America | Australasian | genetics | Native Americans | Pacific coastal route

Anthropologie

BEAUDET 2021

Amélie Beaudet, *The enigmatic origins of the human brain*. [science 372 \(2021\), 124–125](#).

Evolutionary history of the human brain appears more complex than thought.

GIBBONS 2021

Ann Gibbons, *When modern humans met Neanderthals*. [science 372 \(2021\), 115–116](#).

Ancient genomes from first moderns in Europe tell stories of diverse origins, ancient trysts.

HAJDINJAK 2021

Mateja Hajdinjak, Janet Kelso & Svante Pääbo et al., *Initial Upper Palaeolithic humans in Europe had recent Neanderthal ancestry*. [nature 592 \(2021\), 253–257](#).

[n592-0253-Supplement.pdf](#)

Modern humans appeared in Europe by at least 45,000 years ago^{1–5}, but the extent of their interactions with Neanderthals, who disappeared by about 40,000 years ago⁶, and their relationship to the broader expansion of modern humans outside Africa are poorly understood. Here we present genome-wide data from three individuals dated to between 45,930 and 42,580 years ago from Bacho Kiro Cave,

Bulgaria^{1,2}. They are the earliest Late Pleistocene modern humans known to have been recovered in Europe so far, and were found in association with an Initial Upper Palaeolithic artefact assemblage. Unlike two previously studied individuals of similar ages from Romania⁷ and Siberia⁸ who did not contribute detectably to later populations, these individuals are more closely related to present-day and ancient populations in East Asia and the Americas than to later west Eurasian populations. This indicates that they belonged to a modern human migration into Europe that was not previously known from the genetic record, and provides evidence that there was at least some continuity between the earliest modern humans in Europe and later people in Eurasia. Moreover, we find that all three individuals had Neanderthal ancestors a few generations back in their family history, confirming that the first European modern humans mixed with Neanderthals and suggesting that such mixing could have been common.

Mateja Hajdinjak, Fabrizio Mafessoni, Laurits Skov, Benjamin Vernot, Alexander Hübner, Qiaomei Fu, Elena Essel, Sarah Nagel, Birgit Nickel, Julia Richter, Oana Teodora Moldovan, Silviu Constantin, Elena Endarova, Nikolay Zahariev, Rosen Spasov, Frido Welker, Geoff M. Smith, Virginie Sinet-Mathiot, Lindsey Paskulin, Helen Fewlass, Sahra Talamo, Zeljko Rezek, Svoboda Sirakova, Nikolay Sirakov, Shannon P. McPherron, Tsenka Tsanova, Jean-Jacques Hublin, Benjamin M. Peter, Matthias Meyer, Pontus Skoglund, Janet Kelso & Svante Pääbo

PONCE DE LEÓN 2021

Marcia S. Ponce de León, Thibault Bienvenu, Assaf Marom & Christoph P. E. Zollikofer et al., *The primitive brain of early Homo*. [science 372 \(2021\), 165–171](#).

[s372-0165-Supplement.pdf](#)

The brains of modern humans differ from those of great apes in size, shape, and cortical organization, notably in frontal lobe areas involved in complex cognitive tasks, such as social cognition, tool use, and language. When these differences arose during human evolution is a question of ongoing debate. Here, we show that the brains of early Homo from Africa and Western Asia (Dmanisi) retained a primitive, great ape-like organization of the frontal lobe. By contrast, African Homo younger than 1.5 million years ago, as well as all Southeast Asian Homo erectus, exhibited a more derived, humanlike brain organization. Frontal lobe reorganization, once considered a hallmark of earliest Homo in Africa, thus evolved comparatively late, and long after Homo first dispersed from Africa.

Marcia S. Ponce de León, Thibault Bienvenu, Assaf Marom, Silvano Engel, Paul Tafforeau, José Luis Alatorre Warren, David Lordkipanidze, Iwan Kurniawan, Delta Bayu Murti, Rusyad Adi Suriyanto, Toetik Koesbardiati & Christoph P. E. Zollikofer

PRÜFER 2021

Kay Prüfer, Cosimo Posth & Johannes Krause et al., *A genome sequence from a modern human skull over 45,000 years old from Zlatý kůň in Czechia*. [Nature Ecology & Evolution \(2021\), preprint, 1–19](#). DOI:10.1038/s41559-021-01443-x.

[NatEcoEvo2021.04-Prufer-Supplement.pdf](#)

Modern humans expanded into Eurasia more than 40,000 years ago following their dispersal out of Africa. These Eurasians carried $\approx 2\text{--}3\%$ Neanderthal ancestry in their genomes, originating from admixture with Neanderthals that took place sometime between 50,000 and 60,000 years ago, probably in the Middle East. In Europe, the modern human expansion preceded the disappearance of Neanderthals from the fossil record by 3,000–5,000 years. The genetic makeup of the first

Europeans who colonized the continent more than 40,000 years ago remains poorly understood since few specimens have been studied. Here, we analyse a genome generated from the skull of a female individual from Zlaty kun, Czechia. We found that she belonged to a population that appears to have contributed genetically neither to later Europeans nor to Asians. Her genome carries $\approx 3\%$ Neanderthal ancestry, similar to those of other Upper Palaeolithic hunter-gatherers. However, the lengths of the Neanderthal segments are longer than those observed in the currently oldest modern human genome of the $\approx 45,000$ -year-old Ust'-Ishim individual from Siberia, suggesting that this individual from Zlaty kun is one of the earliest Eurasian inhabitants following the expansion out of Africa.

Kay Prüfer, Cosimo Posth, He Yu, Alexander Stoessel, Maria A. Spyrou, Thibaut Deviese, Marco Mattonai, Erika Ribechini, Thomas Higham, Petr Velemínský, Jaroslav Brůžek & Johannes Krause

Bibel

BAUR 2013

Wolfgang Baur, *Die Prophetinnen und Propheten des Alten Testaments. Welt und Umwelt der Bibel* **2013**, iii, 34–39.

In dieser Übersicht wird bewusst zwischen erzählter Zeit, Wirkungszeit und Abfassungszeit unterschieden. Das liegt daran, dass zum einen alle Prophetenbücher erst nach der Zeit dieser Propheten aufgeschrieben – und inhaltlich erweitert und gestaltet – wurden. Bei einigen (wie Mose oder Mirjam) entstanden die Texte sogar erst viele Jahrhunderte nach den Ereignissen, auf die sie sich beziehen. Das bedeutet, dass wir in diesen Texten keine historischen Überlieferungen suchen sollten. Vielmehr projizieren sie Erfahrungen und Glaubensinhalte ihrer Zeit (z. B. der Exilszeit im 6. Jh. vC) in eine fiktive Vergangenheit (z. B. eine Mosezeit, die theoretisch im 12. Jh. vC angenommen werden könnte). Bücher wie Jona oder Maleachi lassen sich gar nicht historisch lesen. Sie sind religiöse Lehrschriften mit Botschaften über Gott und die Welt.

ZWICKEL 2020

Wolfgang Zwickel, *Das Leben am Königshof in Jerusalem und Samaria, Was archäologische und schriftliche Zeugnisse verraten. Welt und Umwelt der Bibel* **2020**, ii, 34–39.

Sowohl in Hazor als auch in Samaria sind im 9. Jh. v.C bereits jeweils sechs Schreiberkammern mit wohl ebenso vielen Schreibern archäologisch belegt.

Wie lebten und wohnten die Könige Israels und Judas? Wie organisierten sie ihre verhältnismäßig kleinen Reiche? Was wissen wir heute über Alltag und Lebensumstände von Männern und Frauen am Hof? Dank der zahlreichen archäologischen Ausgrabungen in den einstigen Hauptstädten Samaria und Jerusalem können wir ein wenig Licht in diese Welt bringen.

Kultur

BENATI 2021

Giacomo Benati & Carmine Guerriero, *Climate change and state evolution. PNAS* **118** (2021), e2020893118.

pnas118-e2020893118-Supplement.pdf

Despite the vast evidence on the short-run effects of adverse climate shocks on the economy, our understanding of their long-run impact on institutions is limited.

To tackle such a key issue, a vast body of research has focused on ancient societies because of the limited complexity of their economies and their unparalleled experience with environmental and institutional change. Notably, the “collapse archaeology” literature has reported countless correlations consistent with the mantra that severe droughts are bound to trigger institutional crises. This conclusion, however, has been recently challenged by a stream of papers that, building on more detailed data on Bronze Age Mesopotamia and a more credible theory-based empirical strategy, have yielded the following two results. First, severe droughts pushed the elites to grant strong political and property rights to the nonelites to convince them that a sufficient part of the returns on joint investments would be shared via public good provision and, thus, to cooperate and accumulate a culture of cooperation. Second, a more favorable climate allowed the elites to elicit cooperation under less inclusive political regimes as well as a weaker culture of cooperation and, possibly, incomplete property rights. These patterns emphasize the importance of considering the asymmetric effect of droughts and, more generally, combining natural and social sciences for the evaluation of climate-related policies.

Keywords: climate change | inclusive political institutions | property rights | culture of cooperation | state evolution

BENATI 2021

Giacomo Benati, Carmine Guerriero & Federico Zaina, *The Origins of Political Institutions and Property Rights, Time inconsistency vs. opacity*. SSRN 2021, Jan. 14, 1–125. <<http://ssrn.com/abstract=3395353>> (2021-04-09).

Despite the economic relevance of strong political and property rights, we still lack an organic and empirically sound theory of their origins and interaction. In our model, the elite can elicit the nonelite’s cooperation in investment by enacting a more inclusive political process, which allows the latter to select the tax rate and organize public good provision, and by punishing suspected shirking through the restriction of the nonelite’s private rights. When the expected investment return is small, cooperation can only be attained under strong political and property rights and full taxation. When it is intermediate, the elite keeps control over fiscal policies and can implement partial taxation. When, finally, the expected investment return is large, the elite can also weaken the nonelite’s private rights. Embracing the stick, however, is optimal only if production is sufficiently transparent and, thus, punishment effectively disciplines a shirking nonelite. These predictions are consistent with novel data on the division of the decision-making power, strength of the farmers’ rights to land, provision of public goods and geographic conditions determining the expected return on farming and its opacity in a panel of 44 major Mesopotamian polities spanning each half-century between 3050 and 1750 BCE. Crucially, our estimates are similar when we also control for trade potential, severity of external and internal conflicts and degree of urbanization.

Keywords: Geography | Time Inconsistency | Opacity | Inclusive Political Institutions | Property Rights.

Mathematik

KENNEDY 2021

P. Kennedy, S. Sumner, P. Botha, N. J. Welton, A. D. Higginson & A. N. Radford, *Diminishing returns drive altruists to help extended family*. *Nature Ecology & Evolution* 5 (2021), 468–479.

Altruism between close relatives can be easily explained. However, paradoxes arise when organisms divert altruism towards more distantly related recipients. In some social insects, workers drift extensively between colonies and help raise less related foreign brood, seemingly reducing inclusive fitness. Since being highlighted by W. D. Hamilton, three hypotheses (bet hedging, indirect reciprocity and diminishing returns to cooperation) have been proposed for this surprising behaviour. Here, using inclusive fitness theory, we show that bet hedging and indirect reciprocity could only drive cooperative drifting under improbable conditions. However, diminishing returns to cooperation create a simple context in which sharing workers is adaptive. Using a longitudinal dataset comprising over a quarter of a million nest cell observations, we quantify cooperative payoffs in the Neotropical wasp *Polistes canadensis*, for which drifting occurs at high levels. As the worker-to-brood ratio rises in a worker's home colony, the predicted marginal benefit of a worker for expected colony productivity diminishes. Helping related colonies can allow effort to be focused on related brood that are more in need of care. Finally, we use simulations to show that cooperative drifting evolves under diminishing returns when dispersal is local, allowing altruists to focus their efforts on related recipients. Our results indicate the power of nonlinear fitness effects to shape social organization, and suggest that models of eusocial evolution should be extended to include neglected social interactions within colony networks.

Politik

HAMORY 2021

Joan Hamory, Edward Miguel, Michael Walker, Michael Kremer & Sarah Baird, *Twenty-year economic impacts of deworming*. [PNAS 118 \(2021\), e2023185118](#).

[pnas118-e2023185118-Supplement.pdf](#)

Estimating the impact of child health investments on adult living standards entails multiple methodological challenges, including the lack of experimental variation in health status, an inability to track individuals over time, and accurately measuring living standards and productivity in low-income settings. This study exploits a randomized school health intervention that provided deworming treatment to Kenyan children, and uses longitudinal data to estimate impacts on economic outcomes up to 20 y later. The effective respondent tracking rate was 84%. Individuals who received two to three additional years of childhood deworming experienced a 14% gain in consumption expenditures and 13% increase in hourly earnings. There are also shifts in sectors of residence and employment: treatment group individuals are 9% more likely to live in urban areas, and experience a 9% increase in nonagricultural work hours. Most effects are concentrated among males and older individuals. The observed consumption and earnings benefits, together with deworming's low cost when distributed at scale, imply that a conservative estimate of its annualized social internal rate of return is 37%, a high return by any standard.

Keywords: deworming | child health | long-run impacts | Kenya

Significance: The belief that investing in child health and nutrition can generate improvements in individuals' future quality of life is the rationale for many policy initiatives around the world. Yet there remains limited evidence on the causal impacts of child health gains on adult living standards, especially in developing countries. This study contributes evidence that addresses leading methodological concerns, by using variation in child health via a randomized health intervention that provided deworming treatment to Kenyan children. We estimate impacts on

individual living standards up to 20 y later among a representative sample of participants, and find those in the deworming treatment group experience meaningful gains in adult living standards and earnings, and shifts in sectors of residence and employment.