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References

Aktuell

ABBOTT 2016

Alison Abbott, *GM-crop papers spark probe.* nature **529** (2016), 268–269.

Work describing harm from genetically modified crops was cited in Italian Senate hearing.

The work has been widely cited on anti-GM websites — and results of the experiments that the papers describe were referenced in an Italian Senate hearing last July on whether the country should allow cultivation of safety-approved GM crops.

Cattaneo noted what looked like problems in all three papers: sections of images of electrophoresis gels appeared to have been obliterated, and some of the images in different papers appeared to be identical but with captions describing different experiments.

BUTLER 2016

Declan Butler & Ewen Callaway, *Scientists in the dark after fatal French clinical trial.* nature **529** (2016), 263–264.

Knowledge about the drug's structure would help researchers understand what happened.

One possible safety issue in the trial of BIA 10-2474, notes trial-design specialist Hill, is that all six participants seem to have been administered the doses simultaneously, rather than one receiving a test dose and being checked for adverse effects before others were given it.

Simultaneous rather than sequential administration was identified as problematic in a disastrous UK clinical trial in 2006 that caused multiple organ failure in six participants. “From the 2006 catastrophe in London, I had concluded that treating several individuals with the same dose on the same day in a phase I trial was a big mistake,” says Hill.

CAREY 2016

John Carey, *Rewilding, Core Concepts.* PNAS **113** (2016), 806–808.

JOHN 2016

Leslie K. John, Kate Barasz & Michael I. Norton, *Hiding personal information reveals the worst.* PNAS **113** (2016), 954–959.

Seven experiments explore people's decisions to share or withhold personal information, and the wisdom of such decisions. When people choose not to reveal information—to be “hiders”—they are judged negatively by others (experiment 1). These negative judgments emerge when hiding is volitional (experiments 2A and 2B) and are driven by decreases in trustworthiness engendered by decisions to hide (experiments 3A and 3B). Moreover, hiders do not intuit these negative consequences: given the choice to withhold or reveal unsavory information, people often choose to withhold, but observers rate those who reveal even questionable behavior more positively (experiments 4A and 4B). The negative impact of hiding holds whether opting not to disclose unflattering (drug use, poor grades, and sexually transmitted diseases) or flattering (blood donations) information, and

across decisions ranging from whom to date to whom to hire. When faced with decisions about disclosure, decision-makers should be aware not just of the risk of revealing, but of what hiding reveals.

Keywords: disclosure | transparency | trust | policy making | privacy

Significance: Disclosure is a critical element of social life, especially given Internet media that afford many opportunities (and demands from friends, partners, and even employers) to share personal information—making withholding anomalous, conspicuous, and therefore suspect. Seven experiments explore people's decisions to withhold or disclose personal information—and the wisdom of such decisions. Declining a request to disclose often makes a worse impression even than divulging unsavory personal information. Moreover, those who withhold fail to intuit this negative consequence: people withhold even when they would make a better impression by "coming clean." In short, people should be aware not just of the risk of revealing, but the risk of hiding.

Anthropologie

BETTINGER 2016

Robert L. Bettinger, *Prehistoric hunter-gatherer population growth rates rival those of agriculturalists.* PNAS **113** (2016), 812–814.

It suggests a trajectory of continuous, long-term WyomingColorado hunter–gatherer population growth of 0.041 % from 13,000–6,000 cal BP, doubling roughly every 1,700 y, within which there were short-term fluctuations during which growth rates were sometimes more than an order of magnitude larger (i.e., $r > 0.4\,\%$), doubling in less than 200 y. Spanning the transition from a highly mobile, large-game-focused Paleoindian adaptation to a less mobile Archaic adaptation that made greater use of small game and plants (5), the long-term WyomingColorado rate is broadly consistent with radiocarbon estimates for North America overall [i.e., including both hunter-gatherers and agriculturalists and bridging from one to the other (6)], almost exclusively hunter-gatherers in Australia (7), European agriculturalists (8), and prehistoric population worldwide (9). That the rates of population growth indicated by these studies are so consistent with each other has important theoretical implications.

That hunter-gatherer populations grow just as fast as agriculturali populations likely explains the failure of agriculture to develop and spread in the Pleistocene, when climate varied so rapidly that populations never reached carrying capacity (14), giving agriculture no advantage until the Holocene, when climate stabilized dramatically.

HENN 2016

Brenna M. Henn et al., *Distance from sub-Saharan Africa predicts mutational load in diverse human genomes.* PNAS **113** (2016), E440–E449.

Brenna M. Henn, Laura R. Botigué, Stephan Peischl, Isabelle Dupanloup, Mikhail Lipatov, Brian K. Maples, Alicia R. Martin, Shaila Musharoff, Howard Cann, Michael P. Snyder, Laurent Excoffier, Jeffrey M. Kidd & Carlos D. Bustamante

The Out-of-Africa (OOA) dispersal ≈50,000 y ago is characterized by a series of founder events as modern humans expanded into multiple continents. Population genetics theory predicts an increase of mutational load in populations undergoing serial founder effects during range expansions. To test this hypothesis, we have sequenced full genomes and high-coverage exomes from seven geographically divergent human populations from Namibia, Congo, Algeria, Pakistan, Cambodia, Siberia, and Mexico. We find that individual genomes vary modestly in the overall number of predicted deleterious alleles. We show via spatially explicit simulations that the observed distribution of deleterious allele frequencies is consistent with the OOA dispersal, particularly under a model where deleterious mutations are recessive. We conclude that there is a strong signal of purifying selection at conserved genomic positions within Africa, but that many predicted deleterious mutations have evolved as if they were neutral during the expansion out of Africa. Under a model where selection is inversely related to dominance, we show that OOA populations are likely to have a higher mutation load due to increased allele frequencies of nearly neutral variants that are recessive or partially recessive.

Keywords: mutation | founder effect | range expansion | expansion load | purifying selection

Significance: Human genomes carry hundreds of mutations that are predicted to be deleterious in some environments, potentially affecting the health or fitness of an individual. We characterize the distribution of deleterious mutations among diverse human populations, modeled under different selection coefficients and dominance parameters. Using a new dataset of diverse human genomes from seven different populations, we use spatially explicit simulations to reveal that classes of deleterious alleles have very different patterns across populations, reflecting the interaction between genetic drift and purifying selection. We show that there is a strong signal of purifying selection at conserved genomic positions within African populations, but most predicted deleterious mutations have evolved as if they were neutral during the expansion out of Africa.

McCoy 2016

Rajiv C. McCoy & Joshua M. Akey, *Patterns of deleterious variation between human populations reveal an unbalanced load.* PNAS **113** (2016), 809–811.

It is becoming increasingly clear that some population genetic characteristics of deleterious mutations vary among populations, but as is the case with neutral mutations, differences among populations are small relative to differences among individuals. Nonetheless, there remains much to learn about the dynamics of nonneutral variation in nonequilibrium populations, particularly for more realistic, complex, and spatially explicit models of human history.

Zahid 2016

H. Jabran Zahid, Erick Robinson & Robert L. Kelly, *Agriculture, population growth, and statistical analysis of the radiocarbon record.* PNAS **113** (2016), 931–935.

The human population has grown significantly since the onset of the Holocene about 12,000 y ago. Despite decades of research, the factors determining prehistoric population growth remain uncertain. Here, we examine measurements of the rate of growth of the prehistoric human population based on statistical analysis of the radiocarbon record. We find that, during most of the Holocene, human populations worldwide grew at a long-term annual rate of 0.04 %. Statistical analysis of the radiocarbon record shows that transitioning farming societies experienced the same rate of growth as contemporaneous foraging societies. The same rate of growth measured for populations dwelling in a range of environments and practicing a variety of subsistence strategies suggests that the global climate and/or endogenous biological factors, not adaptability to local environment or subsistence practices, regulated the long-term growth of the human population during most of the Holocene. Our results demonstrate that statistical analyses of large ensembles of radiocarbon dates are robust and valuable for quantitatively investigating the demography of prehistoric human populations worldwide.

Keywords: archeology | paleodemography | radiocarbon dating | hunter-gatherers | agriculture

Significance: We statistically analyze the radiocarbon record and show that early farming societies in Europe grew at the same rate as contemporaneous foraging societies in North America. Thus, our results challenge the commonly held view that the advent of agriculture was linked to accelerated growth of the human population. The same rates of prehistoric population growth measured worldwide suggest that the global climate and/or biological factors intrinsic to the species and not factors related to the regional environment or subsistence practices regulated the growth of the human population for most of the last 12,000 y. This study demonstrates that statistical analysis of the radiocarbon record is a robust quantitative approach for studying prehistoric human demography.

Bibel

Sanders 2015

Seth L. Sanders, *What if There Aren't Any Empirical Models for Pentateuchal Criticism?* In: Brian B. Schmidt (Hrsg.), *Contextualizing Israel's Sacred Writings*, *Ancient Literacy, Orality, and Literary Production.* Ancient Israel and Its Literature 22 (Atlanta 2015), 281–304.

What we may see here are the traces of a shift in the ancient Hebrew literary dominant. At the knowable beginnings of Hebrew literature, which created the extended narratives attested in the Primeval History, the value of coherence drove the integration of separate preexisting stories into larger arcs. At the later stage of interweaving we find a literary culture that valued comprehensiveness above all. And in Second Temple literature we see not a rupture but a dialectical response, with new religious and literary values that impelled writers and readers to seek harmonization.

This historically anchored comparison of the literary values implicit in the Primeval History's distinctive form teaches us a lesson. This is that it is at the points of ancient Hebrew literature's greatest assertion of continuity that we find its most radical reinvention. New text-making techniques and literary values arose together in response to the now-problematic older ones. Scholem argued that rabbinic Judaism's late invention of the oral torah, imagined already at Sinai, its most aggressive assertion of continuity, was also a point of profound rupture—a fiction and a total anachronism. What the philological and historical evidence we have surveyed shows is that these moments of rupture that create and invoke new forms of continuity go much farther back than he'd imagined, to the genesis of Hebrew literature itself.

Biologie

Bakker 2016

Elisabeth S. Bakker et al., *Combining paleo-data and modern exclosure experiments to assess the impact of megafauna extinctions on woody vegetation.* PNAS **113** (2016), 847–855.

Elisabeth S. Bakker, Jacquelyn L. Gill, Christopher N. Johnson, Frans W. M. Vera, Christopher J. Sandom, Gregory P. Asner & Jens-Christian Svenning

Until recently in Earth history, very large herbivores (mammoths, ground sloths, diprotodons, and many others) occurred in most of the World's terrestrial ecosystems, but the majority have gone extinct as part of the late-Quaternary extinctions. How has this large-scale removal of large herbivores affected landscape structure and ecosystem functioning? In this review, we combine paleo-data with information from modern exclosure experiments to assess the impact of large herbivores (and their disappearance) on woody species, landscape structure, and ecosystem functions. In modern landscapes characterized by intense herbivory, woody plants can persist by defending themselves or by association with defended species, can persist by growing in places that are physically inaccessible to herbivores, or can persist where high predator activity limits foraging by herbivores. At the landscape scale, different herbivore densities and assemblages may result in dynamic gradients in woody cover. The late-Quaternary extinctions were natural experiments in large-herbivore removal; the paleoecological record shows evidence of widespread changes in community composition and ecosystem structure and function, consistent with modern exclosure experiments. We propose a conceptual framework that describes the impact of large herbivores on woody plant abundance mediated by herbivore diversity and density, predicting that herbivore suppression of woody plants is strongest where herbivore diversity is high. We conclude that the decline of large herbivores induces major alterations in landscape structure and ecosystem functions.

Keywords: browsers | ecosystem functions | herbivore diversity | landscape structure | megaherbivore

BARNOSKY 2016

Anthony D. Barnosky et al., *Variable impact of late-Quaternary megafaunal extinction in causing ecological state shifts in North and South America*. PNAS **113** (2016), 856–861.

Anthony D. Barnosky, Emily L. Lindsey, Natalia A. Villavicencio, Enrique Bostelmann, Elizabeth A. Hadly, James Wanket & Charles R. Marshall

Loss of megafauna, an aspect of defaunation, can precipitate many ecological changes over short time scales. We examine whether megafauna loss can also explain features of lasting ecological state shifts that occurred as the Pleistocene gave way to the Holocene. We compare ecological impacts of late-Quaternarymegafauna extinction in five American regions: southwestern Patagonia, the Pampas, northeastern United States, northwestern United States, and Beringia. We find that major ecological state shifts were consistent with expectations of defaunation in North American sites but not in South American ones. The differential responses highlight two factors necessary for defaunation to trigger lasting ecological state shifts discernable in the fossil record: (i) lost megafauna need to have been effective ecosystem engineers, like proboscideans; and (ii) historical contingencies must have provided the ecosystem with plant species likely to respond to megafaunal loss. These findings help in identifying modern ecosystems that are most at risk for disappearing should current pressures on the ecosystems' large animals continue and highlight the critical role of both individual species ecologies and ecosystem context in predicting the lasting impacts of defaunation currently underway.

Keywords: megafauna | extinction | Quaternary | North America | South America

Significance: Removing megafauna from contemporary ecosystems changes vegetation and small mammal communities over ecological time scales. We show that similar dynamics seem to operate over millennial time scales but only if the megafaunal loss includes ecosystem engineers in settings that also contain plant species susceptible to ecological release. Under such conditions, megafauna extinction can initiate changes that quickly lead to new, lasting ecological states. This implies that should some megafauna currently at risk for extinction actually become extinct, their characteristic ecosystems—for example, mosaics of savannah and forest—would also disappear, rapidly transforming into novel systems with respect to what is considered normal in today's world.

KORPELA 2016

Katri Korpela, Anne Salonen, Lauri J. Virta, Riina A. Kekkonen, Kristoffer Forslund, Peer Bork & Willem M. de Vos, *Intestinal microbiome is related to lifetime antibiotic use in Finnish pre-school children.* Nature Communications **7** (2016), 10410. DOI:10.1038/ncomms10410.

NatComm07-10410-Supplement.pdf

Early-life antibiotic use is associated with increased risk for metabolic and immunological diseases, and mouse studies indicate a causal role of the disrupted microbiome. However, little is known about the impacts of antibiotics on the developing microbiome of children. Here we use phylogenetics, metagenomics and individual antibiotic purchase records to show that macrolide use in 2–7 year-old Finnish children (N=142; sampled at two time points) is associated with a long-lasting shift in microbiota composition and metabolism. The shift includes depletion of Actinobacteria, increase in Bacteroidetes and Proteobacteria, decrease in bile-salt hydrolase and increase in macrolide resistance. Furthermore, macrolide use in early life is associated with increased risk of asthma and predisposes to antibiotic-associated weight gain. Overweight and asthmatic children have distinct microbiota compositions. Penicillins leave a weaker mark on the microbiota than macrolides. Our results support the idea that, without compromising clinical practice, the impact on the intestinal microbiota should be considered when prescribing antibiotics.

LEITE 2016

Yuri L. R. Leite et al., *Neotropical forest expansion during the last glacial period challenges refuge hypothesis.* PNAS **113** (2016), 1008–1013.

pnas113-01008-Supplement1.rtf, pnas113-01008-Supplement2.xlsx

Yuri L. R. Leite, Leonora P. Costa, Ana Carolina Loss, Rita G. Rocha, Henrique Batalha-Filho, Alex C. Bastos, Valéria S. Quaresma, Valéria Fagundes, Roberta Paresque, Marcelo Passamani & Renata Pardini

The forest refuge hypothesis (FRH) has long been a paradigm for explaining the extreme biological diversity of tropical forests. According to this hypothesis, forest retraction and fragmentation during glacial periods would have promoted reproductive isolation and consequently speciation in forest patches (ecological refuges) surrounded by open habitats. The recent use of paleoclimatic models of species and habitat distributions revitalized the FRH, not by considering refuges as the main drivers of allopatric speciation, but instead by suggesting that high contemporary diversity is associated with historically stable forest areas. However, the role of the emerged continental shelf on the Atlantic Forest biodiversity hotspot of eastern South America during glacial periods has been ignored in the literature. Here, we combined results of species distribution models with coalescent simulations based on DNA sequences to explore the congruence between scenarios of forest dynamics through time and the genetic structure of mammal species cooccurring in the central region of the Atlantic Forest. Contrary to the FRH predictions, we found more fragmentation of suitable habitats during the last interglacial (LIG) and the present than in the last glacial maximum (LGM), probably due to topography. We also detected expansion of suitable climatic conditions onto the emerged continental shelf during the LGM, which would have allowed forests and forest-adapted species to expand. The interplay of sea level and land distribution must have been crucial in the biogeographic history of the Atlantic Forest, and forest refuges played only a minor role, if any, in this biodiversity hotspot during glacial periods.

Keywords: last glacial maximum | sea level | Atlantic Forest | Quaternary | continental shelf

Significance: The tropical forests of South America are among the most diverse and unique habitats in the world in terms of plant and animal species. One of the most popular explanations for this diversity and endemism is the idea that forests retracted and fragmented during glacial periods, forming ecological refuges, surrounded by dry lands or savannas. These historically stable forest refuges would have been responsible for maintaining the pattern of diversity and endemism observed today. Here, we show that the Atlantic Forest of eastern South America probably expanded, rather than contracted, during the last glacial period. In addition, the emerged Brazilian continental shelf played a major, yet neglected, role on the evolution of this biodiversity hotspot during the last glacial period.

MALHI 2016

Yadvinder Malhi, Christopher E. Doughty, Mauro Galetti, Felisa A. Smith, Jens-Christian Svenning & John W. Terborgh, *Megafauna and ecosystem function from the Pleistocene to the Anthropocene.* PNAS **113** (2016), 838–846.

Large herbivores and carnivores (the megafauna) have been in a state of decline and extinction since the Late Pleistocene, both on land and more recently in the oceans. Much has been written on the timing and causes of these declines, but only recently has scientific attention focused on the consequences of these declines for ecosystem function. Here, we review progress in our understanding of how megafauna affect ecosystem physical and trophic structure, species composition, biogeochemistry, and climate, drawing on special features of PNAS and Ecography that have been published as a result of an international workshop on this topic held in Oxford in 2014. Insights emerging from this work have consequences for our understanding of changes in biosphere function since the Late Pleistocene and of the functioning of contemporary ecosystems, as well as offering a rationale and framework for scientifically informed restoration of megafaunal function where possible and appropriate.

Keywords: extinctions | trophic cascades | vegetation structure | biogeochemistry | rewilding

PERES 2016

Carlos A. Peres, Thaise Emilio, Juliana Schietti, Sylvain J. M. Desmoulière & Taal Levi, *Dispersal limitation induces long-term biomass collapse in overhunted Amazonian forests.* PNAS **113** (2016), 892–897.

Tropical forests are the global cornerstone of biological diversity, and store 55 % of the forest carbon stock globally, yet sustained provisioning of these forest ecosystem services may be threatened by hunting-induced extinctions of plant–animal mutualisms that maintain long-term forest dynamics. Large-bodied Atelinae primates and tapirs in particular offer nonredundant seed-dispersal services for many large-seeded Neotropical tree species, which on average have higher wood density than smaller-seeded and wind-dispersed trees. We used field data and models to project the spatial impact of hunting on large primates by ≈1 million rural households throughout the Brazilian Amazon. We then used a unique baseline dataset on 2,345 1-ha tree plots arrayed across the Brazilian Amazon to model changes in aboveground forest biomass under different scenarios of hunting-induced large-bodied frugivore extirpation. We project that defaunation of the most harvest-sensitive species will lead to losses in aboveground biomass of between 2.5–5.8 % on average, with some losses as high as 26.5–37.8 %. These findings highlight an urgent need to manage the sustainability of game hunting in both protected and unprotected tropical forests, and place full biodiversity integrity, including populations of large frugivorous vertebrates, firmly in the agenda of reducing emissions from deforestation and forest degradation (REDD+) programs.

Keywords: tropical forest | hunting | forest carbon | ecosystem services | large frugivores

Significance: A standardized network of wildlife surveys across 166 Amazonian hunted and nonhunted forests, combined with basin-wide spatial modeling of central-place hunting pressure, reveal the degree to which arboreal frugivores have been extirpated by hunters and the spatial extent of overhunting for harvest-sensitive frugivore species across the Brazilian Amazon. Simulations based on data from 2,345 1-ha tree plots inventoried throughout Brazilian Amazonia then show widespread erosion of forest carbon stocks in the world's largest tropical forest region.

Surovell 2016

Todd A. Surovell, Spencer R. Pelton, Richard Anderson-Sprecher & Adam D. Myers, *Test of Martin's overkill hypothesis using radiocarbon dates on extinct megafauna.* PNAS **113** (2016), 886–891.

pnas113-00886-Supplement1.xlsx, pnas113-00886-Supplement2.xlsx, pnas113-00886-Supplement3.xlsx, pnas113-00886-Supplement4.docx, pnas113-00886-Supplement5.docx

Following Martin [Martin PS (1973) Science 179:969–974], we propose the hypothesis that the timing of human arrival to the New World can be assessed by examining the ecological impacts of a small population of people on extinct Pleistocene megafauna. To that end, we compiled lists of direct radiocarbon dates on paleontological specimens of extinct genera from North and South America with the expectation that the initial decline of extinct megafauna should correspond in time with the initial evidence for human colonization and that those declines should occur first in eastern Beringia, next in the contiguous United States, and last in South America. Analyses of spacings and frequency distributions of radiocarbon dates for each region support the idea that the extinction event first commenced in Beringia, roughly 13,300–15,000 BP. For the United States and South America, extinctions commenced considerably later but were closely spaced in time. For the contiguous United States, extinction began at ca. 12,900–13,200 BP, and at ca. 12,600–13,900 BP in South America. For areas south of Beringia, these estimates correspond well with the first significant evidence for human presence and are consistent with the predictions of the overkill hypothesis.

Keywords: Pleistocene extinctions | overkill | radiocarbon | temporal frequency distributions

Significance: Coincident with the human colonization of the Western Hemisphere, dozens of genera of Pleistocene megafauna were lost to extinction. FollowingMartin, we argue that declines in the record of radiocarbon dates of extinct genera may be used as an independent means of detecting the first presence of humans in the New World. Our results, based on analyses of radiocarbon dates from Eastern Beringia, the contiguous United States, and South America, suggest north to south, time, and space transgressive declines in megafaunal populations as predicted by the overkill hypothesis. This finding is difficult to reconcile with other extinction hypotheses. However, it remains to be determined whether these findings will hold with larger samples of radiocarbon dates from all regions.

SVENNING 2016

Jens-Christian Svenning et al., *Science for a wilder Anthropocene, Synthesis and future directions for trophic rewilding research.* PNAS **113** (2016), 898–906.

Jens-Christian Svenning, Pil B. M. Pedersen, C. Josh Donlan, Rasmus Ejrnæs, Søren Faurby, Mauro Galetti, Dennis M. Hansen, Brody Sandel, Christopher J. Sandom, John W. Terborgh & Frans W. M. Vera

Trophic rewilding is an ecological restoration strategy that uses species introductions to restore top-down trophic interactions and associated trophic cascades to promote self-regulating biodiverse ecosystems. Given the importance of large animals in trophic cascades and their widespread losses and resulting trophic downgrading, it often focuses on restoring functional megafaunas. Trophic rewilding is increasingly being implemented for conservation, but remains controversial. Here, we provide a synthesis of its current scientific basis, highlighting trophic cascades as the key conceptual framework, discussing the main lessons learned from ongoing rewilding projects, systematically reviewing the current literature, and highlighting unintentional rewilding and spontaneous wildlife comebacks as underused sources of information. Together, these lines of evidence show that trophic cascades may be restored via species reintroductions and ecological replacements. It is clear, however, that megafauna effects may be affected by poorly understood trophic complexity effects and interactions with landscape settings, human activities, and other factors. Unfortunately, empirical research on trophic rewilding is still rare, fragmented, and geographically biased, with the literature dominated by essays and opinion pieces. Wehighlight the need for applied programs to include hypothesis testing and science-based monitoring, and outline priorities for future research, notably assessing the role of trophic complexity, interplay with landscape settings, land use, and climate change, as well as developing the global scope for rewilding and tools to optimize benefits and reduce human–wildlife conflicts. Finally, we recommend developing a decision framework for species selection, building on functional and phylogenetic information and with attention to the potential contribution from synthetic biology.

Keywords: conservation | megafauna | reintroduction | restoration | trophic cascades

VAN VALKENBURGH 2016

Blaire Van Valkenburgh, Matthew W. Hayward, William J. Ripple, Carlo Meloro & V. Louise Roth, *The impact of large terrestrial carnivores on Pleistocene ecosystems.* PNAS **113** (2016), 862–867.

Large mammalian terrestrial herbivores, such as elephants, have dramatic effects on the ecosystems they inhabit and at high population densities their environmental impacts can be devastating. Pleistocene terrestrial ecosystems included a much greater diversity of megaherbivores (e.g., mammoths, mastodons, giant ground sloths) and thus a greater potential for widespread habitat degradation if population sizes were not limited. Nevertheless, based on modern observations, it is generally believed that populations of megaherbivores (>800 kg) are largely immune to the effects of predation and this perception has been extended into the

Pleistocene. However, as shown here, the species richness of big carnivores was greater in the Pleistocene and many of them were significantly larger than their modern counterparts. Fossil evidence suggests that interspecific competition among carnivores was relatively intense and reveals that some individuals specialized in consuming megaherbivores. To estimate the potential impact of Pleistocene large carnivores, we use both historic and modern data on predator–prey body mass relationships to predict size ranges of their typical and maximum prey when hunting as individuals and in groups. These prey size ranges are then compared with estimates of juvenile and subadult proboscidean body sizes derived from extant elephant growth data. Young proboscideans at their most vulnerable age fall within the predicted prey size ranges of many of the Pleistocene carnivores. Predation on juveniles can have a greater impact on megaherbivores because of their long interbirth intervals, and consequently, we argue that Pleistocene carnivores had the capacity to, and likely did, limit megaherbivore population sizes.

Keywords: predator | megafauna | hypercarnivore | Carnivora | megaherbivore

Significance: At very high densities, populations of the largest herbivores, such as elephants, have devastating effects on the environment. What prevented widespread habitat destruction in the Pleistocene, when the ecosystem sustained many species of huge herbivores? We use data on predator–prey body mass relationships to predict the prey size ranges of large extinct mammalian carnivores, which were more diverse and much larger than living species. We then compare these prey size ranges with estimates of young mammoth sizes and show that juvenile mammoths and mastodons were within predicted prey size ranges of many of the Pleistocene carnivores. From this and other fossil evidence we argue that, by limiting population sizes of megaherbivores, large carnivores had a major impact on Pleistocene ecosystems.

Kultur

Mirazón Lahr 2016

M. Mirazón Lahr et al., *Inter-group violence among early Holocene hunter-gatherers of West Turkana, Kenya*. nature **529** (2016), 394–398.

n529-0394-Supplement1.pdf, n529-0394-Supplement2.pdf

M. Mirazón Lahr, F. Rivera, R. K. Power, A. Mounier, B. Copsey, F. Crivellaro, J. E. Edung, J. M. Maillo Fernandez, C. Kiarie, J. Lawrence, A. Leakey, E. Mbua, H. Miller, A. Muigai, D. M. Mukhongo, A. Van Baelen, R. Wood, J.-L. Schwenninger, R. Grün, H. Achyuthan, A. Wilshaw & R. A. Foley

The nature of inter-group relations among prehistoric huntergatherers remains disputed, with arguments in favour and against the existence of warfare before the development of sedentary societies1,2. Here we report on a case of inter-group violence towards a group of hunter-gatherers from Nataruk, west of Lake Turkana, which during the late Pleistocene/early Holocene period extended about 30 km beyond its present-day shore3. Ten of the twelve articulated skeletons found at Nataruk show evidence of having died violently at the edge of a lagoon, into which some of the bodies fell. The remains from Nataruk are unique, preserved by the particular conditions of the lagoon with no evidence of deliberate burial. They offer a rare glimpse into the life and death of past foraging people, and evidence that warfare was part of the repertoire of inter-group relations among prehistoric hunter-gatherers.

WATSON 1999

Aaron Watson & David Keating, *Architecture and sound, An acoustic analysis of megalithic monuments in prehistoric Britain*. Antiquity **73** (1999), 325–336.

Prehistoric monuments in Britain are often dominant features in the landscape, and archaeological theory has tended to consider the visual and spatial influences of their architecture upon peoples' movement and perception. The articulation of sound within these structures has not been widely discussed, despite evidence which suggests that many monuments provided settings for gatherings of people. This possibility was explored at two contrasting sites in Scotland, a recumbent stone circle and a passagegrave, revealing that the elemental acoustic properties inherent in each may have literally orchestrated encounters with the stones.

Keywords: sound | megaliths | prehistoric monuments | Camster Round | experimental archaeology | Easter Aquorthies | Caithness

Neolithikum

ARBUCKLE 2014

Benjamin S. Arbuckle et al., *Data Sharing Reveals Complexity in the Westward Spread of Domestic Animals across Neolithic Turkey*. PLoS ONE **9** (2014), e99845. DOI:10.1371/journal.pone.0099845.

pone09-e0099845-Supplement.pdf

Benjamin S. Arbuckle, Sarah Whitcher Kansa, Eric Kansa, David Orton, Canan Çakırlar, Lionel Gourichon, Levent Atici, Alfred Galik, Arkadiusz Marciniak, Jacqui Mulville, Hijlke Buitenhuis, Denise Carruthers, Bea De Cupere, Arzu Demirergi, Sheelagh Frame, Daniel Helmer, Louise Martin, Joris Peters, Nadja Pöllath, Kamilla Pawłowska, Nerissa Russell, Katheryn Twiss & Doris Würtenberger

This study presents the results of a major data integration project bringing together primary archaeozoological data for over 200,000 faunal specimens excavated from seventeen sites in Turkey spanning the Epipaleolithic through Chalcolithic periods, c. 18,000-4,000 cal BC, in order to document the initial westward spread of domestic livestock across Neolithic central and western Turkey. From these shared datasets we demonstrate that the westward expansion of Neolithic subsistence technologies combined multiple routes and pulses but did not involve a set 'package' comprising all four livestock species including sheep, goat, cattle and pig. Instead, Neolithic animal economies in the study regions are shown to be more diverse than deduced previously using quantitatively more limited datasets. Moreover, during the transition to agro-pastoral economies interactions between domestic stock and local wild fauna continued. Through publication of datasets with Open Context (opencontext.org), this project emphasizes the benefits of data sharing and web-based dissemination of large primary data sets for exploring major questions in archaeology.

NEIL 2016

Samantha Neil, Jane Evans, Janet Montgomery & Chris Scarre, *Isotopic evidence for residential mobility of farming communities during the transition to agriculture in Britain*. Royal Society Open Science **3** (2016), 150522.

Development of agriculture is often assumed to be accompanied by a decline in residential mobility, and sedentism is frequently proposed to provide the basis for economic intensification, population growth and increasing social complexity. In

Britain, however, the nature of the agricultural transition (ca 4000 BC) and its effect on residence patterns has been intensely debated. Some authors attribute the transition to the arrival of populations who practised a system of sedentary intensive mixed farming similar to that of the very earliest agricultural regimes in central Europe, ca 5500 BC, with cultivation of crops in fixed plots and livestock keeping close to permanently occupied farmsteads. Others argue that local hunter–gatherers within Britain adopted selected elements of a farming economy and retained a mobile way of life. We use strontium and oxygen isotope analysis of tooth enamel from an Early Neolithic burial population in Gloucestershire, England, to evaluate the residence patterns of early farmers. Our results are consistent with the hypothesis that early farming communities in Britain were residentially mobile and were not fully sedentary. Results highlight the diverse nature of settlement strategies associated with early farming in Europe and are of wider significance to understanding the effect of the transition to agriculture on residence patterns.

Keywords: development of agriculture | Neolithic | sedentism | mobility | strontium | isotope | analysis

Physik

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Thomas J. Phillips, *Antimatter may matter.* nature **529** (2016), 294–295.

The charge neutrality of the antimatter atom antihydrogen has been confirmed with unprecedented accuracy, paving the way for experiments that could simultaneously solve several of physics' biggest mysteries.

In addition to the lack of antimatter, every list of the biggest mysteries in physics includes the natures of three things: dark energy, dark matter and cosmic inflation. These three were all posited as ad hoc solutions to problems posed by cosmological observations that do not fit predictions arising from the general theory of relativity.

Furthermore, in this model the Universe would have zero net gravitational charge, so dark energy would not be needed to explain why its expansion is not slowing down. Such a coasting Universe also obviates the need for cosmic inflation, because its expansion would have been sufficiently slow for the entire visible Universe to have been causally connected. Finally, antimatter that has negative gravitational charge would change the nature of vacuum (a process called vacuum polarization) such that it could provide enough gravity to hold galaxies together without the need for dark matter.