Liste erstellt am 2011-11-23

Literatur

Afrika

GOUEM GOUEM 2011

Bienvenu Gouem Gouem, *Des premières communautés villageoises aux sociétés complexes sur le littoral méridional du Cameroun.* Dissertation (Bruxelles 2011).

NEUMANN 2011

Katharina Neumann, Koen Bostoen, Alexa Höhn, Stefanie Kahlheber, Alfred Ngomanda & Barthelémy Tchiengué, *First farmers in the Central African rainforest: A view from southern Cameroon.* Quaternary International (2011) preprint, 1–10. DOI:10.1016/j.quaint.2011.03.024.

Agriculture was introduced into the Central African rainforest from the drier West African savanna, in concert with a major climatic change that amplified seasonality just after 2500 BP. The savanna crop pearl millet (Pennisetum glaucum), dated to 2400–2200 BP, could only be cultivated due to the development of a distinct dry season. Increasing seasonality and the replacement of mature forests by pioneer formations is indicated by Trema orientalis in the pollen diagram of Nyabessan after 2400 BP. However, charcoal data do not point to the existence of savannas in South Cameroon during this period, but rather to a mosaic of mature and pioneer forests. The early rainforest farmers combined the cultivation of pearl millet with the exploitation of wild oil-containing tree fruits, such as oil palm and Canarium. The existence of pioneer formations that can be easily cut favoured the establishment of shifting cultivation. The archaeobotanical finds fit into a linguistic scenario of West-Bantu speakers making the cultivation of pearl millet one of their food production strategies before expanding further to the South. The reconstructed inherited pearl millet vocabulary for the early phases of Bantu language history provides strong circumstantial evidence for an overlap of the major stages of the Bantu expansion with the dispersal of food production.

Aktuell

CROCKER 2011

Jennifer Crocker, *The road to fraud starts with a single step.* nature **479** (2011), 151.

The extensive academic fraud of Diederik Stapel has rocked science. Social psychologist Jennifer Crocker traces the destructive path that cheats follow.
To understand fraud, we should think about how it begins and escalates, not how it ends. By the time such fraud is exposed, bad choices that would usually lead to only minor transgressions have escalated into outright career-killing behaviour. In this regard, we should all admire the colleagues and researchers who took the risk to stop something unacceptable when they saw it in the Stapel case. Surely, they too experienced egotistical fears. Will people believe me? What will happen to me? Will my own reputation be tarnished? The slippery slope beckoned, but they acted for the common good, and we should thank them.

Jones 2011

Benjamin F. Jones & Bruce A. Weinberg, *Age dynamics in scientific creativity*. PNAS **108** (2011), 18910–18914.

Data on Nobel Laureates show that the age-creativity relationship varies substantially more over time than across fields. The age dynamics within fields closely mirror field-specific shifts in (i) training patterns and (ii) the prevalence of theoretical contributions. These dynamics are especially pronounced in physics and coincide with the emergence of quantum mechanics. Taken together, these findings show fundamental shifts in the life cycle of research productivity, inform theories of the age-creativity relationship, and provide observable predictors for the age at which great achievements are made.
innovation | history of science | scientific revolutions

Monastersky 2011

Richard Monastersky, *The quake killer*. nature **479** (2011), 166–170.

The US government says that a huge earthquake risk lurks in the heart of the country, where a series of large shocks hit 200 years ago. Seth Stein says that kind of warning is dead wrong.

Anthropologie

Carrier 2011

David R. Carrier, Christoph Anders & Nadja Schilling, *The musculoskeletal system of humans is not tuned to maximize the economy of locomotion*. PNAS **108** (2011), 18631–18636.

Humans are known to have energetically optimal walking and running speeds at which the cost to travel a given distance is minimized. We hypothesized that “optimal” walking and running speeds would also exist at the level of individual locomotor muscles. Additionally, because humans are 60-70 % more economical when they walk than when they run, we predicted that the different muscles would exhibit a greater degree of tuning to the energetically optimal speed during walking than during running. To test these hypotheses, we used electromyography to measure the activity of 13 muscles of the back and legs over a range of walking and running speeds in human subjects and calculated the cumulative activity required from each muscle to traverse a kilometer. We found that activity of each of these muscles was minimized at specific walking and running speeds but the different muscles were not tuned to a particular speed in either gait. Although humans are clearly highly specialized for terrestrial locomotion compared with other great apes, the results of this study indicate that our locomotor muscles are not tuned to specific walking or running speeds and, therefore, do not maximize the economy of locomotion. This pattern may have evolved in response to selection to broaden the range of sustainable running speeds, to improve performance in motor behaviors not related to endurance locomotion, or in response to selection for both.
cost of transport | human evolution | persistence hunting | locomotor energetics | electromyography

Shultz 2011

Susanne Shultz, Christopher Opie & Quentin D. Atkinson, *Stepwise evolution of stable sociality in primates*. nature **479** (2011), 219–222.
n479-0219-Supplement.pdf

Although much attention has been focused on explaining and describing the diversity of social grouping patterns among primates1-3, less effort has been devoted to understanding the evolutionary history of social living4. This is partly because social behaviours do not fossilize, making it difficult to infer changes over evolutionary time. However, primate social behaviour shows strong evidence for phylogenetic inertia, permitting the use of Bayesian comparative methods to infer changes in social behaviour through time, thereby allowing us to evaluate alternative models of social evolution. Here we present a model of primate social evolution, whereby sociality progresses fromsolitary foraging individuals directly to large multi-male/multi-female aggregations (approximately 52 million years (Myr) ago), with pair-living (approximately 16 Myr ago) or single-male harem systems (approximately 16 Myr ago) derivative from this second stage. This model fits the data significantly better than the two widely accepted alternatives (an unstructured model implied by the socioecological hypothesis or a model that allows linear stepwise changes in social complexity through time). We also find strong support for the co-evolution of social living with a change from nocturnal to diurnal activity patterns, but not with sex-biased dispersal. This supports suggestions that social living may arise because of increased predation risk associated with diurnal activity. Sociality based on loose aggregation is followed by a second shift to stable or bonded groups. This structuring facilitates the evolution of cooperative behaviours5 and may provide the scaffold for other distinctive anthropoid traits including coalition formation, cooperative resource defence and large brains.

SILK 2011

Joan B. Silk, *The path to sociality*. nature **479** (2011), 182–183.

A comparative analysis traces the trajectory of change in social organization among primates and establishes a firm foundation for modelling the origins of social complexity.
The existence of a strong phylogenetic signal spells trouble for socioecological models that aim to explain the evolution of primate social organization. The models hypothesize that food distribution shapes competitive regimes, and that these, in turn, shape dispersal patterns and the nature of relationships within groups3-5. These models generally assume that phylogeny does not impose notable constraints on social organization, and that changes from one form of social organization to another are all equally likely. But there is a growing realization that history does have a role6-8, and the new results1 strengthen that view.
The direction of the transition from stable groups with multiple males and females to pair-bonded groups is of particular interest for at least two reasons. First, it challenges assumptions about the nature of social complexity. In the past few decades, the social-brain hypothesis has held sway in primatology10,11. According to this hypothesis, the demands of living in large groups with a host of potential rivals favoured the evolution of greater cognitive abilities: the larger the group, the more complicated the social terrain and the greater the need for cognitive sophistication. But Shultz and colleagues' finding that there has not been a steady progression from small groups to larger ones suggests that social complexity is not a simple function of group size.

Biologie

BOS 2011

Kirsten I. Bos et al., *A draft genome of Yersinia pestis from victims of the Black Death*. nature **478** (2011), 506–510.

n478-0506-Supplement1.pdf, n478-0506-Supplement2.zip

Kirsten I. Bos, Verena J. Schuenemann, G. Brian Golding, Hernán A. Burbano, Nicholas Waglechner, Brian K. Coombes, Joseph B. McPhee, Sharon N.DeWitte, Matthias Meyer, Sarah Schmedes, James Wood, David J. D. Earn, D. Ann Herring, Peter Bauer, Hendrik N. Poinar & Johannes Krause

Technological advances in DNA recovery and sequencing have drastically expanded the scope of genetic analyses of ancient specimens to the extent that full genomic investigations are now feasible and are quickly becoming standard1. This trend has important implications for infectious disease research because genomic data from ancient microbes may help to elucidate mechanisms of pathogen evolution and adaptation for emerging and re-emerging infections. Here we report a reconstructed ancient genome of Yersinia pestis at 30-fold average coverage from Black Death victims securely dated to episodes of pestilence-associated mortality in London, England, 1348-1350. Genetic architecture and phylogenetic analysis indicate that the ancient organismis ancestral to most extant strains and sits very close to the ancestral node of all Y. pestis commonly associated with human infection. Temporal estimates suggest that the Black Death of 1347-1351 was the main historical event responsible for the introduction and widespread dissemination of the ancestor to all currently circulating Y. pestis strains pathogenic to humans, and further indicates that contemporary Y. pestis epidemics have their origins in the medieval era. Comparisons against modern genomes reveal no unique derived positions in the medieval organism, indicating that the perceived increased virulence of the disease during the Black Death may not have been due to bacterial phenotype. These findings support the notion that factors other than microbial genetics, such as environment, vector dynamics and host susceptibility, should be at the forefront of epidemiological discussions regarding emerging Y. pestis infections.

Pruvost 2011

Melanie Pruvost et al., *Genotypes of predomestic horses match phenotypes painted in Paleolithic works of cave art.* PNAS **108** (2011), 18626–18630.

Melanie Pruvost, Rebecca Bellone, Norbert Benecke, Edson Sandoval-Castellanos, Michael Cieslak, Tatyana Kuznetsova, Arturo Morales-Muñiz, Terry O'Connor, Monika Reissmann, Michael Hofreiter and Arne Ludwig

Archaeologists often argue whether Paleolithic works of art, cave paintings in particular, constitute reflections of the natural environment of humans at the time. They also debate the extent to which these paintings actually contain creative artistic expression, reflect the phenotypic variation of the surrounding environment, or focus on rare phenotypes. The famous paintings "The Dappled Horses of Pech-Merle," depicting spotted horses on the walls of a cave in Pech-Merle, France, date back ≈25,000 y, but the coat pattern portrayed in these paintings is remarkably similar to a pattern known as "leopard" in modern horses. We have genotyped nine coat-color loci in 31 predomestic horses from Siberia, Eastern and Western Europe, and the Iberian Peninsula. Eighteen horses had bay coat color, seven were black, and six shared an allele associated with the leopard complex spotting (LP), representing the only spotted phenotype that has been discovered in wild, predomestic horses thus far. LP was detected in four Pleistocene and two Copper Age samples from Western and Eastern Europe, respectively. In contrast, this phenotype was absent from predomestic Siberian horses. Thus, all horse color phenotypes that seem to be distinguishable in cave paintings have now been found to exist in prehistoric horse populations, suggesting that cave paintings of this species represent remarkably realistic depictions of the animals shown. This finding lends support to hypotheses arguing that cave paintings might have contained less of a symbolic or transcendental connotation than often assumed.

ancient DNA | transient receptor potential cation channel subfamily M1 | single nucleotide polymorphism | leopard complex spotting | Franco-Cantabrian region

Strier 2011

Karen B. Strier, Paulo B. Chaves, Sérgio L. Mendes, Valéria Fagundes & Anthony Di Fiore, *Low paternity skew and the influence of maternal kin in an egalitarian, patrilocal primate.* PNAS **108** (2011), 18915–18919.

Levels of reproductive skew vary in wild primates living in multimale groups depending on the degree to which high-ranking males monopolize access to females. Still, the factors affecting paternity in egalitarian societies remain unexplored. We combine unique behavioral, life history, and genetic data to evaluate the distribution of paternity in the northern muriqui (Brachyteles hypoxanthus), a species known for its affiliative, nonhierarchical relationships. We genotyped 67 individuals (22 infants born over a 3-y period, their 21 mothers, and all 24 possible sires) at 17 micro-satellite marker loci and assigned paternity to all infants. None of the 13 fathers were close maternal relatives of females with which they sired infants, and the most successful male sired a much lower percentage of infants (18 %) than reported for the most successful males in other species. Our findings of inbreeding avoidance and low male reproductive skew are consistent with the muriqui's observed social and sexual behavior, but the long delay (≥2.08 y) between the onset of male sexual behavior and the age at which males first sire young is unexpected. The allocation of paternity implicates individual male life histories and access to maternal kin as key factors influencing variation in paternal—and grandmaternal—fitness. The apparent importance of lifelong maternal investment in coresident sons resonates with other recent examinations of maternal influences on offspring reproduction. This importance also extends the implications of the "grandmother hypothesis" in human evolution to include the possible influence of mothers and other maternal kin on male reproductive success in patrilocal societies.
mating system | reproductive strategy | development | molecular ecology | Platyrrhini

Datierung

BLAAUW 2003

Maarten Blaauw, Gerard B. M. Heuvelink, Dmitri Mauquoy, Johannes van der Plicht & Bas van Geel, *A numerical approach to* ^{14}C *wiggle-match dating of organic deposits: best fits and confidence intervals*. Quaternary Science Reviews **22** (2003), 1485–1500.

14C wiggle-match dating (WMD) of peat deposits uses the non-linear relationship between 14C age and calendar age to match the shape of a sequence of closely spaced peat 14C dates with the 14C calibration curve. A numerical approach to WMD enables the quantitative assessment of various possible wiggle-match solutions and of calendar year confidence intervals for sequences of 14C dates. We assess the assumptions, advantages, and limitations of the method. Several case-studies show that WMD results in more precise chronologies than when individual 14C dates are calibrated. WMD is most successful during periods with major excursions in the 14C calibration curve (e.g., in one case WMD could narrow down confidence intervals from 230 to 36 yr).

BLAAUW 2004

Maarten Blaauw, Bas van Geel, Dmitri Mauquoy & Johannes van der Plicht, *Carbon-14 wiggle-match dating of peat deposits: advantages and limitations*. Journal of Quaternary Science **19** (2004), 177–181.

Carbon-14 wiggle-match dating (WMD) of peat deposits uses the non-linear relationship between 14C age and calendar age to match the shape of a series of closely spaced peat 14C dates with the 14C calibration curve. The method of WMD is discussed, and its advantages and limitations are compared with calibration of individual dates. A numerical approach to WMD is introduced that makes it possible to assess the precision of WMD chronologies. During several intervals of the Holocene, the 14C calibration curve shows less pronounced fluctuations. We assess whether wigglematching is also a feasible strategy

for these parts of the 14C calibration curve. High-precision chronologies, such as obtainable with WMD, are needed for studies of rapid climate changes and their possible causes during the Holocene.

KEYWORDS: 14C chronologies; 14C calibration; 14C wiggle-match dating.