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References

Afrika

SADR 2015

Karim Sadr, *Livestock First Reached Southern Africa in Two Separate Events.* PLoS ONE **10** (2015), e134215. DOI:10.1371/journal.pone.0134215.

After several decades of research on the subject, we now know when the first livestock reached southern Africa but the question of how they got there remains a contentious topic. Debate centres on whether they were brought with a large migration of Khoe-speakers who originated from East Africa; or whether the livestock were traded down-the-line among hunter-gatherer communities; or indeed whether there was a long history of diverse small scale population movements in this part of the world, one or more of which 'infiltrated' livestock into southern Africa. A new analysis of the distribution of stone toolkits from a sizeable sample of sub-equatorial African Later Stone Age sites, coupled with existing knowledge of the distribution of the earliest livestock remains and ceramics vessels, has allowed us to isolate two separate infiltration events that brought the first livestock into southern Africa just over 2000 years ago; one infiltration was along the Atlantic seaboard and another entered the middle reaches of the Limpopo River Basin. These findings agree well with the latest results of genetic research which together indicate that multiple, small-scale infiltrations probably were responsible for bringing the first livestock into southern Africa.

Aktuell

BERER 2017

Kerstin Berer et al., *Gut microbiota from multiple sclerosis patients enables spontaneous autoimmune encephalomyelitis in mice.* PNAS **114** (2017), 10719–10724.

Kerstin Berer, Lisa Ann Gerdes, Egle Cekanaviciute, Xiaoming Jia, Liang Xiao, Zhongkui Xia, Chuan Liu, Luisa Klotz, Uta Stauffer, Sergio E. Baranzini, Tania Kümpfel, Reinhard Hohlfeld, Gurumoorthy Krishnamoorthy & Hartmut Wekerle

There is emerging evidence that the commensal microbiota has a role in the pathogenesis of multiple sclerosis (MS), a putative autoimmune disease of the CNS. Here, we compared the gut microbial composition of 34 monozygotic twin pairs discordant for MS. While there were no major differences in the overall microbial profiles, we found a significant increase in some taxa such as Akkermansia in untreated MS twins. Furthermore, most notably, when transplanted to a transgenic mouse model of spontaneous brain autoimmunity, MS twin-derived microbiota induced a significantly higher incidence of autoimmunity than the healthy twin-derived microbiota. The microbial profiles of the colonized mice showed a high intraindividual and remarkable temporal stability with several differences, including Sutterella, an organism shown to induce a protective immunoregulatory profile in vitro. Immune cells from mouse recipients of MS-twin samples produced less IL-10 than immune cells from mice colonized with healthy-twin samples. IL-10 may have a regulatory role in spontaneous CNS autoimmunity, as neutralization of the cytokine in mice colonized with healthy-twin fecal samples increased disease incidence. These findings provide evidence that MS-derived microbiota contain factors that precipitate an MS-like autoimmune disease in a transgenic mouse model. They hence encourage the detailed search for protective and pathogenic microbial components in human MS.

Keywords: gut microbiome | multiple sclerosis | experimental autoimmune encephalomyelitis | twin study | germ-free mice

Significance: Studies using experimental models have indicated that multiple sclerosis (MS)-like disease can be triggered in the gut following interactions of brain autoimmune T lymphocytes with local microbiota. Here we studied the gut microbiota from monozygotic human twin pairs discordant for multiple sclerosis. When we transferred human-derived microbiota into transgenic mice expressing a myelin autoantigen-specific T cell receptor, we found that gut microbiota from multiple sclerosis-affected twins induced CNS-specific autoimmunity at a higher incidence than microbiota from healthy co-twins. Our results offer functional evidence that human microbiome components contribute to CNS-specific autoimmunity.

KUPFERSCHMIDT 2017

Kai Kupferschmidt, *Bot-hunters eye mischief in German election.* science **357** (2017), 1081–1082.

Fake social media profiles are proliferating, but their potency is unclear.

Bots can inflate a topic's importance or tarnish reputations by flooding social networks with fake news and by manipulating the currency of Twitter: likes and shares, follows and retweets. Just how that translates into votes is unclear, says Simon Hegelich.

Hegelich [...] examines factors such as the distribution of exclamation marks to pinpoint bots. Humans are inconsistent, he says. “Most bots either use a lot of exclamation marks or never.” [He] tracks hundreds of features, including an account's age and use of emoticons. (Bot-generated content tends to be emotionally charged.)

MARCUS 2017

Adam Marcus, *Pay up or retract? Drug survey spurs conflict.* science **357** (2017), 1085–1086.

Researchers' zealous effort to protect intellectual property has included legal threats.

Morisky is well within his rights to seek payment for use of his copyrighted tool. U.S. law encourages academic scientists and their universities to protect and profit from their inventions, including those developed with public funds.

Anthropologie

GIBSON 2017

Edward Gibson et al., *Color naming across languages reflects color use.* PNAS **114** (2017), 10785–10790.

Edward Gibson, Richard Futrell, Julian Jara-Ettinger, Kyle Mahowald, Leon Bergen, Sivalogeswaran Ratnasingam, Mitchell Gibson, Steven T. Piantadosi & Bevil R. Conway

What determines how languages categorize colors? We analyzed results of the World Color Survey (WCS) of 110 languages to show that despite gross differences across languages, communication of chromatic chips is always better for warm colors (yellows/reds) than cool colors (blues/greens). We present an analysis of color statistics in a large databank of natural images curated by human observers for salient objects and show that objects tend to have warm rather than cool colors. These results suggest that the cross-linguistic similarity in color-naming efficiency reflects colors of universal usefulness and provide an account of a principle (color use) that governs how color categories come about. We show that potential methodological issues with the WCS do not corrupt information-theoretic analyses, by collecting original data using two extreme versions of the colornaming task, in three groups: the Tsimane', a remote Amazonian hunter-gatherer isolate; Bolivian-Spanish speakers; and English speakers. These data also enabled us to test another prediction of the color-usefulness hypothesis: that differences in color categorization between languages are caused by differences in overall usefulness of color to a culture. In support, we found that color naming among Tsimane' had relatively low communicative efficiency, and the Tsimane' were less likely to use color terms when describing familiar objects. Color-naming among Tsimane' was boosted when naming artificially colored objects compared with natural objects, suggesting that industrialization promotes color usefulness.

Keywords: color categorization | information theory | color cognition | Whorfian hypothesis | basic color terms

Significance: The number of color terms varies drastically across languages. Yet despite these differences, certain terms (e.g., red) are prevalent, which has been attributed to perceptual salience. This work provides evidence for an alternative hypothesis: The use of color terms depends on communicative needs. Across languages, from the hunter-gatherer Tsimane' people of the Amazon to students in Boston, warm colors are communicated more efficiently than cool colors. This cross-linguistic pattern reflects the color statistics of the world: Objects (what we talk about) are typically warm-colored, and backgrounds are cool-colored. Communicative needs also explain why the number of color terms varies across languages: Cultures vary in how useful color is. Industrialization, which creates objects distinguishable solely based on color, increases color usefulness.

Datierung

DEVIÈSE 2017

Thibaut Devièse et al., *Direct dating of Neanderthal remains from the site of Vindija Cave and implications for the Middle to Upper Paleolithic transition.* PNAS **114** (2017), 10606–10611.

Thibaut Devièse, Ivor Karavanić, Daniel Comeskey, Cara Kubiak, Petra Korlević, Mateja Hajdinjak, Siniša Radović, Noemi Procopio, Michael Buckley, Svante Pääbo & Tom Higham Previous dating of the Vi-207 and Vi-208 Neanderthal remains from Vindija Cave (Croatia) led to the suggestion that Neanderthals survived there as recently as 28,000–29,000 B.P. Subsequent dating yielded older dates, interpreted as ages of at least ≈32,500 B.P. We have redated these same specimens using an approach based on the extraction of the amino acid hydroxyproline, using preparative highperformance liquid chromatography (Prep-HPLC). This method is more efficient in eliminating modern contamination in the bone collagen. The revised dates are older than 40,000 B.P., suggesting the Vindija Neanderthals did not live more recently than others across Europe, and probably predate the arrival of anatomically modern humans in Eastern Europe. We applied zooarchaeology by mass spectrometry (ZooMS) to find additional hominin remains. We identified one bone that is Neanderthal, based on its mitochondrial DNA, and dated it directly to 46,200±1,500 B.P. We also attempted to date six early Upper Paleolithic bone points from stratigraphic units G1, Fd/d+G1 and Fd/d, Fd.

One bone artifact gave a date of 29,500±400 B.P., while the remainder yielded no collagen. We additionally dated animal bone samples from units G1 and G1–G3. These dates suggest a co-occurrence of early Upper Paleolithic osseous artifacts, particularly split-based points, alongside the remains of Neanderthals is a result of postdepositional mixing, rather than an association between the two groups, although more work is required to show this definitively.

Keywords: Vindija Cave (Croatia) | single-compound AMS dating | DNA analysis | zooarchaeology by mass spectrometry | Middle to Upper Paleolithic transition

Significance: Radiocarbon dating of Neanderthal remains recovered from Vindija Cave (Croatia) initially revealed surprisingly recent results: 28,000–29,000 B.P. This implied the remains could represent a late-surviving, refugial Neanderthal population and suggested they could have been responsible for producing some of the early Upper Paleolithic artefactsmore usually produced by anatomically modern humans. This article presents revised radiocarbon dates of the human bones from this site obtained using a more robust purification method targeting the amino acid hydroxyproline. The data show that all the Neanderthal remains are from a much earlier period (>40,000 cal B.P.). These revised dates change our interpretation of this important site and demonstrate that the Vindija Neanderthals probably did not overlap temporally with early modern humans.

HUBLIN 2017

Jean-Jacques Hublin, *The last Neanderthal.* PNAS **114** (2017), 10520–10522.

Devièse et al. provide new radiocarbon dates for the same Vindija Neanderthal samples, dating them to before 40,000 14C B.P., significantly older than previous efforts dating this material to 29–28,000 and 33–32,000 radiocarbon years. The situation in Vindija is therefore not at all exceptional, and previous results can be explained by the effect of sample contamination and layer admixture.

Since other cases of Neanderthal late survival, such as RipparoMezzena in Northern Italy, have now been falsified, the latest occurrences of Neanderthal remains in the European fossil record can now be documented by specimens discovered in association with so-called transitional industries. These industries display features inherited from local Middle Paleolithic assemblages produced by Neanderthals, combined with Upper Paleolithic innovations similar to those encountered in the Aurignacian. At Saint-Cesaire and at the Grotte du Renne, France, Neanderthal remains associated with a transitional industry called Chatelperronian, which already displays many Upper Paleolithic features, were directly dated to 36,200±750 and 36,840±660 14C B.P., respectively. Another series of Neanderthal remains from the cave of Spy, Belgium, has also been directly dated to ca. 36,000 14C B.P. This age falls in the time range of the Lincombian-Ranisian-Jerzmanowician (LRJ), a European transitional industry identified in this site. If one assumes that the entire Chatelperronian and LRJ were produced by late Neanderthals, this would push the last occurrence date for these populations to ca. 35,000 14C B.P. Converting this radiocarbon date into a calendar age corresponds to ≈40,000 y ago. By that time, modern humans producing Aurignacian industries had already occupied the neighboring regions of Austria, Germany, and Northern Italy for some time. Interactions with modern groups may explain the cultural evolution of the last Neanderthals, but a puzzling issue remains regarding possible biological interactions between the two groups.

Judentum

Stillman 1995

Norman A. Stillman, *The Jew in the Medieval Islamic City*. In: Daniel Frank (Hrsg.), *The Jews of medieval Islam: community, society, and identity*, *Proceedings of an international conference held by the Institute of Jewish Studies, University College London, 1992.* Études sur le judaïsme médiéval 16 (Leiden 1995), 3–13.

As a result of the Islamic conquests, the majority of Jews living in the world at that time came under Arab rule. During this period of urbanization, the Jews—particularly in their great demographic center of Bavel, which now became Arab Iraq—completed the transition that had already begun in talmudic times from an agrarian to a cosmopolitan way of life.

Jews never came to dominate the financial scene in Baghdad or other medieval Islamic cities, despite the arguments to the contrary of the late Louis Massignon in a famous article, based, unfortunately, upon very scanty evidence. Most of the great bankers of the eighth through tenth centuries in the Abbasid Caliphate seem to have been Christians, and it is Christians—not Jews—who remained the stereotypical men of money in Arabic literature and lore. Even during the period of decline in the later Middle Ages, however, there were still a small number of Jews who played a significant role in the commercial and financial life of several major Islamic cities.

Stroumsa 1995

Sarah Stroumsa, *On Jewish Intellectuals Who Converted in the Early Middle Ages*. In: Daniel Frank (Hrsg.), *The Jews of medieval Islam: community, society, and identity*, *Proceedings of an international conference held by the Institute of Jewish Studies, University College London, 1992.* Études sur le judaïsme médiéval 16 (Leiden 1995), 179–197.

And although it is true that Ibn Kammuna too mentions the relativist argument, this argument was, as we have seen, sufficiently widespread and well-known for him to have received it from many other sources. To a certain degree, Ibn Kammuna confirms the impression that relativism typified the spirit of the age: his detached, objective attitude toward the three faiths is generally presented against the background of toleration which characterized the Mongol regime prior to its conversion to Islam. There is certainly a great deal of truth to this. It seems, nevertheless, that we must factor in as well the relativist tradition in Islamic philosophy—a tradition which paradoxically expressed itself in the polemical words of Samau'al the apostate.

Kultur

Müller 2015

Johannes Müller, Vesa P. J. Arponen, Robert Hofmann & René Ohlrau, *The Appearance of Social Inequalities*, *Cases of Neolithic and Chalcolithic Societies*. Origini **38** (2015), 65–85.

By using a new methodological approach, which is based on the reconstruction of social roles of households by comparing architecture and inventories, the origin of social inequality is detected in a Neolithic village. In contrast the identification of manifold social identities in a Chalcolithic mega-site (including social inequalities) describes other forms of social control.

Keywords: Origin of social inequality | Late Neolithic Balkan | Chalcolithic North Pontic | household economies

Methoden

Musco 2017

Cameron Musco, Hsin-Hao Su & Nancy A. Lynch, *Ant-inspired density estimation via random walks*. PNAS **114** (2017), 10534–10541.

Many ant species use distributed population density estimation in applications ranging from quorum sensing, to task allocation, to appraisal of enemy colony strength. It has been shown that ants estimate local population density by tracking encounter rates: The higher the density, the more often the ants bump into each other. We study distributed density estimation from a theoretical perspective. We prove that a group of anonymous agents randomly walking on a grid are able to estimate their density within a small multiplicative error in few steps by measuring their rates of encounter with other agents. Despite dependencies inherent in the fact that nearby agents may collide repeatedly (and, worse, cannot recognize when this happens), our bound nearly matches what would be required to estimate density by independently sampling grid locations. From a biological perspective, our work helps shed light on how ants and other social insects can obtain relatively accurate density estimates via encounter rates. From a technical perspective, our analysis provides tools for understanding complex dependencies in the collision probabilities of multiple random walks. We bound the strength of these dependencies using local mixing properties of the underlying graph. Our results extend beyond the grid to more general graphs, and we discuss applications to size estimation for social networks, density estimation for robot swarms, and random walk-based sampling for sensor networks.

Keywords: population density estimation | random walk sampling | network exploration | ant colony algorithms | biological distributed algorithms

Significance: Highly complex distributed algorithms are ubiquitous in nature: from the behavior of social insect colonies and bird flocks, to cellular differentiation in embryonic development, to neural information processing. In our research, we study biological computation theoretically, combining a scientific perspective, which seeks to better understand the systems being studied, with an engineering perspective, which takes inspiration from these systems to improve algorithm design. In this work, we focus on the problem of population density estimation in ant colonies, demonstrating that extremely simple algorithms, similar to those used by ants, solve the problem with strong theoretical guarantees and have a number of interesting computational applications.

Neolithikum

Müller 2017

Johannes Müller, *Großsteingräber Grabenwerke Langhügel*, *Frühe Monumentalbauten Mitteleuropas*. Archäologie in Deutschland **2017**, Sonderheft 11.

Bis zu 5800 Jahre alte Monumente prägen noch heute die Landschaften Norddeutschlands: Großsteingräber sind als Landmarken über Jahrtausende hinweg den Bewohnern gegenwärtig und erzählen aus einer Zeit, als der Mensch erstmals großräumig Kulturlandschaften in Nordmitteleuropa und Südskandinavien geschaffen hat. So sichtbar und nah Großsteingräber uns heute erscheinen, so schwierig und langwierig ist ihre Erforschung: Wer hat sie errichtet und warum? Wie waren die damaligen Lebensbedingungen? Was bedeuteten megalithische, aber auch nichtmegalithische Monumente für die Gesellschaften? Um dies zu verstehen, müssen wir die ökologischen, ökonomischen, sozialen und kulturellen Aspekte der damaligen Zeit rekonstruieren.

Dieser Aufgabe hat sich in den letzten Jahren eine Gruppe von Wissenschaftlerinnen und Wissenschaftlern verschiedener universitärer und außeruniversitärer Forschungseinrichtungen gestellt, die im Rahmen des Schwerpunktprogramms 1400 der Deutschen Forschungsgemeinschaft “Frühe Monumentalität und soziale Differenzierung” Großsteingräber, Grabenwerke, Siedlungen und Umweltbedingungen insbesondere der Trichterbechergesellschaften (4100–2800 v. Chr.) untersucht haben (www.schwerpunkt-monumente.de). Mithilfe kultur-, natur- und lebenswissenschaftlicher Methoden ließ sich der Kenntnisstand um das Geschehen insbesondere im norddeutschen Raum erheblich erweitern. Dieses Sonderheft der “Archäologie in Deutschland” fasst einige der Forschungsergebnisse zusammen und bietet einen Einstieg in die Thematik.

Ozeanien

Bergström 2017

Anders Bergström et al., *A Neolithic expansion, but strong genetic structure, in the independent history of New Guinea.* science **357** (2017), 1160–1163.

Anders Bergström, Stephen J. Oppenheimer, Alexander J. Mentzer, Kathryn Auckland, Kathryn Robson, Robert Attenborough, Michael P. Alpers, George Koki, William Pomat, Peter Siba, Yali Xue, Manjinder S. Sandhu & Chris Tyler-Smith

New Guinea shows human occupation since ≈50 thousand years ago (ka), independent adoption of plant cultivation ≈10 ka, and great cultural and linguistic diversity today. We performed genome-wide single-nucleotide polymorphism genotyping on 381 individuals from 85 language groups in Papua New Guinea and find a sharp divide originating 10 to 20 ka between lowland and highland groups and a lack of non–New Guinean admixture in the latter. All highlanders share ancestry within the last 10 thousand years, with major population growth in the same period, suggesting population structure was reshaped following the Neolithic lifestyle transition. However, genetic differentiation between groups in Papua New Guinea is much stronger than in comparable regions in Eurasia, demonstrating that such a transition does not necessarily limit the genetic and linguistic diversity of human societies.

Ancient DNA studies in Europe and the Near East have documented a gradual, but dramatic, decrease in differentiation, showing that the genetic homogeneity of present-day west Eurasia emerged in the last few thousand years. FST values in PNG fall between those of hunter-gatherers and present-day populations ofwest Eurasia, suggesting that a transition to cultivation alone does not necessarily lead to genetic homogenization. A key difference might be that PNG had no Bronze Age, which in west Eurasia was driven by an expansion of herders and led to massive population replacement, admixture, and cultural and linguistic change, or Iron Age such as that linked to the expansion of Bantu-speaking farmers in Africa. Such cultural events have resulted in rapid Y-chromosome lineage expansions due to increasedmale reproductive variance, but we consistently find no evidence for this in PNG (fig. S13). Thus, in PNG, we may be seeing the genetic, linguistic, and cultural diversity that sedentary human societies can achieve in the absence of massive technology-driven expansions.

GIBBONS 2017

Ann Gibbons, *Papua New Guinea's genetic diversity withstood farming.* science **357** (2017), 1086.

Island somehow resisted homogenization seen elsewhere.

Regardless of the cause, PNG's sharp genetic distinctions suggest that the spread of farmers may not be enough to homogenize DNA across large regions. Other, later waves of migration may have wiped out differences in Europe and Asia. "People in PNG did not experience the Bronze Age and Iron Age transformation," adds evolutionary geneticist Simon Easteal of the Australian National University in Canberra. The new study, he says, indicates that "there is a general erosion of local genomic diversity in human populations associated with technological change—a process that is continuing today."

Politik

BOXELL 2017

Levi Boxell, Matthew Gentzkow & Jesse M. Shapiro, *Greater Internet use is not associated with faster growth in political polarization among US demographic groups.* PNAS **114** (2017), 10612–10617.

pnas114-10612-Supplement.zip

We combine eight previously proposed measures to construct an index of political polarization among US adults. We find that polarization has increased the most among the demographic groups least likely to use the Internet and social media. Our overall index and all but one of the individual measures show greater increases for those older than 65 than for those aged 18–39. A linear model estimated at the age-group level implies that the Internet explains a small share of the recent growth in polarization.

Keywords: politics | polarization | Internet | social media

Significance: By many measures, Americans have become increasingly polarized in recent decades. We study the role of the Internet and social media in explaining this trend. We find that polarization has increased the most among the demographic groups least likely to use the Internet and social media, suggesting that the role of these factors is limited.