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References

Afrika

McDonald 1998

Mary M. A. McDonald, *Early African Pastoralism*, *View from Dakhleh Oasis (South Central Egypt)*. Journal of Anthropological Archaeology **17** (1998), 124–142.

The late prehistoric archaeological sequence from Dakhleh Oasis, South Central Egypt, is examined for evidence on the origins and development of pastoralism in northeastern Africa, under the dry but fluctuating environmental conditions of the early to mid-Holocene. Around 8800 B.P., relatively sedentary groups of the Masara cultural unit have a broad-based subsistence system but no sign of food production. Herding appears ca. 7000 B.P., at a time of increased and possibly less seasonal rainfall, on large late Bashendi A sites with stone-built structures and a still-diversified food economy. With the drying trend after 6500 B.P., mobile Bashendi B cattle and goat herders continue to aggregate in the oasis for a millennium, still utilizing a variety of resources. More settled Sheikh Muftah groups occupy the oasis lowlands until Old Kingdom times. Throughout the sequence, the early pastoralism of Dakhleh seems more African than West Asian in character.

Aktuell

Abatzoglou 2016

John T. Abatzoglou & A. Park Williams, *Impact of anthropogenic climate change on wildfire across western US forests*. PNAS **113** (2016), 11770–11775.

pnas113-11770-Supplement1.csv, pnas113-11770-Supplement2.csv, pnas113-11770-Supplement3.csv

Increased forest fire activity across the western continental United States (US) in recent decades has likely been enabled by a number of factors, including the legacy of fire suppression and human settlement, natural climate variability, and human-caused climate change. We use modeled climate projections to estimate the contribution of anthropogenic climate change to observed increases in eight fuel aridity metrics and forest fire area across the western United States. Anthropogenic increases in temperature and vapor pressure deficit significantly enhanced fuel aridity across western US forests over the past several decades and, during 2000–2015, contributed to 75 % more forested area experiencing high ($> 1\sigma$) fire-season fuel aridity and an average of nine additional days per year of high fire potential. Anthropogenic climate change accounted for ≈55 % of observed increases in fuel aridity from 1979 to 2015 across western US forests, highlighting both anthropogenic climate change and natural climate variability as important contributors to increased wildfire potential in recent decades. We estimate that human-caused climate change contributed to an additional 4.2 million ha of forest fire area during 1984– 2015, nearly doubling the forest fire area expected in its absence. Natural climate variability will continue to alternate between modulating and compounding anthropogenic increases in fuel aridity, but anthropogenic

climate change has emerged as a driver of increased forest fire activity and should continue to do so while fuels are not limiting.

Keywords: wildfire | climate change | attribution | forests

Significance: Increased forest fire activity across the western United States in recent decades has contributed to widespread forest mortality, carbon emissions, periods of degraded air quality, and substantial fire suppression expenditures. Although numerous factors aided the recent rise in fire activity, observed warming and drying have significantly increased fire-season fuel aridity, fostering a more favorable fire environment across forested systems. We demonstrate that human-caused climate change caused over half of the documented increases in fuel aridity since the 1970s and doubled the cumulative forest fire area since 1984. This analysis suggests that anthropogenic climate change will continue to chronically enhance the potential for western US forest fire activity while fuels are not limiting.

CHANG 2016

Melanie L. Chang & April Nowell, *How To Make Stone Soup, Is the "Paleo Diet" a Missed Opportunity for Anthropologists?* Evolutionary Anthropology **25** (2016), 228–231.

"Evolutionary biology has much to teach us about how we should eat and live for best health. It would be good for evolutionary biologists to spend themselves for the worthy cause of identifying those truths."

This is not to say that it is inappropriate to criticize aspects of the Paleo movement that seem misguided or based on flawed understandings of our evolutionary past. Nevertheless, it may be important to revisit our tone and recognize that our responses should not be framed and, indeed, may be not perceived the same way they would if we were speaking to colleagues at an academic conference.

The Paleo movement represents an opportunity for public engagement and dialogue that our discipline has largely failed to take advantage of; we should not squander future opportunities. As paleoanthropologists, we have a public responsibility to use what we know about our evolutionary history to promote a richer, more complex understanding of the biological underpinnings of human health and to increase awareness of the relevance of anthropology during what is a socially and politically difficult period for the both discipline specifically and science in general.

KNAPP 2016

Roland A. Knapp et al., *Large-scale recovery of an endangered amphibian despite ongoing exposure to multiple stressors.* PNAS **113** (2016), 11889–11894.

Roland A. Knapp, Gary M. Fellers, Patrick M. Kleeman, David A. W. Miller, Vance T. Vredenburg, Erica Bree Rosenblum & Cheryl J. Briggs

Amphibians are one of the most threatened animal groups, with 32 % of species at risk for extinction. Given this imperiled status, is the disappearance of a large fraction of the Earth's amphibians inevitable, or are some declining species more resilient than is generally assumed? We address this question in a species that is emblematic of many declining amphibians, the endangered Sierra Nevada yellowlegged frog (Rana sierrae). Based on >7,000 frog surveys conducted across Yosemite National Park over a 20-y period, we show that, after decades of decline and despite ongoing exposure tomultiple stressors, including introduced fish, the recently emerged disease chytridiomycosis, and pesticides, R. sierrae abundance increased sevenfold during the study and at a rate of 11 % per year. These increases occurred in hundreds of populations throughout Yosemite, providing a rare example of amphibian recovery at an ecologically relevant spatial scale. Results from a laboratory experiment indicate that these increases may be in part because of reduced frog susceptibility to chytridiomycosis. The disappearance of nonnative fish from numerous water bodies after cessation of stocking also contributed to the recovery. The large-scale increases in R. sierrae abundance that we document suggest that, when habitats are relatively intact and stressors are reduced in their importance by active management or species' adaptive responses, declines of some amphibians may be partially reversible, at least at a regional scale. Other studies conducted over similarly large temporal and spatial scales are critically needed to provide insight and generality about the reversibility of amphibian declines at a global scale.

Keywords: amphibians | recovery | disease | Rana sierrae | Yosemite

Significance: Human influences are causing the disappearance of species at a rate unprecedented in millions of years. Amphibians are being particularly affected, and extinctions of many species may be inevitable. The Sierra Nevada yellow-legged frog (Rana sierrae) was once common in the mountains of California (United States), but human impacts have driven it near extinction. Repeated surveys of thousands of water bodies in Yosemite National Park show that the decline of R. sierrae has recently reversed and that population abundance is now increasing markedly in part because of reduced influence of stressors, including disease and introduced fish. These results suggest that some amphibians may be more resilient than is assumed, and with appropriate management, declines of such species may be reversible.

PERRON 2016

J. Taylor Perron & Jeremy G. Venditti, *Megafloods downsized.* nature **538** (2016), 174–175.

A fresh look at the Channeled Scablands of North America shows that the ancient floods that scarred that landscape were smaller than is commonly assumed. This result could revise estimates of similar floods on Mars.

Anthropologie

CULOTTA 2016

Elizabeth Culotta & Ann Gibbons, *Aborigines and Eurasians rode one migration wave.* science **353** (2016), 1352–1353.

Tide of genetic data refutes idea that an earlier expansion of modern humans populated the island continent.

Australian Aborigines have long been cast as a people apart. Although Australia is halfway around the world from our species's accepted birthplace in Africa, the continent is nevertheless home to some of the earliest undisputed signs of modern humans outside Africa, and Aborigines have unique languages and cultural adaptations. Some researchers have posited that the ancestors of the Aborigines were the first modern humans to surge out of Africa, spreading swiftly eastward along the coasts of southern Asia thousands of years before a second wave of migrants populated Eurasia. Not so, according to a trio of genomic studies, the first to analyze many full genomes from Australia and New Guinea. They conclude that, like most other living Eurasians, Aborigines descend from a single group of modern humans who swept out of Africa 50,000 to 60,000 years ago and then spread in different directions.

But the third paper, by a team led by Mait Metspalu of the Estonian Biocentre in Tartu, makes a different claim. Analyzing 379 new genomes from 125 populations worldwide, the group concludes that at least 2 % of the genomes of people from Papua New Guinea comes from an early dispersal of modern humans, who left Africa perhaps 120,000 years ago. Their paper proposes that Homo sapiens left Africa in at least two waves. Reich questions that result, but says that his and Willerslev's studies can't rule out a contribution of only 1 % or 2 % from an earlier H. sapiens migration. Akey says: "As population geneticists, we could spend the next decade arguing about that 2 %, but in practical terms it doesn't matter." The most recent migration "explains more than 90 % of the ancestry of living people."

Dong 2016

Xiao Dong, Brandon Milholland & Jan Vijg, *Evidence for a limit to human lifespan*. nature **538** (2016), 257–259.

Driven by technological progress, human life expectancy has increased greatly since the nineteenth century. Demographic evidence has revealed an ongoing reduction in old-age mortality and a rise of the maximum age at death, which may gradually extend human longevity1,2. Together with observations that lifespan in various animal species is flexible and can be increased by genetic or pharmaceutical intervention, these results have led to suggestions that longevity may not be subject to strict, species-specific genetic constraints. Here, by analysing global demographic data, we show that improvements in survival with age tend to decline after age 100, and that the age at death of the world's oldest person has not increased since the 1990s. Our results strongly suggest that the maximum lifespan of humans is fixed and subject to natural constraints.

Malaspinas 2016

Anna-Sapfo Malaspinas et al., *A genomic history of Aboriginal Australia*. nature **538** (2016), 207–214.

n538-0207-Supplement.pdf

Anna-Sapfo Malaspinas, Michael C. Westaway, Craig Muller, Vitor C. Sousa, Oscar Lao, Isabel Alves, Anders Bergström, Georgios Athanasiadis, Jade Y. Cheng, Jacob E. Crawford, Tim H. Heupink, Enrico Macholdt, Stephan Peischl, Simon Rasmussen, Stephan Schiffels, Sankar Subramanian, Joanne L. Wright, Anders Albrechtsen, Chiara Barbieri, Isabelle Dupanloup, Anders Eriksson, Ashot Margaryan, Ida Moltke, Irina Pugach, Thorfinn S. Korneliussen, Ivan P. Levkivskyi, J. Víctor Moreno-Mayar, Shengyu Ni, Fernando Racimo, Martin Sikora, Yali Xue, Farhang A. Aghakhanian, Nicolas Brucato, Søren Brunak, Paula F. Campos, Warren Clark, Sturla Ellingvåg, Gudjugudju Fourmile, Pascale Gerbault, Darren Injie, George Koki, Matthew Leavesley, Betty Logan, Aubrey Lynch, Elizabeth A. Matisoo-Smith, Peter J. McAllister, Alexander J. Mentzer, Mait Metspalu, Andrea B. Migliano, Les Murgha, Maude E. Phipps, William Pomat, Doc Reynolds, Francois-Xavier Ricaut, Peter Siba, Mark G. Thomas, Thomas Wales, Colleen Ma'run Wall, Stephen J. Oppenheimer, Chris Tyler-Smith, Richard Durbin, Joe Dortch, Andrea Manica, Mikkel H. Schierup, Robert A. Foley, Marta Mirazón Lahr, Claire Bowern, Jeffrey D. Wall, Thomas Mailund, Mark Stoneking, Rasmus Nielsen, Manjinder S. Sandhu, Laurent Excoffier, David M. Lambert & Eske Willerslev

The population history of Aboriginal Australians remains largely uncharacterized. Here we generate high-coverage genomes for 83 Aboriginal Australians (speakers of Pama–Nyungan languages) and 25 Papuans from the New Guinea Highlands. We find that Papuan and Aboriginal Australian ancestors diversified 25–40 thousand years ago (kya), suggesting pre-Holocene population structure in the ancient continent of Sahul (Australia, New Guinea and Tasmania). However, all of the studied Aboriginal Australians descend from a single founding population that differentiated ≈10–32 kya. We infer a population expansion in northeast

Australia during the Holocene epoch (past 10,000 years) associated with limited gene flow from this region to the rest of Australia, consistent with the spread of the Pama–Nyungan languages. We estimate that Aboriginal Australians and Papuans diverged from Eurasians 51–72 kya, following a single out-of-Africa dispersal, and subsequently admixed with archaic populations. Finally, we report evidence of selection in Aboriginal Australians potentially associated with living in the desert.

MALLICK 2016

Swapan Mallick et al., *The Simons Genome Diversity Project, 300 genomes from 142 diverse populations.* nature **538** (2016), 201–206.

n538-0201-Supplement.pdf

Swapan Mallick, Heng Li, Mark Lipson, Iain Mathieson, Melissa Gymrek, Fernando Racimo, Mengyao Zhao, Niru Chennagiri, Susanne Nordenfelt, Arti Tandon, Pontus Skoglund, Iosif Lazaridis, Sriram Sankararaman, Qiaomei Fu, Nadin Rohland, Gabriel Renaud, Yaniv Erlich, Thomas Willems, Carla Gallo, Jeffrey P. Spence, Yun S. Song, Giovanni Poletti, Francois Balloux, George van Driem, Peter de Knijff, Irene Gallego Romero, Aashish R. Jha, Doron M. Behar, Claudio M. Bravi, Cristian Capelli, Tor Hervig, Andres Moreno-Estrada, Olga L. Posukh, Elena Balanovska, Oleg Balanovsky, Sena Karachanak-Yankova, Hovhannes Sahakyan, Draga Toncheva, Levon Yepiskoposyan, Chris Tyler-Smith, Yali Xue, M. Syafiq Abdullah, Andres Ruiz-Linares, Cynthia M. Beall, Anna Di Rienzo, Choongwon Jeong, Elena B. Starikovskaya, Ene Metspalu, Jüri Parik, Richard Villems, Brenna M. Henn, Ugur Hodoglugil, Robert Mahley, Antti Sajantila, George Stamatoyannopoulos, Joseph T. S. Wee, Rita Khusainova, Elza Khusnutdinova, Sergey Litvinov, George Ayodo, David Comas, Michael F. Hammer, Toomas Kivisild, William Klitz, Cheryl A. Winkler, Damian Labuda, Michael Bamshad, Lynn B. Jorde, Sarah A. Tishkoff, W. Scott Watkins, Mait Metspalu, Stanislav Dryomov, Rem Sukernik, Lalji Singh, Kumarasamy Thangaraj, Svante Pääbo, Janet Kelso, Nick Patterson & David Reich

Here we report the Simons Genome Diversity Project data set: high quality genomes from 300 individuals from 142 diverse populations. These genomes include at least 5.8 million base pairs that are not present in the human reference genome. Our analysis reveals key features of the landscape of human genome variation, including that the rate of accumulation of mutations has accelerated by about 5 % in non-Africans compared to Africans since divergence. We show that the ancestors of some pairs of present-day human populations were substantially separated by 100,000 years ago, well before the archaeologically attested onset of behavioural modernity. We also demonstrate that indigenous Australians, New Guineans and Andamanese do not derive substantial ancestry from an early dispersal of modern humans; instead, their modern human ancestry is consistent with coming from the same source as that of other nonAfricans.

PAGANI 2016

Luca Pagani et al., *Genomic analyses inform on migration events during the peopling of Eurasia.* nature **538** (2016), 238–242.

n538-0238-Supplement1.pdf, n538-0238-Supplement2.xlsx

Luca Pagani, Daniel John Lawson, Evelyn Jagoda, Alexander Mörseburg, Anders Eriksson, Mario Mitt, Florian Clemente, Georgi Hudjashov, Michael DeGiorgio, Lauri Saag, Jeffrey D. Wall, Alexia Cardona, Reedik Mägi, Melissa A. Wilson Sayres, Sarah Kaewert, Charlotte Inchley, Christiana L. Scheib, Mari Järve, Monika Karmin, Guy S. Jacobs, Tiago Antao, Florin Mircea Iliescu, Alena Kushniarevich, Qasim Ayub, Chris Tyler-Smith, Yali Xue, Bayazit Yunusbayev, Kristiina Tambets, Chandana Basu Mallick, Lehti Saag, Elvira Pocheshkhova, George Andriadze, Craig Muller, Michael C. Westaway, David M. Lambert, Grigor Zoraqi, Shahlo Turdikulova, Dilbar Dalimova, Zhaxylyk Sabitov, Gazi Nurun Nahar Sultana, Joseph Lachance, Sarah Tishkoff, Kuvat Momynaliev, Jainagul Isakova, Larisa D. Damba, Marina Gubina, Pagbajabyn Nymadawa, Irina Evseeva, Lubov Atramentova, Olga Utevska, François-Xavier Ricaut, Nicolas Brucato, Herawati Sudoyo, Thierry Letellier, Murray P. Cox, Nikolay A. Barashkov, Vedrana Škaro, Lejla Mulahasanović, Dragan Primorac, Hovhannes Sahakyan, Maru Mormina, Christina A. Eichstaedt, Daria V. Lichman, Syafiq Abdullah, Gyaneshwer Chaubey, Joseph T. S. Wee, Evelin Mihailov, Alexandra Karunas, Sergei Litvinov, Rita Khusainova, Natalya Ekomasova, Vita Akhmetova, Irina Khidiyatova, Damir Marjanoviæ, Levon Yepiskoposyan, Doron M. Behar, Elena Balanovska, Andres Metspalu, Miroslava Derenko, Boris Malyarchuk, Mikhail Voevoda, Sardana A. Fedorova, Ludmila P. Osipova, Marta Mirazón Lahr, Pascale Gerbault, Matthew Leavesley, Andrea Bamberg Migliano, Michael Petraglia, Oleg Balanovsky, Elza K. Khusnutdinova, Ene Metspalu, Mark G. Thomas, Andrea Manica, Rasmus Nielsen, Richard Villems, Eske Willerslev, Toomas Kivisild,2 & Mait Metspalu

High-coverage whole-genome sequence studies have so far focused on a limited number1 of geographically restricted populations2–5, or been targeted at specific diseases, such as cancer6. Nevertheless, the availability of high-resolution genomic data has led to the development of new methodologies for inferring population history7–9 and refuelled the debate on the mutation rate in humans10. Here we present the Estonian Biocentre Human Genome Diversity Panel (EGDP), a dataset of 483 high-coverage human genomes from 148 populations worldwide, including 379 new genomes from 125 populations, which we group into diversity and selection sets. We analyse this dataset to refine estimates of continent-wide patterns of heterozygosity, long- and short-distance gene flow, archaic admixture, and changes in effective population size through time as well as for signals of positive or balancing selection. We find a genetic signature in present-day Papuans that suggests that at least 2 % of their genome originates from an early and largely extinct expansion of anatomically modern humans (AMHs) out of Africa. Together with evidence from the western Asian fossil record11, and admixture between AMHs and Neanderthals predating the main Eurasian expansion12, our results contribute to the mounting evidence for the presence of AMHs out of Africa earlier than 75,000 years ago.

PAGEL 2016

Mark Pagel, *Lethal violence deep in the human lineage.* nature **538** (2016), 180–181.

Researchers estimate that the incidence of human lethal violence at the time of the origin of our species was about six times higher than for the average mammal, but about as violent as expected, given our great-ape ancestry.

The authors' estimates of rates of lethal violence in humans vary widely over time, in most cases too quickly to be attributable to genetic changes. Their palaeolithic samples have rates very close to the 2 % predicted at the origin of our species, but then rates rise to as high as 15–30 % (with high statistical uncertainty) in samples from between 3,000 and 500 years ago, before declining in contemporary populations (approximately 100 years ago to the present day). The rise tends to correlate with moving from an early pre-societal 'state of nature' to tribal groupings and then to organized political societies that have a warrior class.

TELENTI 2016

Amalio Telenti et al., *Deep sequencing of 10,000 human genomes.* PNAS **113** (2016), 11901–11906.

Amalio Telenti, Levi C. T. Pierce, William H. Biggs, Julia di Iulio, Emily H. M. Wong, Martin M. Fabani, Ewen F. Kirkness, Ahmed Moustafa, Naisha Shah, Chao Xie, Suzanne C. Brewerton, Nadeem Bulsara, Chad Garner, Gary Metzker, Efren Sandoval, Brad A. Perkins, Franz J. Och, Yaron Turpaz & J. Craig Venter

We report on the sequencing of 10,545 human genomes at 30×–40× coverage with an emphasis on quality metrics and novel variant and sequence discovery. We find that 84 % of an individual human genome can be sequenced confidently. This high-confidence region includes 91.5 % of exon sequence and 95.2 % of known pathogenic variant positions. We present the distribution of over 150 million single-nucleotide variants in the coding and noncoding genome. Each newly sequenced genome contributes an average of 8,579 novel variants. In addition, each genome carries on average 0.7 Mb of sequence that is not found in the main build of the hg38 reference genome. The density of this catalog of variation allowed us to construct high-resolution profiles that define genomic sites that are highly intolerant of genetic variation. These results indicate that the data generated by deep genome sequencing is of the quality necessary for clinical use.

Keywords: genomics | noncoding genome | human genetic diversity

Significance: Large-scale initiatives toward personalized medicine are driving a massive expansion in the number of human genomes being sequenced. Therefore, there is an urgent need to define quality standards for clinical use. This includes deep coverage and sequencing accuracy of an individual's genome. Our work represents the largest effort to date in sequencing human genomes at deep coverage with these new standards. This study identifies over 150 million human variants, a majority of them rare and unknown. Moreover, these data identify sites in the genome that are highly intolerant to variation—possibly essential for life or health. We conclude that high-coverage genome sequencing provides accurate detail on human variation for discovery and clinical applications.

TUCCI 2016

Serena Tucci & Joshua M. Akey, *A map of human wanderlust*. nature **538** (2016), 179–180.

Genetic studies of individuals from geographically diverse human populations provide insights into the dispersal of modern humans across the globe and how geography shaped genomic variation.

However, neither Mallick et al. nor Malaspinas et al. exclude the possibility of multiple out-of-Africa dispersals. Indeed, their models are consistent with earlier dispersals, as long as these early voyagers made little or no contribution to the gene pool of contemporary non-African populations (which is essentially what Pagani et al. find). Studies of ancient DNA clearly show that large-scale population turnovers have happened throughout human history: populations that once lived in Eurasia, for example, vanished without a trace, except for their bones11,12. Thus, although some differences between the proposed models are yet to be reconciled, they are not as disparate as they might seem to be.

The three studies also provide resources to better define models of genetic mixing between modern humans and their archaic hominin relatives, such as Neanderthals and Denisovans. Malaspinas and colleagues propose that the genomes of present-day Aboriginal Australians might harbour traces of an ancient liaison with an unknown hominin group. Although evidence for gene flow from an unknown hominin group is tentative, it highlights the potentially surprising things that can be learnt from a comprehensive sampling of human genomic variation.

Archäologie

EGGERT 2000

Manfred K. H. Eggert, *Bedeutung der Ethnoarchäologie*. In: MANFRED K. H. EGGERT (Hrsg.), *Prähistorische Archäologie, Konzepte und Methoden*. Uni-Taschenbücher 2092 (Tübingen ^{4}2012), 361–381.

EGGERT 2014

Manfred K. H. Eggert, *Ethnoarchäologie*. In: SABINE WOLFRAM & DOREEN MÖLDERS (Hrsg.), *Schlüsselbegriffe der Prähistorischen Archäologie*. Tübinger Archäologische Taschenbücher 11 (Münster 2014), 81–85.

Biologie

GÓMEZ 2016

José María Gómez, Miguel Verdú, Adela González-Megías & Marcos Méndez, *The phylogenetic roots of human lethal violence*. nature **538** (2016), 233–237.

n538-0233-Supplement.pdf

The psychological, sociological and evolutionary roots of conspecific violence in humans are still debated, despite attracting the attention of intellectuals for over two millennia1–11. Here we propose a conceptual approach towards understanding these roots based on the assumption that aggression in mammals, including humans, has a significant phylogenetic component. By compiling sources of mortality from a comprehensive sample of mammals, we assessed the percentage of deaths due to conspecifics and, using phylogenetic comparative tools, predicted this value for humans. The proportion of human deaths phylogenetically predicted to be caused by interpersonal violence stood at 2 %. This value was similar to the one phylogenetically inferred for the evolutionary ancestor of primates and apes, indicating that a certain level of lethal violence arises owing to our position within the phylogeny of mammals. It was also similar to the percentage seen in prehistoric bands and tribes, indicating that we were as lethally violent then as common mammalian evolutionary history would predict. However, the level of lethal violence has changed through human history and can be associated with changes in the socio-political organization of human populations. Our study provides a detailed phylogenetic and historical context against which to compare levels of lethal violence observed throughout our history.

HELDSTAB 2016

Sandra A. Heldstab, Carel P. van Schaik & Karin Isler, *Being fat and smart, A comparative analysis of the fat-brain trade-off in mammals*. Journal of Human Evolution **100** (2016), 25–34.

JHumEvo100-0025-Supplement1.docx, JHumEvo100-0025-Supplement2.xlsx

Humans stand out among non-aquatic mammals by having both an extremely large brain and a relatively large amount of body fat. To understand the evolution of this human peculiarity we report a phylogenetic comparative study of 120 mammalian species, including 30 primates, using seasonal variation in adult body mass as a proxy of the tendency to store fat. Species that rely on storing fat to survive lean periods are expected to be less active because of higher costs of locomotion and have increased predation risk due to reduced agility. Because a fat-storage strategy reduces the net cognitive benefit of a large brain without reducing its cost, such species should be less likely to evolve a larger brain than non-fat-storing species. We therefore predict that the two strategies to buffer food shortages (storing body fat and cognitive flexibility) are compensatory, and therefore predict negative co-evolution between relative brain size and seasonal variation in body mass. This trade-off is expected to be stronger in predominantly arboreal species than in more terrestrial ones, as the cost of transporting additional adipose depots is higher for climbing than for horizontal locomotion. We did, indeed, find a significant negative correlation between brain size and coefficient of variation (CV) in body mass in both sexes for the subsample of arboreal species, both in all mammals and within primates. In predominantly terrestrial species, in contrast, this correlation was not significant. We therefore suggest that the adoption of habitually terrestrial locomotor habits, accompanied by a reduced reliance on climbing, has allowed for a primate of our body size the unique human combination of unusually large brains and unusually large adipose depots.

Keywords: Locomotion costs | Bipedalism | Terrestriality | Body fat | Brain size | Seasonality

Judentum

Reichmann 1974

Eva G. Reichmann, *Max Horkheimer the Jew, Critical Theory and Beyond*. Leo Baeck Institute Year Book **19** (1974), 181–195.

'Thou shalt not make a graven image of God' says the Bible. You cannot depict the absolute good. The devout Jew tries to avoid if possible the word 'God'; he does not spell it out, he makes a sign instead [. . .] Should we not ask ourselves why this shyness exists ? No other religion apart from Judaism knows it. I believe it exists because what matters primarily to the Jewish religion is not so much what God is as what Man is. In the same way Critical Theory calls the Absolute cautiously 'the Other'. What instigates me is the challenge to apply the theological idea to a sensible theory of society.

Klima

Chen 2016

Nan Chen & Andrew J. Majda, *Simple dynamical models capturing the key features of the Central Pacific El Niño*. PNAS **113** (2016), 11732–11737.

The Central Pacific El Niño (CP El Niño) has been frequently observed in recent decades. The phenomenon is characterized by an anomalous warm sea surface temperature (SST) confined to the central Pacific and has different teleconnections from the traditional El Niño. Here, simple models are developed and shown to capture the key mechanisms of the CP El Niño. The starting model involves coupled atmosphere–ocean processes that are deterministic, linear, and stable. Then, systematic strategies are developed for incorporating several major mechanisms of the CP El Niño into the coupled system. First, simple nonlinear zonal advection with no ad hoc parameterization of the background SST gradient is introduced that creates coupled nonlinear advective modes of the SST. Secondly, due to the recent multidecadal strengthening of the easterly trade wind, a stochastic parameterization of the wind bursts including a mean easterly tradewind anomaly is coupled to the simple atmosphere–ocean processes. Effective stochastic noise in the wind burst model facilitates the intermittent occurrence of the CP El Niño with realistic amplitude and duration. In addition to the anomalous warm SST in the central Pacific, other major features of the CP El Niño such as the rising branch of the anomalous Walker circulation being shifted to the central Pacific and the eastern Pacific cooling with a shallow thermocline are all captured by this simple coupled model. Importantly, the coupled model succeeds in simulating a series of CP El Niño that lasts for 5 y, which resembles the two CP El Niño episodes during 1990–1995 and 2002–2006.

Keywords: nonlinear zonal advection | strengthening of the easterly trade wind | effective stochastic noise | Walker circulation

Significance: The Central Pacific El Niño (CP El Niño) has been frequently observed in recent decades. The phenomenon is characterized by an anomalous warm sea surface temperature (SST) confined to the central Pacific and has different teleconnections from the traditional El Niño with major societal impact. Here, a simple modeling framework is developed and shown to capture the key mechanisms of the CP El Niño. In addition to the SST, other major characteristics of the CP El Niño such as the rising branch of the anomalous Walker circulation being shifted to the central Pacific and the eastern Pacific cooling with a shallow thermocline are all captured by this simple coupled model. Key features of the model are nonlinear advection of SST and effective stochastic wind bursts.

Osprey 2016

Scott M. Osprey et al., *An unexpected disruption of the atmospheric quasi-biennial oscillation.* science **353** (2016), 1424–1427.

Scott M. Osprey, Neal Butchart, Jeff R. Knight, Adam A. Scaife, Kevin Hamilton, James A. Anstey, Verena Schenzinger & Chunxi Zhang

One of the most repeatable phenomena seen in the atmosphere, the quasi-biennial oscillation (QBO) between prevailing eastward and westward wind jets in the equatorial stratosphere (approximately 16 to 50 kilometers altitude), was unexpectedly disrupted in February 2016. An unprecedented westward jet formed within the eastward phase in the lower stratosphere and cannot be accounted for by the standard QBO paradigm based on vertical momentum transport. Instead, the primary cause was waves transporting momentum from the Northern Hemisphere. Seasonal forecasts did not predict the disruption, but analogous QBO disruptions are seen very occasionally in some climate simulations. A return to more typical QBO behavior within the next year is forecast, although the possibility ofmore frequent occurrences of similar disruptions is projected for a warming climate.

Snyder 2016

Carolyn W. Snyder, *Evolution of global temperature over the past two million years.* nature **538** (2016), 226–228.

n538-0226-Supplement1.pdf, n538-0226-Supplement2.xlsx

Reconstructions of Earth's past climate strongly influence our understanding of the dynamics and sensitivity of the climate system. Yet global temperature has been reconstructed for only a few isolated windows of time1,2, and continuous reconstructions across glacial cycles remain elusive. Here I present a spatially weighted proxy reconstruction of global temperature over the past 2 million years estimated from a multi-proxy database of over 20,000 sea surface temperature point reconstructions. Global temperature gradually cooled until roughly 1.2 million years ago and cooling then stalled until the present. The cooling trend probably stalled before the beginning of the mid-Pleistocene transition3, and predated the increase in the maximum size of ice sheets around 0.9 million years ago4–6. Thus, global cooling may have been a precondition for, but probably is not the sole causal mechanism of, the shift to quasi-100,000-year glacial cycles at the mid-Pleistocene transition. Over the past 800,000 years, polar amplification (the amplification of temperature change at the poles relative to global temperature change) has been stable over time, and global temperature and atmospheric greenhouse gas concentrations have been closely coupled across glacial cycles. A comparison of the new temperature reconstruction with radiative forcing from greenhouse gases estimates an Earth system sensitivity of 9 degrees Celsius (range 7 to 13 degrees Celsius, 95 per cent credible interval) change in global average surface temperature per doubling of atmospheric carbon dioxide over millennium timescales. This result suggests that stabilization at today's greenhouse gas levels may already commit Earth to an eventual total warming of 5 degrees Celsius (range 3 to 7 degrees Celsius, 95 per cent credible interval) over the next few millennia as ice sheets, vegetation and atmospheric dust continue to respond to global warming.

Kultur

ERARD 2016

Michael Erard, *Solving Australia's Language Puzzle.* science **353** (2016), 1357–1359.

Methods borrowed from evolutionary biology show how people spread across the continent, giving birth to new languages.

The 25 Aboriginal languages still being passed to new generations make up one of the last and most diverse great hunter-gatherer linguistic groups left. So understanding how they and their extinct relatives diversified could open a window on how language itself emerged among small social groups in the distant human past. "We need to look at places like Australia, which offer models of language diversification closest to the earliest state that shaped humankind," Evans says.

To the researchers' amazement, the genetic pattern mirrored the linguistic one. "It's incredible that those two trees match. None of us expected that," says paleoanthropologist Michael Westaway of Griffith University, Nathan, in Australia, a co-author on the Willerslev paper. "But it's confusing: The [genetic splits] date to 30,000 years ago or more but the linguistic divisions are only maybe 6000 years old." Willerslev says he first thought the languages must be much older than thought. "But the linguists told me, 'no way."' Both types of data also show that the population expanded from the northeast to the southwest. This migration occurred within the last 10,000 years and likely came in successive waves, Bowern says, in which existing languages were overlaid by new ones. This expansion also seems to correspond with a stone tool innovation called a backed edge blade. But the accompanying gene flow was just a trickle, suggesting that only a few people had an outsize cultural impact, Willerslev says. "It's like you had two men entering a village, convincing everyone to speak a new language and adopt new tools, having a little sexual interaction, then disappearing," he says. Then the new languages continued to develop, following the older patterns of population separation. "It's really strange but it's the best way we can interpret the data at this stage."

KAMEDA 2016

Tatsuya Kameda, Keigo Inukai, Satomi Higuchi, Akitoshi Ogawa, Hackjin Kim, Tetsuya Matsuda & Masamichi Sakagami, *Rawlsian maximin rule operates as a common cognitive anchor in distributive justice and risky decisions.* PNAS **113** (2016), 11817–11822.

Distributive justice concerns the moral principles by which we seek to allocate resources fairly among diverse members of a society. Although the concept of fair allocation is one of the fundamental building blocks for societies, there is no clear consensus on how to achieve “socially just” allocations. Here, we examine neurocognitive commonalities of distributive judgments and risky decisions. We explore the hypothesis that people’s allocation decisions for others are closely related to economic decisions for oneself at behavioral, cognitive, and neural levels, via a concern about the minimum, worst-off position. In a series of experiments using attention-monitoring and brain-imaging techniques, we investigated this “maximin” concern (maximizing the minimum possible payoff) via responses in two seemingly disparate tasks: third-party distribution of rewards for others, and choosing gambles for self. The experiments revealed three robust results: (i) participants’ distributive choices closely matched their risk preferences—”Rawlsians,” who maximized theworst-off position in distributions for others, avoided riskier gambles for themselves,whereas “utilitarians,” who favored the largesttotal distributions, preferred riskier but more profitable gambles; (ii) across such individual choice preferences, however, participants generally showed the greatest spontaneous attention to information about the worst possible outcomes in both tasks; and (iii) this robust concern about the minimum outcomes was correlated with activation of the right temporoparietal junction (RTPJ), the region associated with perspective taking. The results provide convergent evidence that social distribution for others is psychologically linked to risky decision making for self, drawing on common cognitive–neural processes with spontaneous perspective taking of the worst-off position.

Keywords: distributive justice | risky decisions | maximin rule | perspective taking | right temporoparietal junction

Significance: Distributive justice is a highly controversial issue across many societies. Compared with the accumulation of various normative (”ought”) theories by philosophers over the centuries, our empirical (”is”) understanding of people’s distributive judgments remains insufficient. In a series of experiments, we show that the “maximin” concern (maximizing the minimum possible payoff) operates as a strong cognitive anchor in both distributive decisions for others and economic decisions for self, and that the right temporoparietal junction, associated with perspective taking, plays a key role in this linkage. Our approach illustrates how rigorous methods from behavioral, cognitive, and neural sciences can be combined to shed light on functional elements of distributive justice in our minds, and potential neural underpinnings shared by other nonsocial decisions.

KAPPES 2016

Andreas Kappes, Guy Kahane & M. J. Crockett, *From risk to fairness.* PNAS **113** (2016), 11651–11653.

A key insight of this work is that considering the worst possible outcome is a common feature of both risky and distributive choices. In the former, we imagine ourselves on the losing end of the bet; in the latter, we take the perspective of the least fortunate recipient. Thus, just as distributive choices involve a conflict of interests between individuals, risky choices can be described as a conflict of interest between lucky and unlucky selves. Others have used a similar logic to show that intertemporal choices between immediate and delayed rewards resemble a kind of social dilemma between present and future selves. The common thread binding all these kinds of decisions is perspective taking, which has been linked to the right temporoparietal junction (RTPJ).

Intriguingly, although most participants used similar strategies for distributive and risky decisions, they were significantly more likely to follow a maximin strategy for distributive decisions. This behavioral tendency to be more risk-averse for others than self was reflected in the neural data, where connectivity between RTPJ and caudate was stronger for distributive than risky choices. These findings may indicate that the worst possible outcome carries more weight when deciding for others than for self, perhaps because choosing for others has potential moral consequences whereas choosing for oneself does not. This idea finds additional support in a recent study where participants chose whether to inflict painful electric shocks on either themselves or an anonymous other person in exchange for money. Strikingly, most people were more averse to inflicting pain on others than themselves. One potential explanation is that people were more uncertain about how others would experience the shocks, and therefore were afraid that an amount of pain acceptable for them might be unbearable for the other person. This uncertainty could have induced a sort of risk premium on the moral costs of imposing potentially intolerable pain on another, leading people to deploy a pain-minimizing strategy when deciding about others' pain but a profit-maximizing strategy when deciding about their own pain—just as many participants in the study by Kameda et al. were loss-minimizing for distributive decisions affecting others but profit-maximizing for risky decisions affecting only themselves.

Mesolithikum

Rowley-Conwy 2011

Peter Rowley-Conwy & Robert Layton, *Foraging and farming as niche construction*, *Stable and unstable adaptations*. Phil. Trans. Royal Society B **366** (2011), 849–862.

All forager (or hunter–gatherer) societies construct niches, many of them actively by the concentration of wild plants into useful stands, small-scale cultivation, burning of natural vegetation to encourage useful species, and various forms of hunting, collectively termed 'low-level food production'. Many such niches are stable and can continue indefinitely, because forager populations are usually stable. Some are unstable, but these usually transform into other foraging niches, not geographically expansive farming niches. The Epipalaeolithic (final hunter–gatherer) niche in the Near East was complex but stable, with a relatively high population density, until destabilized by an abrupt climatic change. The niche was unintentionally transformed into an agricultural one, due to chance genetic and behavioural attributes of some wild plant and animal species. The agricultural niche could be exported with modifications over much of the Old World. This was driven by massive population increase and had huge impacts on local people, animals and plants wherever the farming niche was carried. Farming niches in some areas may temporarily come close to stability, but the history of the last 11 000 years does not suggest that agriculture is an effective strategy for achieving demographic and political stability in the world's farming populations. Keywords: hunter–gatherer; forager; farmer; niche construction; origins of agriculture; low-level food production

Metallzeiten

Ünlü 2016

Elif Ünlü, *The Handle Wagging The Cup – formal aspects of alcohol consumption in the transfer of ideology*, *Anatolia and the Aegean towards the end of the third millennium BC*. Oxford Journal of Archaeology **35** (2016), 345–358.

Fermented drinks have been socially and economically important since their advent, not only because they are functionally significant in preserving calories, but also as value-added foodstuffs incorporated into symbolically important ceremonies and feasts to increase the social value of an individual or a group's status. Towards the end of the third millennium BC, just as wine was becoming an important commodity, the manifestation of this emphasis on the communal consumption of alcoholic beverages can be observed in the material culture of Anatolia and the Aegean with the so-called 'west Anatolian drinking set' consisting of drinking cups with characteristically oversized handles and beak-spouted pitchers. Against the backdrop of the socio-economic reasons for the distribution of this particular drinking set over a wide geographical area, the focus of this article is on their impact upon the prevailing local pottery traditions and the local adaptation of these vessels into the traditional repertoire where the importance of the oversized handles is recognized.

Mittelpaläolithikum

WADE 2016

Lizzie Wade, *Neandertals made jewelry, proteins confirm.* science **353** (2016), 1350.

"Landmark" study firmly links sophisticated artifacts from France to our extinct cousins.