Liste erstellt am 2015-06-18

References

Aktuell

CALLAWAY 2015

Ewen Callaway, *DNA deluge reveals Bronze Age secrets.* nature **522** (2015), 140–141.

Population-scale studies of ancient genomes hint at roots of technology, languages and diet.

“Christ, what does this mean?” says Greger Larson, an evolutionary geneticist at the University of Oxford, UK. “In another five years, we’ll be talking about tens of thousands of ancient genomes.”

“It’s an interesting time, because the technology is moving faster than our ability to ask questions of it,” says Larson, whose lab has also amassed around 4,000 samples from ancient dogs and wolves to chart the origins of domestic dogs. “Let’s just sequence everything and ask questions later.”

CERNANSKY 2015

Rachel Cernansky, *Super vegetables.* nature **522** (2015), 146–148.

Long overlooked in parts of Africa, indigenous greens are now capturing attention for their nutritional and environmental benefits.

Research by Abukutsa and others shows that amaranth greens, spider plant and African nightshade pack substantial amounts of protein and iron — in many cases, more than kale and cabbage. These vegetables are generally rich in calcium and folate as well as vitamins A, C and E. In recent years, Abukutsa has been studying how to maximize nutritional benefits using different cooking methods. Compared with raw vegetables, boiled and fried greens contain much more usable iron and could help to combat the high rates of anaemia in parts of East Africa. They can also be important sources of protein, she says. “Some people just live on vegetables, and they cannot maybe afford meat.”

But efforts to improve indigenous vegetables could come at a cost, say researchers. If breeders focus only on increasing yields, they could accidentally eliminate nutritional benefits. And if farmers seek to drive up production through monocrop agriculture — planting just one crop — they risk losing some of the qualities that make these vegetables such a draw. Plots with single crops, for example, face higher risks of being completely wiped out by insects or diseases.

GREIVES 2015

Timothy J. Greives et al., *Costs of sleeping in*, *Circadian rhythms influence cuckoldry risk in a songbird.* Functional Ecology (2015), preprint, 1–8. DOI:10.1111/1365-2435.12440.

FuncEcol2015-Greives-Supplement1.pdf, FuncEcol2015-Greives-Supplement2.docx

Timothy J. Greives, Sjouke A. Kingma, Bart Kranstauber, Kim Mortega, Martin Wikelski, Kees van Oers, Christa Mateman, Glen A. Ferguson, Giulia Beltrami and Michaela Hau

1. Circadian (i.e. daily) regulation of behaviours is thought to provide fitness benefits to organisms by enabling them to anticipate diel changes in the environment, such as sunrise.

2. A common behaviour among socially monogamous songbirds that usually takes place in the early mornings is extra-pair mating, that is copulating with partners outside of the social pair bond.
3. Thus, variation in when individuals begin their daily activity may influence their reproductive success; early risers may be better able to gain copulations and guard their partners, thus minimizing their risk of being cuckolded compared with late risers. Sexual selection may thus play an important role in shaping circadian behaviours, but this assumption has yet to be tested in free-living animals.
4. Here, we experimentally weakened endogenous circadian rhythmicity, and thus, anticipation of dawn in male great tits (Parus major) in the wild through the subcutaneous administration of implants filled with melatonin shortly before egg-laying began in this population. Melatonin is a hormone released during the dark phase at night and is one important cue animals use to entrain their circadian clock.
5. Experimental individuals delayed the onset of daily activity compared with controls and were more likely to be cuckolded compared with control males. Manipulation did not alter other behavioural traits observed; no difference between treatments was observed in activity levels during the day or in the end time of daily activity.
6. These results strongly support the assumption that selection, particularly sexual selection, shapes the circadian phenotypes of wild vertebrates which enable anticipation of important and predictive diel changes in an individual's biotic and abiotic environment.

Keywords: biological rhythms, daily rhythms, melatonin, passerine

HOCKINGS 2015

Kimberley J. Hockings et al., *Tools to tipple, Ethanol ingestion by wild chimpanzees using leaf-sponges.* Royal Society Open Science **2** (2015), 150150.

RSocOpenSci02-150150-Supplement1.mp4, RSocOpenSci02-150150-Supplement2.pdf, RSocOpenSci02-150150-Supplement3.docx

Kimberley J. Hockings, Nicola Bryson-Morrison, Susana Carvalho, Michiko Fujisawa, Tatyana Humle, William C. McGrew, Miho Nakamura, Gaku Ohashi, Yumi Yamanashi, Gen Yamakoshi & Tetsuro Matsuzawa

African apes and humans share a genetic mutation that enables them to effectively metabolize ethanol. However, voluntary ethanol consumption in this evolutionary radiation is documented only inmodern humans. Here, we report evidence of the long-term and recurrent ingestion of ethanol from the raffia palm (Raphia hookeri, Arecaceae) by wild chimpanzees (Pan troglodytes verus) at Bossou in Guinea, West Africa, from 1995 to 2012. Chimpanzees at Bossou ingest this alcoholic beverage, often in large quantities, despite an average presence of ethanol of 3.1 % alcohol by volume (ABV) and up to 6.9 % ABV. Local people tap raffia palms and the sap collects in plastic containers, and chimpanzees use elementary technology—a leafy tool—to obtain this fermenting sap. These data show that ethanol does not act as a deterrent to feeding in this community of wild apes, supporting the idea that the last common ancestor of living African apes and modern humans was not averse to ingesting foods containing ethanol.

Keywords: ethanol ingestion | elementary tool-use | great apes | raffia palm

KE 2015

Qing Ke, Emilio Ferrara, Filippo Radicchi & Alessandro Flammini, *Defining and identifying Sleeping Beauties in science.* PNAS **112** (2015), 7426–7431.

A Sleeping Beauty (SB) in science refers to a paper whose importance is not recognized for several years after publication. Its citation history exhibits a long hibernation period followed by a sudden spike of popularity. Previous studies suggest a relative scarcity of SBs. The reliability of this conclusion is, however, heavily dependent on identification methods based on arbitrary threshold parameters for sleeping time and number of citations, applied to small or monodisciplinary bibliographic datasets. Here we present a systematic, large-scale, and multidisciplinary analysis of the SB phenomenon in science. We introduce a parameter-free measure that quantifies the extent to which a specific paper can be considered an SB. We apply our method to 22 million scientific papers published in all disciplines of natural and social sciences over a time span longer than a century. Our results reveal that the SB phenomenon is not exceptional. There is a continuous spectrum of delayed recognition where both the hibernation period and the awakening intensity are taken into account. Although many cases of SBs can be identified by looking at monodisciplinary bibliographic data, the SB phenomenon becomes much more apparent with the analysis of multidisciplinary datasets, where we can observe many examples of papers achieving delayed yet exceptional importance in disciplines different from those where they were originally published. Our analysis emphasizes a complex feature of citation dynamics that so far has received little attention, and also provides empirical evidence against the use of short-term citation metrics in the quantification of scientific impact.

Keywords: delayed recognition | Sleeping Beauty | bibliometrics

Significance: Scientific papers typically have a finite lifetime: their rate to attract citations achieves its maximum a few years after publication, and then steadily declines. Previous studies pointed out the existence of a few blatant exceptions: papers whose relevance has not been recognized for decades, but then suddenly become highly influential and cited. The Einstein, Podolsky, and Rosen “paradox” paper is an exemplar Sleeping Beauty. We study how common Sleeping Beauties are in science. We introduce a quantity that captures both the recognition intensity and the duration of the “sleeping” period, and show that Sleeping Beauties are far from exceptional. The distribution of such quantity is continuous and has power-law behavior, suggesting a common mechanism behind delayed but intense recognition at all scales.

Mohlenhoff 2015

Kathryn A. Mohlenhoff, Joan Brenner Coltrain & Brian F. Codding, *Optimal foraging theory and niche-construction theory do not stand in opposition*. PNAS **112** (2015), E3093.

However, in addressing the frameworks used to explain domestication, Zeder (1) presents optimal foraging theory (OFT) and niche-construction theory (NCT) as two mutually exclusive approaches. In order for NCB to make sense, economic decisions founded within OFT are useful. We agree with Zeder that in most research focusing on OFT models, researchers do not make NCB explicit, and agree that this outcome should be highlighted. Although Zeder’s recent article follows a discussion of whether or not these two approaches can be integrated, we believe that understanding the utility of both approaches is a more constructive outlook than the current and extremely polarized atmosphere permits.

Sweeney 2013

Latanya Sweeney, *Discrimination in Online Ad Delivery*. unknown **2013**, Jan. 28, 1–36. <`http://ssrn.com/abstract=2208240`>.

A Google search for a person’s name, such as “Trevon Jones”, may yield a personalized ad for public records about Trevon that may be neutral, such as “Looking for Trevon Jones? . . . “, or may be suggestive of an arrest record, such as “Trevon Jones, Arrested?...”. This writing investigates the delivery of these kinds of ads by Google AdSense using a sample of racially associated names and finds statistically significant discrimination in ad delivery based on searches of 2184 racially associated personal names across two websites. First names, previously identified by others as being assigned at birth to more black or white babies, are found predictive of race (88 % black, 96 % white), and those assigned primarily to black babies, such as DeShawn, Darnell and Jermaine, generated ads suggestive of an arrest in 81 to 86 percent of name searches on one website and 92 to 95 percent on the other, while those assigned at birth primarily to whites, such as Geoffrey, Jill and Emma, generated more neutral copy: the word “arrest” appeared in 23 to 29 percent of name searches on one site and 0 to 60 percent on the other. On the more ad trafficked website, a black—identifying name was 25 % more likely to get an ad suggestive of an arrest record.

A few names did not follow these patterns: Dustin, a name predominantly given to white babies, generated an ad suggestive of arrest 81 and 100 percent of the time. All ads return results for actual individuals and ads appear regardless of whether the name has an arrest record in the company’s database. Notwithstanding these findings, the company maintains Google received the same ad text for groups of last names (not first names), raising questions as to whether Google’s advertising technology exposes racial bias in society and how ad and search technology can develop to assure racial fairness.

Keywords: online advertising | public records | racial discrimination | data privacy | information retrieval | computers and society | search engine marketing

WITTMAACK 2015

Klaus Wittmaack, *The joys of research in retirement.* nature **522** (2015), 156.

ZEDER 2015

Melinda A. Zeder, *Human behavioral ecology needs a rethink that niche-construction theory can provide, Reply to Mohlenhoff et al.* PNAS **112** (2015), E3094.

Thus, far from arguing for some form of human exceptionalism by emphasizing the role of human agency in evolution, NCT provides a framework for understanding how human cognitive capacities fall within a larger set of mechanisms by which both humans and nonhuman organisms shape selective environments and codirect their evolution. Cultural niche construction, then, provides the “general theory of behavior” that Mohlenhoff et al. and others claim NCT lacks.

Anthropologie

DEAN 2001

Christopher Dean, Meave G. Leakey, Donald Reid, Friedemann Schrenk, Gary T. Schwartz, Christopher Stringer & Alan Walker, *Growth processes in teeth distinguish modern humans from Homo erectus and earlier hominins.* nature **414** (2001), 628–631.

A modern human-like sequence of dental development, as a proxy for the pace of life history, is regarded as one of the diagnostic hallmarks of our own genus Homo1 ± 3. Brain size, age at first reproduction, lifespan and other life-history traits correlate tightly with dental development. Here we report differences in enamel growth that show the earliest fossils attributed to Homo do not resemble modern humans in their development. We used daily incremental markings in enamel to calculate rates of enamel formation in 13 fossil hominins and identified differences in this key determinant of tooth formation time. Neither australopiths nor fossils currently attributed to early Homo shared the slow trajectory of enamel growth typical of modern humans; rather, both resembled modern and fossil African apes. We then reconstructed tooth formation times in australopiths, in the ≈1.5-Myr-old Homo erectus skeleton from Nariokotome, Kenya, and in another Homo erectus specimen, Sangiran S7-37 from Java. These times were shorter than those in modern humans. It therefore seems likely that truly modern dental development emerged relatively late in human evolution.

DEAN 2006

M. Christopher Dean, *Tooth microstructure tracks the pace of human life-history evolution*. Proc. Royal Society B **273** (2006), 2799–2808.

A number of fundamental milestones define the pace at which animals develop, mature, reproduce and age. These include the length of gestation, the age at weaning and at sexual maturity, the number of offspring produced over a lifetime and the length of life itself. Because a time-scale for dental development can be retrieved from the internal structure of teeth and many of these life-history variables tend to be highly correlated, we can discover more than might be imagined about fossil primates and more, in particular, about fossil hominids and our own evolutionary history. Some insights into the evolutionary processes underlying changes in dental development are emerging from a better understanding of the mechanisms controlling enamel and dentine formation. Our own 18–20-year period of growth and development probably evolved quite recently after ca 17 million years of a more ape-like life-history profile.

Keywords: life history; enamel; dentine; incremental markings; hominid; evolution

ITAN 2009

Yuval Itan, Adam Powell, Mark A. Beaumont, Joachim Burger & Mark G. Thomas, *The Origins of Lactase Persistence in Europe*. PLoS Computational Biology **5** (2009), e1000491. DOI:10.1371/journal.pcbi.1000491.

Lactase persistence (LP) is common among people of European ancestry, but with the exception of some African, Middle Eastern and southern Asian groups, is rare or absent elsewhere in the world. Lactase gene haplotype conservation around a polymorphism strongly associated with LP in Europeans (213,910 C/T) indicates that the derived allele is recent in origin and has been subject to strong positive selection. Furthermore, ancient DNA work has shown that the 213,910*T (derived) allele was very rare or absent in early Neolithic central Europeans. It is unlikely that LP would provide a selective advantage without a supply of fresh milk, and this has lead to a gene-culture coevolutionary model where lactase persistence is only favoured in cultures practicing dairying, and dairying is more favoured in lactase persistent populations. We have developed a flexible demic computer simulation model to explore the spread of lactase persistence, dairying, other subsistence practices and unlinked genetic markers in Europe and western Asia's geographic space. Using data on 213,910*T allele frequency and farming arrival dates across Europe, and approximate Bayesian computation to estimate parameters of interest, we infer that the 213,910*T allele first underwent selection among dairying farmers around 7,500 years ago in a region between the central Balkans and central Europe, possibly in association with the dissemination of the

Neolithic Linearbandkeramik culture over Central Europe. Furthermore, our results suggest that natural selection favouring a lactase persistence allele was not higher in northern latitudes through an increased requirement for dietary vitamin D. Our results provide a coherent and spatially explicit picture of the coevolution of lactase persistence and dairying in Europe.

KRAMER 2015

Karen L. Kramer & Erik Otárola-Castillo, *When mothers need others, The impact of hominin life history evolution on cooperative breeding.* Journal of Human Evolution **84** (2015), 16–24.

JHumEvo084-0016-Supplement.docx

The evolution of cooperative breeding is particularly complex in humans because many other traits that directly affect parental care (shorter birth intervals, increased offspring survivorship, juvenile dependence, and older ages at dispersal) also emerge during the Pleistocene. If human cooperative breeding is ancient, it likely evolved in a hominin lacking a fully modern life history. However, the impact that changing life history traits has on parental care and cooperative breeding has not been analytically investigated. We develop an exploratory model to simulate an economic problem that would have arisen over the course of hominin life history evolution to identify those transitions that produced the strongest pressures for cooperative childrearing. The model generates two central predictions. First, help within maternal-offspring groups can support early changes in juvenile dependence, dispersal age, birth intervals, and fertility. If so, maternal-juvenile cooperation may be an important but understudied step in the evolution of human cooperative breeding. Second, pressure to recruit adult cooperation is most pronounced under more derived conditions of late dispersal and later ages of juvenile dependence, with a strong interaction at short birth intervals. Our findings indicate that changes in life history traits that affect parental care are critical in considering background selective forces that shaped the evolution of cooperative breeding.

Keywords: Human evolution | Juvenility | Intergenerational transfers | Parental care

MOGGI-CECCHI 2001

Jacopo Moggi-Cecchi, *Questions of growth.* nature **414** (2001), 595–597.

The evolution of an extended childhood had implications for human society and culture. New analyses of dental development in fossil hominins suggest that our lengthy growth processes arose quite late in evolution.

Dean et al. propose that the developmental processes in H. erectus differ only slightly from those of earlier hominins (australopiths). This proposal is in agreement with the view that H. erectus/H. ergaster is only slightly different from australopiths in its relative brain size (there is suggested to be a relationship between an increase in brain size and extension of the postnatal period of development). The slow rate of enamel growth that is typical of modern humans, and is associated with an extended growth period, is first seen with the large-brained Neanderthals.

Second, the new results support the idea that specific morphological characters (such as brain size, enamel thickness or bipedalism), as observed or inferred in fossil specimens, cannot be interpreted in isolation to indicate affinities with modern humanity. It is becoming increasingly clear that many features thought to be typical of modern humans may have evolved more than once.

MOORJANI 2013

Priya Moorjani et al., *Genetic Evidence for Recent Population Mixture in India*. American Journal of Human Genetics **93** (2013), 422–438.

AmJHumGen93-0422-Supplement.pdf

Priya Moorjani, Kumarasamy Thangaraj, Nick Patterson, Mark Lipson, Po-Ru Loh, Periyasamy Govindaraj, Bonnie Berger, David Reich & Lalji Singh

Most Indian groups descend from a mixture of two genetically divergent populations: Ancestral North Indians (ANI) related to Central Asians, Middle Easterners, Caucasians, and Europeans; and Ancestral South Indians (ASI) not closely related to groups outside the subcontinent. The date of mixture is unknown but has implications for understanding Indian history. We report genome-wide data from 73 groups from the Indian subcontinent and analyze linkage disequilibrium to estimate ANI-ASI mixture dates ranging from about 1,900 to 4,200 years ago. In a subset of groups, 100 % of the mixture is consistent with having occurred during this period. These results show that India experienced a demographic transformation several thousand years ago, from a region in which major population mixture was common to one in which mixture even between closely related groups became rare because of a shift to endogamy.

PATTERSON 2012

Nick Patterson et al., *Ancient Admixture in Human History*. Genetics **192** (2012), 1065–1093.

Nick Patterson, Priya Moorjani, Yontao Luo, Swapan Mallick, Nadin Rohland, Yiping Zhan, Teri Genschoreck, Teresa Webster & David Reich

Population mixture is an important process in biology. We present a suite of methods for learning about population mixtures, implemented in a software package called ADMIXTOOLS, that support formal tests for whether mixture occurred and make it possible to infer proportions and dates of mixture. We also describe the development of a new single nucleotide polymorphism (SNP) array consisting of 629,433 sites with clearly documented ascertainment that was specifically designed for population genetic analyses and that we genotyped in 934 individuals from 53 diverse populations. To illustrate the methods, we give a number of examples that provide new insights about the history of human admixture. The most striking finding is a clear signal of admixture into northern Europe, with one ancestral population related to present-day Basques and Sardinians and the other related to present-day populations of northeast Asia and the Americas. This likely reflects a history of admixture between Neolithic migrants and the indigenous Mesolithic population of Europe, consistent with recent analyses of ancient bones from Sweden and the sequencing of the genome of the Tyrolean “Iceman.”

SMITH 2015

Alex R. Smith, Rachel N. Carmody, Rachel J. Dutton & Richard W. Wrangham, *The significance of cooking for early hominin scavenging*. Journal of Human Evolution **84** (2015), 62–70.

Meat scavenged by early Homo could have contributed importantly to a higher-quality diet. However, it has been suggested that because carrion would normally have been contaminated by bacteria it would have been dangerous and therefore eaten rarely prior to the advent of cooking. In this study, we quantified bacterial loads on two tissues apparently eaten by hominins, meat and bone marrow. We tested the following three hypotheses: (1) the bacterial loads on exposed surfaces of raw meat increase within 24 h to potentially dangerous levels, (2) simple roasting of meat on hot coals kills most bacteria, and (3) fewer bacteria grow on marrow than on meat, making marrow a relatively safe food. Our results supported all three hypotheses. Our experimental data imply that early hominins would have found it difficult to scavenge safely without focusing on marrow, employing strategies of carrion selection to minimize pathogen load, or cooking.

Keywords: Diet | Meat | Marrow | Bacteria | Hominin ecology | Chimpanzee

ZIHLMAN 2015

Adrienne L. Zihlman & Debra R. Bolter, *Body composition in Pan paniscus compared with Homo sapiens has implications for changes during human evolution*. PNAS **112** (2015), 7466–7471.

The human body has been shaped by natural selection during the past 4–5 million years. Fossils preserve bones and teeth but lack muscle, skin, fat, and organs. To understand the evolution of the human form, information about both soft and hard tissues of our ancestors is needed. Our closest living relatives of the genus Pan provide the best comparative model to those ancestors. Here, we present data on the body composition of 13 bonobos (Pan paniscus) measured during anatomical dissections and compare the data with Homo sapiens. These comparative data suggest that both females and males (i) increased body fat, (ii) decreased relative muscle mass, (iii) redistributed muscle mass to lower limbs, and (iv) decreased relative mass of skin during human evolution. Comparison of soft tissues between Pan and Homo provides new insights into the function and evolution of body composition.

Keywords: body composition | bonobo | Pan paniscus | human evolution | Homo sapiens

Significance: During human evolution, the body changed in shape, partially to accommodate bipedal locomotion. Concurrently, brain size underwent a threefold increase recorded in evidence from fossils and from comparative anatomy of chimpanzees, Homo sapiens' closest living relatives. Because soft tissues like muscle, skin, and fat do not fossilize, and little information is available on these components for the genus Pan, reconstructing tissue changes has primarily relied on what is known about humans. This study presents unique quantitative data on major body components of muscle, bone, skin, and fat of 13 bonobos (Pan paniscus) for interpreting evolutionary forces that have shaped the human form for survival in a savanna mosaic environment.

Bibel

FAGAN 2015

Brian Fagan, *Did Akhenaten's monotheism influence Moses?* Biblical Archaeology Review **41** (2015), iv, 42–49, 70–71.

Pharaoh Akhenaten, who abolished the Egyptian pantheon and instituted worship of a single deity, the sun-disk Aten, in the mid-14th century B.C , may have established the world's first monotheism. Did this influence the birth of Israelite monotheism?

Israelite monotheism developed through centuries of discussion, declarations of faith and interactions with other societies and other beliefs. In contrast, Akhenaten's monotheism developed very largely at the behest of a single, absolute monarch presiding over an isolated land, where the pharaoh's word was divine and secular law. It was an experiment that withered on the vine.

A great deal of scholarship has been devoted to Biblical monotheism and its origins, but, to an archaeologist schooled in the importance of accurate dating and historical contexts, there are no connections between two quite different forms of monotheism—the one an expression of pharaonic authority imposing religious conformity, the other a matter of profound abstraction. And it's important to realize that the cultural milieu of both Egyptian and Israelite religious beliefs were entirely different and far from compatible. There were two experiments in monotheism—the Egyptian one, which vanished, and the more abstract Israelite version that ensued and survived.

Mumcuoglu 2015

Madeleine Mumcuoglu & Yosef Garfinkel, *The puzzling doorways of Solomon's temple.* Biblical Archaeology Review **41** (2015), iv, 34–41.

In the Bible, the inner shrine of Solomon's Temple is described as having five mezuzot. What are they? The question has puzzled Biblical scholars for centuries. Does a recently discovered shrine model from Khirbet Qeiyafa hold the answer?

We do not know when the Biblical text describing the period of David and Solomon was composed—contemporaneously or hundreds of years later. From the Qeiyafa stone model, however, we can conclude that recessed doorframes, or mezuzot, were known in that region at that time, thus strengthening the Bible's claim to historicity in this detail of the Biblical tradition. It seems that after about 3,000 years, the Qeiyafa model shrine has definitely solved the mystery of the Biblical mezuzot.

Patterson 2015

The Gospel of Thomas, Translated by Stephen J. Patterson and James M. Robinson. Bible History Daily **2015**, June 3, 1–7.

Klima

Billups 2015

Katharina Billups, *Timing is everything during deglaciations.* nature **522** (2015), 163–164.

Links between various climate records for the North Atlantic Ocean and the Mediterranean Sea have helped to identify a potential mechanism that enhanced sea-level rise during the last interglacial time interval.

The revised chronology of the proxy records examined by Marino and co-workers points to a pivotal difference in climate dynamics between the most recent and the penultimate glacial-to-interglacial transitions, which are also known as Terminations I and II, respectively. Both are associated with times when summer insolation (incoming solar radiation) in the Northern Hemisphere and atmospheric carbon dioxide levels were increasing. One would therefore expect the ensuing ice-sheet melt-back behaviour to have been similar as well. But it was not.

Hartman 2015

Gideon Hartman, Erella Hovers, Jean-Jacques Hublin & Michael Richards, *Isotopic evidence for Last Glacial climatic impacts on Neanderthal gazelle hunting territories at Amud Cave, Israel.* Journal of Human Evolution **84** (2015), 71–82.

JHumEvo084-0071-Supplement.doc

The Middle Paleolithic site of Amud Cave, Israel, was occupied by Neanderthals at two different time periods, evidenced by two chronologically and stratigraphically distinct depositional sub-units (B4 and B2/B1) during MIS 4 and

MIS 3, respectively. The composition of both hunted large fauna and naturally-deposited micromammalian taxa is stable at the site over time, despite a $\approx$10 ky gap between the two occupation phases. However, while gazelle is the most ubiquitous hunted species throughout the occupation, isotopic analysis showed that there is a marked change in Neanderthal hunting ranges between the early (B4) and late (B2/B1) phases. Hunting ranges were reconstructed by comparing oxygen, carbon, and strontium isotopes from gazelle tooth enamel with modern isotope data from the Amud Cave region. This region is characterized by extensive topographic, lithological, and pedological heterogeneity. During the early occupation phase negative oxygen isotope values, low radiogenic 87Sr/86Sr ratios, and low Sr concentrations reveal restricted gazelle hunting in the high elevations west of Amud Cave. In the late occupation phase, hunting ranges became more diverse, but concentrate at low elevations closer to the site. Climatic proxies indicate that conditions were drier in the early occupation phase, which may have pushed gazelle populations into higher, more productive foraging areas. This study showed that Neanderthals adjusted their hunting territories considerably in relation to varying environmental conditions over the course of occupation in Amud Cave. It highlights the utility of multiple isotope analysis in enhancing the resolution of behavioral interpretations based on faunal remains and in reconstructing past hunting behaviors of Paleolithic hominins.

Keywords: Paleoclimate | Paleoenvironment | Middle Paleolithic | Carbon isotopes | Oxygen isotopes | Strontium isotopes

Marino 2015

G. Marino, E. J. Rohling, L. Rodríguez-Sanz, K. M. Grant, D. Heslop, A. P. Roberts, J. D. Stanford & J. Yu, *Bipolar seesaw control on last interglacial sea level.* nature **522** (2015), 197–201.

n522-0197-Supplement.pdf

Our current understanding of ocean–atmosphere–cryosphere interactions at ice-age terminations relies largely on assessments of the most recent (last) glacial–interglacial transition1–3, Termination I (T-I). But the extent to which T-I is representative of previous terminations remains unclear. Testing the consistency of termination processes requires comparison of time series of critical climate parameters with detailed absolute and relative age control.However, such age control has been lacking for even the penultimate glacial termination (T-II), which culminated in a sea-level highstand during the last interglacial period that was several metres above present4. Here we show that Heinrich Stadial 11 (HS11), a prominent North Atlantic cold episode5,6, occurred between 13561 and 13062 thousand years ago and was linked with rapid sea-level rise during T-II. Our conclusions are based on new and existing6–9 data for T-II and the last interglacial that we collate onto a single, radiometrically constrained chronology. The HS11 cold episode5,6 punctuated T-II and coincided directly with amajor deglacialmeltwater pulse, which predominantly entered the NorthAtlantic Ocean and accounted for about 70 per cent of the glacial–interglacial sea-level rise8,9. We conclude that, possibly in response to stronger insolation and CO2 forcing earlier in T-II, the relationship between climate and ice-volume changes differed fundamentally from that of T-I. In T-I, the major sea-level rise clearly post-dates3,10,11 Heinrich Stadial 1. We also find that HS11 coincided with sustained Antarctic warming, probably through a bipolar seesaw temperature response12, and propose that this heat gain at high southern latitudes promoted Antarctic ice-sheet melting that fuelled the last interglacial sea-level peak.

Metallzeiten

ALLENTOFT 2015

Morten E. Allentoft et al., *Population genomics of Bronze Age Eurasia*. nature **522** (2015), 167–172.

n522-0167-Supplement1.pdf, n522-0167-Supplement2.xlsx, n522-0167-Supplement3.xls, n522-0167-Supplement4.xlsx, n522-0167-Supplement5.xlsx, n522-0167-Supplement6.xlsx, n522-0167-Supplement7.xlsx, n522-0167-Supplement8.xlsx, n522-0167-Supplement9.xls

Morten E. Allentoft, Martin Sikora, Karl-Göran Sjögren, Simon Rasmussen, Morten Rasmussen, Jesper Stenderup, Peter B. Damgaard, Hannes Schroeder, Torbjörn Ahlström, Lasse Vinner, Anna-Sapfo Malaspinas, Ashot Margaryan, Tom Higham, David Chivall, Niels Lynnerup, Lise Harvig, Justyna Baron, Philippe Della Casa, Paweł Dąbrowski, Paul R. Duffy, Alexander V. Ebel, Andrey Epimakhov, Karin Frei, Mirosław Furmanek, Tomasz Gralak, Andrey Gromov, Stanisław Gronkiewicz, Gisela Grupe, Tamás Hajdu, Radosław Jarysz, Valeri Khartanovich, Alexandr Khokhlov, Viktória Kiss, Jan Kolář, Aivar Kriiska, Irena Lasak, Cristina Longhi, George McGlynn, Algimantas Merkevicius, Inga Merkyte, Mait Metspalu, Ruzan Mkrtchyan, Vyacheslav Moiseyev, László Paja, György Pálfi, Dalia Pokutta, Łukasz Pospieszny, T. Douglas Price, Lehti Saag, Mikhail Sablin, Natalia Shishlina, Václav Smrčka, Vasilii I. Soenov, Vajk Szeverényi, Gusztáv Tóth, Synaru V. Trifanova, Liivi Varul, Magdolna Vicze, Levon Yepiskoposyan, Vladislav Zhitenev, Ludovic Orlando, Thomas Sicheritz-Pontén, Søren Brunak, Rasmus Nielsen, Kristian Kristiansen & Eske Willerslev

The Bronze Age of Eurasia (around 3000–1000 BC) was a period of major cultural changes. However, there is debate about whether these changes resulted from the circulation of ideas or from human migrations, potentially also facilitating the spread of languages and certain phenotypic traits. We investigated this by using new, improved methods to sequence low-coverage genomes from 101 ancient humans from across Eurasia. We show that the Bronze Age was a highly dynamic period involving large-scale population migrations and replacements, responsible for shaping major parts of present-day demographic structure in both Europe and Asia. Our findings are consistent with the hypothesized spread of Indo-European languages during the Early Bronze Age. We also demonstrate that light skin pigmentation in Europeans was already present at high frequency in the Bronze Age, but not lactose tolerance, indicating a more recent onset of positive selection on lactose tolerance than previously thought.

HAAK 2015

Wolfgang Haak et al., *Massive migration from the steppe was a source for Indo-European languages in Europe*. nature **522** (2015), 207–211.

n522-0207-Supplement1.pdf, n522-0207-Supplement2.xlsx, n522-0207-Supplement3.zip, n522-0207-Supplement4.zip, n522-0207-Supplement5.zip, n522-0207-Supplement6.zip

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We generated genome-wide data from 69 Europeans who lived between 8,000–3,000 years ago by enriching ancient DNA libraries for a target set of almost 400,000 polymorphisms. Enrichment of these positions decreases the sequencing required for genome-wide ancient DNA analysis by a median of around 250-fold, allowing us to study an order of magnitude more individuals than previous studies1–8 and to obtain new insights about the past. We show that the populations ofWestern and Far Eastern Europe followed opposite trajectories between 8,000–5,000 years ago. At the beginning of the Neolithic period in Europe, 8,000–7,000 years ago, closely related groups of early farmers appeared in Germany, Hungary and Spain, different from indigenous hunter-gatherers, whereas Russia was inhabited by a distinctive population of hunter-gatherers with high affinity to a 24,000-year-old Siberian6. By 6,000–5,000 years ago, farmers throughout much of Europe had more hunter-gatherer ancestry than their predecessors, but in Russia, the Yamnaya steppe herders of this time were descended not only from the preceding eastern European hunter-gatherers, but also from a population of Near Eastern ancestry. Western and Eastern Europe came into contact 4,500 years ago, as the Late Neolithic Corded Ware people from Germany traced 75 % of their ancestry to the Yamnaya, documenting a massive migration into the heartland of Europe from its eastern periphery. This steppe ancestry persisted in all sampled central Europeans until at least 3,000 years ago, and is ubiquitous inpresent-day-Europeans. These results provide support for a steppe origin9 of at least some of the Indo-European languages of Europe.

KRISTIANSEN 2012

Kristian Kristiansen, *The Bronze Age expansion of Indo-European languages*, *An archaeological model.* In: CHRISTOPHER PRESCOT & HÅKON GLØRSTAD (Hrsg.), *Becoming European*, *The transformation of third millennium Northern and Western Europe.* (Oxford 2012), 165–181.

Today it can be stated with some certainty that the third millennium BC was a period of major social and economic changes over wide areas in western Eurasia. Furthermore, that this change was in part linked to a complex pattern of interaction, from travels and small-scale population movements to some large-scale migrations. It was based upon the formation of a new economy, and a concomitant new social and religious order of society, with a tremendous capacity for expansion and social incorporation. Regional series of 14C dating define the beginning of this major expansion within a rather narrow time span during the early part of the third millennium BC. This scenario is supported by new evidence from science, ecology and metallurgy.

During the Early and Middle Neolithic periods there were still large forest reserves preserved in Europe, although mainly on lighter soils. However, during the early third millennium BC these areas were colonised by expanding pastoral herders and warriors with an apparently never-ending appetite for new pastures. They rapidly burned down the forests to create grazing lands for their animals, as evidenced in pollen diagrams. The newcomers practiced some cultivation of cereals, especially barley, but the economy was based on animal products, and these agro-pastoral societies expanded through a combination of warfare and recruitment of new members through patron-client-relations and other means of social dominance, including language. This was in some areas replaced by mass migrations, as in the case of western Jutland. Small houses or huts appear during the later stage of the Corded Ware and Single Grave Culture.

From the mid-third millennium this inland economic system, variously termed Corded Ware, Single Grave and Battle Axe cultures, was complemented by a maritime counterpart in the form of the Bell Beaker cultures that expanded along the western Mediterranean and along the Atlantic façade before they moved inland, but never further east than Hungary and they always settled in small pockets. The Bell Beaker people brought with them metallurgical knowledge, in addition to maritime skills, and they migrated as skilled artisans according to recent strontium isotope analyses of teeth and bone.

[...] This is the formation of the Maikop Culture in the Caucasus with royal kurgans and Mesopotamian imports. It led to the formation of new institutions based upon a new concept of rank linked to movable, personal property, mainly in the form of prestige goods and animals (herds). I thus propose that transmission of a new family structure from the city-states of the south (the Uruk expansion) with new definitions of family, property and inheritance helped to facilitate the social formation of a new mobile agro-pastoral society in the steppe region and beyond. It constituted the monogamous family group as a central social and economic institution based on a patrilineal kinship system. It favoured the accumulation of mobile wealth through expansion and the formation of external alliance systems, and mobile wealth could be carried along and even transmitted between generations. The new barrow ritual of individual burials furnished with these very same symbols of wealth represented the ritualised institutionalisation of these new principles as they were now also transferred to the land of death, when property had to be transmitted and redistributed.

Novembre 2015

John Novembre, *Ancient DNA steps into the language debate.* nature **522** (2015), 164–165.

Two studies of ancient human DNA reveal expansions of Bronze Age populations that shed light on the long-running debate about the origins and spread of Indo-European languages.

Previous studies of both modern and ancient DNA have suggested an influx of people into Europe from modern Eurasia after the spread of Neolithic farming. However, the details have been hazy, and any role for steppe populations has been unclear. To resolve this uncertainty, Haak et al. and Allentoft et al. obtained ancient human DNA samples from a broad swathe of archaeological cultures from Europe and central Asia dating from around 6000 bc to 900 bc. Although each study used different strategies (Allentoft et al. sequenced whole genomes, whereas Haak et al. targeted select regions), the groups successfully obtained around 101 and 69 samples, respectively — a remarkable achievement. The sequencing data are poor by the standards applied to modern DNA, but they are sufficient to discern broad brushstrokes of human migration.

Together, these studies argue that Bronze Age population movements were important in shaping the genetics of Eurasia. Ancient DNA cannot prove how language spread, of course, and more data will help to refine our understanding, but expansions of Yamnaya-related peoples add weight to the steppe hypothesis. If genes were moving en masse, it is likely that words were too.

Story or Book

Davies 2015

William Davies, *How we misread our own story.* nature **522** (2015), 154–155.

William Davies ponders a chronicle unwinding the twisted strands of thinking on human evolution.

The Strange Case of the Rickety Cossack: And Other Cautionary Tales from Human Evolution. Ian Tattersall. Palgrave Macmillan: 2015.

The lack of connection between those who recovered the fossilized and archaeological remains of early hominins, and those who sought to interpret them, is perhaps the most striking feature of the first 60–70 years of palaeo anthropology. It ensured that wider archaeological and ecological contexts were all but ignored in the application of pre determined (and untested) theories.

The Strange Case of the Rickety Cossack is an interesting critical evaluation of how palaeo anthropology has developed. Rivalries between teams are delineated and used to explain how we know what we know.

Some of Tattersall's assertions will generate heated debate — particularly the claim that the large-brained Neanderthals were empirical artisans, rather than symbolic artists. Current archaeological evidence indicates that Neanderthals were able to innovate, but that these innovations may have been kept within small-scale social networks. By contrast, the future of palaeo anthropology lies in its ability to make extensive connections.