

References

Aktuell

BRAUNER 2021

Jan M. Brauner et al., *Inferring the effectiveness of government interventions against COVID-19*. *science* **371** (2021), 802.

[DOI:10.1126/science.abd9338](https://doi.org/10.1126/science.abd9338).

[s371-0802-Supplement.pdf](#)

Governments are attempting to control the COVID-19 pandemic with nonpharmaceutical interventions (NPIs). However, the effectiveness of different NPIs at reducing transmission is poorly understood. We gathered chronological data on the implementation of NPIs for several European and non-European countries between January and the end of May 2020. We estimated the effectiveness of these NPIs, which range from limiting gathering sizes and closing businesses or educational institutions to stay-at-home orders. To do so, we used a Bayesian hierarchical model that links NPI implementation dates to national case and death counts and supported the results with extensive empirical validation. Closing all educational institutions, limiting gatherings to 10 people or less, and closing face-to-face businesses each reduced transmission considerably. The additional effect of stay-at-home orders was comparatively small.

Jan M. Brauner, Sören Minderhann, Mrinank Sharma, David Johnston, John Salvatier, Tomáš Gavenèiak, Anna B. Stephenson, Gavin Leech, George Altman, Vladimir Mikulik, Alexander John Norman, Joshua Teperowski Monrad, Tamay Besiroglu, Hong Ge, Meghan A. Hartwick, Yee Whye Teh, Leonid Chindelevitch, Yarin Gal & Jan Kulveit

COHEN 2021

Jon Cohen, *The Long Road*. *science* **371** (2021), 768–772.

[DOI:10.1126/science.371.6531.768](https://doi.org/10.1126/science.371.6531.768).

Early signs suggest COVID-19 vaccines are having an impact, but questions abound about the path to normal.

MUIK 2021

Alexander Muik et al., *Neutralization of SARS-CoV-2 lineage B.1.1.7 pseudovirus by BNT162b2 vaccine-elicited human sera*. *science* **2021**, [abg6105](https://doi.org/10.1126/science.abg6105). [DOI:10.1126/science.abg6105](https://doi.org/10.1126/science.abg6105).

Recently, a new SARS-CoV-2 lineage called B.1.1.7 (variant of concern: VOC 202012/01) emerged in the United Kingdom that was reported to spread more efficiently and faster than other strains. This variant has an unusually large number of mutations with 10 amino acid changes in the spike protein, raising concerns that its recognition by neutralizing antibodies may be affected. Here, we tested SARS-CoV-2-S pseudoviruses bearing either the Wuhan reference strain or the B.1.1.7 lineage spike protein with sera of 40 participants who were vaccinated in a previously reported trial with the mRNA-based COVID-19 vaccine BNT162b2. The immune sera had slightly reduced but overall largely preserved neutralizing titers against the B.1.1.7 lineage pseudovirus. These data indicate that the B.1.1.7 lineage will not escape BNT162b2-mediated protection.

Alexander Muik, Ann-Kathrin Wallisch, Bianca Sanger, Kena A. Swanson, Julia Muhl, Wei Chen, Hui Cai, Daniel Maurus, Ritu Sarkar, ˆzlem Tiireci, Philip R. Dormitzer & Uğur Şahin

PHILLIPS 2021

Nicky Phillips, *The Coronavirus Will Become Endemic.* [nature](#) **590** (2021), 382–384.

A Nature survey shows many scientists expect SARS-CoV-2 is here to stay, but it could pose less danger over time.

RAPPAZZO 2021

C. Garrett Rappazzo et al., *Broad and potent activity against SARS-like viruses by an engineered human monoclonal antibody.* [science](#) **371** (2021), 823–829. DOI:10.1126/science.abf4830.

s371-0823-Supplement.pdf

The recurrent zoonotic spillover of coronaviruses (CoVs) into the human population underscores the need for broadly active countermeasures. We employed a directed evolution approach to engineer three severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) antibodies for enhanced neutralization breadth and potency. One of the affinity-matured variants, ADG-2, displays strong binding activity to a large panel of sarbecovirus receptor binding domains and neutralizes representative epidemic sarbecoviruses with high potency. Structural and biochemical studies demonstrate that ADG-2 employs a distinct angle of approach to recognize a highly conserved epitope that overlaps the receptor binding site. In immunocompetent mouse models of SARS and COVID-19, prophylactic administration of ADG-2 provided complete protection against respiratory burden, viral replication in the lungs, and lung pathology. Altogether, ADG-2 represents a promising broad-spectrum therapeutic candidate against clade 1 sarbecoviruses.

C. Garrett Rappazzo, Longping V. Tse, Chengzi I. Kaku, Daniel Wrapp, Mrunal Sakharkar, Deli Huang, Laura M. Deveau, Thomas J. Yockachonis, Andrew S. Herbert, Michael B. Battles, Cecilia M. O’Brien, Michael E. Brown, James C. Geoghegan, Jonathan Belk, Linghang Peng, Linlin Yang, Yixuan Hou, Trevor D. Scobey, Dennis R. Burton, David Nemazee, John M. Dye, James E. Voss, Bronwyn M. Gunn, Jason S. McLellan, Ralph S. Baric, Lisa E. Gralinski & Laura M. Walker

STARR 2021

Tyler N. Starr, Amin Addetia, William W. Hannon & Jesse D. Bloom et al., *Prospective mapping of viral mutations that escape antibodies used to treat COVID-19.* [science](#) **371** (2021), 850–854.

DOI:10.1126/science.abf9302.

s371-0850-Supplement.pdf

Antibodies are a potential therapy for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), but the risk of the virus evolving to escape them remains unclear. Here we map how all mutations to the receptor binding domain (RBD) of SARS-CoV-2 affect binding by the antibodies in the REGN-COV2 cocktail and the antibody LY-CoV016. These complete maps uncover a single amino acid mutation that fully escapes the REGN-COV2 cocktail, which consists of two antibodies, REGN10933 and REGN10987, targeting distinct structural epitopes. The maps also identify viral mutations that are selected in a persistently infected patient treated with REGN-COV2 and during in vitro viral escape selections. Finally, the maps reveal that mutations escaping the individual antibodies are

already present in circulating SARS-CoV-2 strains. These complete escape maps enable interpretation of the consequences of mutations observed during viral surveillance.

Tyler N. Starr, Allison J. Greaney, Amin Addetia, William W. Hannon, Manish C. Choudhary, Adam S. Diggins, Jonathan Z. Li & Jesse D. Bloom

VLACHOS 2021

Jonas Vlachos, Edvin Hertegård & Helena B. Svaleryd, *The effects of school closures on SARS-CoV-2 among parents and teachers*. [PNAS 118 \(2021\), e2020834118](#). DOI:10.1073/pnas.2020834118.

[pnas118-e2020834118-Supplement.pdf](#)

To reduce the transmission of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), most countries closed schools, despite uncertainty if school closures are an effective containment measure. At the onset of the pandemic, Swedish upper-secondary schools moved to online instruction, while lower-secondary schools remained open. This allows for a comparison of parents and teachers differently exposed to open and closed schools, but otherwise facing similar conditions. Leveraging rich Swedish register data, we connect all students and teachers in Sweden to their families and study the impact of moving to online instruction on the incidence of SARS-CoV-2 and COVID-19. We find that, among parents, exposure to open rather than closed schools resulted in a small increase in PCR-confirmed infections (odds ratio [OR] 1.17; 95% CI [CI95] 1.03 to 1.32). Among lower-secondary teachers, the infection rate doubled relative to upper-secondary teachers (OR 2.01; CI95 1.52 to 2.67). This spilled over to the partners of lowersecondary teachers, who had a higher infection rate than their upper-secondary counterparts (OR 1.29; CI95 1.00 to 1.67). When analyzing COVID-19 diagnoses from healthcare visits and the incidence of severe health outcomes, results are similar for teachers, but weaker for parents and teachers' partners. The results for parents indicate that keeping lower-secondary schools open had minor consequences for the overall transmission of SARS-CoV-2 in society. The results for teachers suggest that measures to protect teachers could be considered.

Keywords: COVID-19 | SARS-CoV-2 | school closures | social distancing

Significance: Many countries closed schools during the pandemic to contain the spread of SARS-CoV-2. Sweden closed upper-secondary schools, while lower-secondary schools remained open, allowing for an evaluation of school closures. This study analyzes the impact of school closures on the spread of SARS-CoV-2 by comparing groups exposed and not exposed to open schools. We find that exposure to open schools resulted in a small increase in infections among parents. Among teachers, the infection rate doubled, and infections spilled over to their partners. This suggests that keeping lower-secondary schools open had a minor impact on the overall spread of SARS-CoV2 in society. However, teachers are affected, and measures to protect them could be considered.

VOYSEY 2021

Merryn Voysey & Oxford COVID Vaccine Trial Group, *Single-dose administration and the influence of the timing of the booster dose on immunogenicity and efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine: a pooled analysis of four randomised trials*. [The Lancet \(2021\), preprint, 1–11](#). DOI:10.1016/S0140-6736(21)00432-3.

The results of this primary analysis of two doses of ChAdOx1 nCoV-19 were consistent with those seen in the interim analysis of the trials and confirm that the vaccine is efficacious, with results varying by dose interval in exploratory analyses.

A 3-month dose interval might have advantages over a programme with a short dose interval for roll-out of a pandemic vaccine to protect the largest number of individuals in the population as early as possible when supplies are scarce, while also improving protection after receiving a second dose.

Biologie

BOURKE 2021

Andrew F. G. Bourke, *The role and rule of relatedness*. [nature](#) **590** (2021), 392–394.

Inclusive fitness theory shows that social partners must be related for altruism to evolve, yet some models suggest that relatedness is not needed. An analysis concludes that assumptions in those models build in a role for relatedness, after all.

KAY 2020

Tomas Kay, Laurent Keller & Laurent Lehmann, *The evolution of altruism and the serial rediscovery of the role of relatedness*. [PNAS](#) **117** (2020), 28894–28898.

[pnas117-28894-Supplement.pdf](#)

The genetic evolution of altruism (i.e., a behavior resulting in a net reduction of the survival and/or reproduction of an actor to benefit a recipient) once perplexed biologists because it seemed paradoxical in a Darwinian world. More than half a century ago, W. D. Hamilton explained that when interacting individuals are genetically related, alleles for altruism can be favored by selection because they are carried by individuals more likely to interact with other individuals carrying the alleles for altruism than random individuals in the population (“kin selection”). In recent decades, a substantial number of supposedly alternative pathways to altruism have been published, leading to controversies surrounding explanations for the evolution of altruism. Here, we systematically review the 200 most impactful papers published on the evolution of altruism and identify 43 evolutionary models in which altruism evolves and where the authors attribute the evolution of altruism to a pathway other than kin selection and/or deny the role of relatedness. An analysis of these models reveals that in every case the life cycle assumptions entail local reproduction and local interactions, thereby leading to interacting individuals being genetically related. Thus, contrary to the authors’ claims, Hamilton’s relatedness drives the evolution to altruism in their models. The fact that several decades of investigating the evolution to altruism have resulted in the systematic and unwitting rediscovery of the same mechanism is testament to the fundamental importance of positive relatedness between actor and recipient for explaining the evolution of altruism.

Keywords: evolution | kin selection | altruism | Hamilton’s rule | rediscovery

Significance: The canonical explanation for the evolution of altruism (“kin selection”)—which was mathematically derived in the 1960s by W. D. Hamilton—emphasizes the importance of genetic relatedness. Over the past three decades, numerous authors claim to have discovered alternative explanations. We systematically analyze the models substantiating these claims and reveal that in every model the interacting individuals are genetically related and that the authors have therefore unwittingly rediscovered Hamilton’s insight.

LECA 2021

Jean-Baptiste Leca, Noëlle Gunst, Matthew Gardiner & I. Nengah Wandia, *Acquisition of object-robbing and object/food-bartering be-*

haviours, *A culturally maintained token economy in free-ranging long-tailed macaques*. *Phil. Trans. Royal Society B* **376** (2021), 20190677.

The token exchange paradigm shows that monkeys and great apes are able to use objects as symbolic tools to request specific food rewards. Such studies provide insights into the cognitive underpinnings of economic behaviour in non-human primates. However, the ecological validity of these laboratorybased experimental situations tends to be limited. Our field research aims to address the need for a more ecologically valid primate model of trading systems in humans. Around the Uluwatu Temple in Bali, Indonesia, a large free-ranging population of long-tailed macaques spontaneously and routinely engage in token-mediated bartering interactions with humans. These interactions occur in two phases: after stealing inedible and more or less valuable objects from humans, the macaques appear to use them as tokens, by returning them to humans in exchange for food. Our field observational and experimental data showed (i) age differences in robbing/ bartering success, indicative of experiential learning, and (ii) clear behavioural associations between value-based token possession and quantity or quality of food rewards rejected and accepted by subadult and adult monkeys, suggestive of robbing/bartering payoff maximization and economic decision-making. This population-specific, prevalent, crossgenerational, learned and socially influenced practice may be the first example of a culturally maintained token economy in free-ranging animals.

Keywords: token exchange | bartering | economic behaviour | symbolic tool | material culture | ecological validity

MATHIAS 2021

Justin M. Mathias & Richard B. Thomas, *Global tree intrinsic water use efficiency is enhanced by increased atmospheric CO₂ and modulated by climate and plant functional types*. *PNAS* **118** (2021), e2014286118.

pnas118-e2014286118-Supplement.pdf

We conducted a meta-analysis of carbon and oxygen isotopes from tree ring chronologies representing 34 species across 10 biomes to better understand the environmental drivers and physiological mechanisms leading to historical changes in tree intrinsic water use efficiency (iWUE), or the ratio of net photosynthesis (Anet) to stomatal conductance (gs), over the last century. We show a $\approx 40\%$ increase in tree iWUE globally since 1901, coinciding with a $\approx 34\%$ increase in atmospheric CO₂ (Ca), although mean iWUE, and the rates of increase, varied across biomes and leaf and wood functional types. While Ca was a dominant environmental driver of iWUE, the effects of increasing Ca were modulated either positively or negatively by climate, including vapor pressure deficit (VPD), temperature, and precipitation, and by leaf and wood functional types. A dual carbon–oxygen isotope approach revealed that increases in Anet dominated the observed increased iWUE in $\approx 83\%$ of examined cases, supporting recent reports of global increases in Anet, whereas reductions in gs occurred in the remaining $\approx 17\%$. This meta-analysis provides a strong process-based framework for predicting changes in tree carbon gain and water loss across biomes and across wood and leaf functional types, and the interactions between Ca and other environmental factors have important implications for the coupled carbon–hydrologic cycles under future climate. Our results furthermore challenge the idea of widespread reductions in gs as the major driver of increasing tree iWUE and will better inform Earth system models regarding the role of trees in the global carbon and water cycles.

Keywords: tree rings | stable isotopes | carbon | oxygen | intrinsic water use efficiency

Significance: Changes in tree physiology driven by environmental change can alter the balance of forest ecosystem carbon and water fluxes. We performed a meta-analysis of published tree ring literature, comprising 36 different species across 84 sites globally, to show stimulated leaf photosynthesis, not reduced stomatal conductance, is primarily responsible for recently increasing tree intrinsic water use efficiency (iWUE), which integrates the balance between carbon and water fluxes. Furthermore, we show trends in tree iWUE are similar in magnitude to the increase in atmospheric CO₂ over the 20th century and that climate interacts with CO₂ to modulate tree iWUE. These findings will help to guide efforts of refining the role of forests in process-based models under future environmental change.

Klima

COOPER 2021

Alan Cooper & Chris S. M. Turney et al., *A global environmental crisis 42,000 years ago*. [science](#) **371** (2021), 811–818.

[s371-0811-Supplement.pdf](#)

Geological archives record multiple reversals of Earth’s magnetic poles, but the global impacts of these events, if any, remain unclear. Uncertain radiocarbon calibration has limited investigation of the potential effects of the last major magnetic inversion, known as the Laschamps Excursion [41 to 42 thousand years ago (ka)]. We use ancient New Zealand kauri trees (*Agathis australis*) to develop a detailed record of atmospheric radiocarbon levels across the Laschamps Excursion. We precisely characterize the geomagnetic reversal and perform global chemistry-climate modeling and detailed radiocarbon dating of paleoenvironmental records to investigate impacts. We find that geomagnetic field minima ≈ 42 ka, in combination with Grand Solar Minima, caused substantial changes in atmospheric ozone concentration and circulation, driving synchronous global climate shifts that caused major environmental changes, extinction events, and transformations in the archaeological record.

Alan Cooper, Chris S. M. Turney, Jonathan Palmer, Alan Hogg, Matt McGlone, Janet Wilmshurst, Andrew M. Lorrey, Timothy J. Heaton, James M. Russell, Ken McCracken, Julien G. Anet, Eugene Rozanov, Marina Friedel, Ivo Suter, Thomas Peter, Raimund Muscheler, Florian Adolphi, Anthony Dosseto, J. Tyler Faith, Pavla Fenwick, Christopher J. Fogwill, Konrad Hughen, Mathew Lipson, Jiabo Liu, Norbert Nowaczyk, Eleanor Rainsley, Christopher Bronk Ramsey, Paolo Sebastianelli, Yassine Souilmi, Janelle Stevenson, Zoë Thomas, Raymond Tobler & Roland Zech

VOOSEN 2021

Paul Voosen, *Kauri trees mark magnetic flip 42,000 years ago*. [science](#) **371** (2021), 766.

Researchers say cosmic ray bombardment unleashed by weaker field drove climate shift.

This is where other scientists say the study gets too speculative. Ice cores from Greenland and Antarctica that span the past 100,000 years capture stark temperature swings every few thousand years. But they show no shifts 42,000 years ago. A few Pacific Ocean records do show swings. But even if the shift occurred mostly in the tropics, as Cooper and colleagues suggest, it should be seen in the ice, says Anders Svensson, a glaciologist at the University of Copenhagen. “We just don’t see that.”

Kultur

BROMHAM 2021

Lindell Bromham, Alexander Skeels, Hilde Schneemann, Russell Dinnage & Xia Hua, *There is little evidence that spicy food in hot countries is an adaptation to reducing infection risk*. [Nature Human Behaviour \(2021\), preprint, 1–16](#). DOI:10.1038/s41562-020-01039-8.

[NatHumBeh2021.02-Bromham-Supplement.pdf](#)

Spicier food in hot countries has been explained in terms of natural selection on human cultures, with spices with antimicrobial effects considered to be an adaptation to increased risk of foodborne infection. However, correlations between culture and environment are difficult to interpret, because many cultural traits are inherited together from shared ancestors, neighbouring cultures are exposed to similar conditions, and many cultural and environmental variables show strong covariation. Here, using a global dataset of 33,750 recipes from 70 cuisines containing 93 different spices, we demonstrate that variation in spice use is not explained by temperature and that spice use cannot be accounted for by diversity of cultures, plants, crops or naturally occurring spices. Patterns of spice use are not consistent with an infection-mitigation mechanism, but are part of a broader association between spice, health, and poverty. This study Highlights the challenges inherent in interpreting patterns of human cultural variation in terms of evolutionary pressures.

MILLS 2014

Barbara J. Mills, *Relational Networks and Religious Sodalities at Çatalhöyük*. In: HODDER & IAN (Hrsg.), *Religion at Work in a Neolithic Society, Vital Matters*. (Cambridge 2014), 159–186.

The development and transformation of sodalities are among the strongest and most important underlying historical themes in Southwestern archaeology. While history houses seem to help us get beyond thinking about kinship, we may need to go even further to understand the range of variation and the ways in which power and property were intertwined with ritual at Çatalhöyük. In the Southwest some of the complexity of organization was the result of dramatic demographic and social changes that is only beginning to be understood in central Anatolia . Further work on how these factors intersect will be important for untangling the many paradoxes of the Neolithic, especially those intriguingly suggested by the detailed work at Çatalhöyük.

Methoden

LORI 2020

Francesca Valentina Luisa Lori & Corinna Rossi, *3D contour detection, A non-photorealistic rendering method for the analysis of Egyptian reliefs*. [Antiquity 94 \(2020\), e34](#).

This paper presents the results of a non-photorealistic rendering technique applied to three different types of reliefs from the ancient Egyptian tomb of Meryneith at Saqqara.

Keywords: Egypt | reliefs | epigraphy | non-photorealistic rendering | 3D contour detection

NICHOLS 2021

James D. Nichols, Madan K. Oli, William L. Kendall & G. Scott Boomer, *A better approach for dealing with reproducibility and replicability in science*. [PNAS 118 \(2021\), e2100769118](#).

Here we emphasize the comparison of study results with model-based predictions as more useful to science than the comparison of results of different pairs of studies. The latter approach produces conclusions about whether two studies do or do not yield similar results, whereas the former leads to accumulated assessments of confidence in specific hypotheses and their predictions.

Neolithikum

CHYLENSKI 2019

Maciej Chyleński et al., *Ancient Mitochondrial Genomes Reveal the Absence of Maternal Kinship in the Burials of Çatalhöyük People and Their Genetic Affinities*. [Genes 10 \(2019\), 207, 1–14](#).

[Genes10-a0207-Supplement1.pdf](#), [Genes10-a0207-Supplement2.ods](#)

Çatalhöyük is one of the most widely recognized and extensively researched Neolithic settlements. The site has been used to discuss a wide range of aspects associated with the spread of the Neolithic lifestyle and the social organization of Neolithic societies. Here, we address both topics using newly generated mitochondrial genomes, obtained by direct sequencing and capture-based enrichment of genomic libraries, for a group of individuals buried under a cluster of neighboring houses from the classical layer of the site's occupation. Our data suggests a lack of maternal kinship between individuals interred under the floors of Çatalhöyük buildings. The findings could potentially be explained either by a high variability of maternal lineages within a larger kin group, or alternatively, an intentional selection of individuals for burial based on factors other than biological kinship. Our population analyses shows that Neolithic Central Anatolian groups, including Çatalhöyük, share the closest affinity with the population from the Marmara Region and are, in contrast, set further apart from the Levantine populations. Our findings support the hypothesis about the emergence and the direction of spread of the Neolithic within Anatolian Peninsula and beyond, emphasizing a significant role of Central Anatolia in this process.

Keywords: ancient DNA | Neolithic | kinship

Maciej Chyleński, Edvard Ehler, Mehmet Somel, Reyhan Yaka, Maja Krzewińska, Mirosława Dabert, Anna Juras & Arkadiusz Marciniak

PILLOUD 2011

Marin A. Pilloud & Clark Spencer Larsen, *“Official” and “Practical” Kin, Inferring Social and Community Structure From Dental Phenotype at Neolithic Çatalhöyük, Turkey*. [American Journal of Physical Anthropology 145 \(2011\), 519–530](#).

The Neolithic site of Çatalhöyük, Turkey (7400–5600 cal BC) is widely acknowledged for its role in the study of early farming communities. To better understand the social and community structure of this setting, an intracemetery biological distance analysis was conducted. Metric and nonmetric observations were recorded in both deciduous and permanent dentitions (n 5266) to explore phenotypic patterning of individuals interred within individual buildings. Specifically, this study tests the hypothesis that individuals within houses and house groupings represent family units and the social structure of Çatalhöyük was largely biological-kin-based.

Multivariate and univariate statistical procedures were applied to phenotypic dental data. Results indicate that inclusion for interment within a house was only minimally related to biological affinity. Moreover, the site does not appear to be organized into larger, biologically related neighborhoods of houses. These findings suggest that Catalhöyük may not have been a kin-based society, largely because membership within a house cemetery was not solely defined on the basis of biological affinity, such as in a family group. Rather, it appears that social structure was centered on the house as the unifying social principle. The choice for interment location may have transcended biological lines thereby creating an alternate and more fluid definition of “kin.” These findings can be used to understand the transition to settled life and biological patterning in this Neolithic community.

Keywords: biological distance | dental morphology | dental metrics | intracemetery variation

Religion

CURRY 2021

Andrew Curry, *England’s Stonehenge was erected in Wales first.* [science 371 \(2021\), 765.](#)

PARKER PEARSON 2021

Mike Parker Pearson et al., *The original Stonehenge? A dismantled stone circle in the Preseli Hills of west Wales.* [Antiquity 95 \(2021\), 85–103.](#)

[Antiquity095-0085-Supplement.pdf](#)

The discovery of a dismantled stone circle—close to Stonehenge’s bluestone quarries in west Wales—raises the possibility that a 900-year-old legend about Stonehenge being built from an earlier stone circle contains a grain of truth. Radiocarbon and OSL dating of Waun Mawn indicate construction c. 3000 BC, shortly before the initial construction of Stonehenge. The identical diameters of Waun Mawn and the enclosing ditch of Stonehenge, and their orientations on the midsummer solstice sunrise, suggest that at least part of the Waun Mawn circle was brought from west Wales to Salisbury Plain. This interpretation complements recent isotope work that supports a hypothesis of migration of both people and animals from Wales to Stonehenge.

Keywords: Britain | Preseli | Stonehenge | Neolithic | megaliths | stone circle

Mike Parker Pearson, Josh Pollard, Colin Richards, Kate Welham, Timothy Kinnaird, Dave Shaw, Ellen Simmons, Adam Stanford, Richard Bevins, Rob Ixer, Clive Ruggles, Jim Rylatt & Kevan Edinborough