Liste erstellt am 2013-10-31

Literatur

Afrika

AMILLS 2013

Marcel Amills, Oscar Ramírez & Ofelia Galman-Omitogun & Alex Clop, *Domestic Pigs in Africa*. African Archaeological Review **30** (2013), 73–82.

The history of African pig breeds is still controversial due to the relative scarcity of archaeological and genetic data clarifying their origins. While these breeds might descend from Near Eastern pigs entering the continent via Egypt during the Neolithic, Africa may be a primary domestication locus for pigs, as indicated for other species such as cattle and donkeys. In this regard, characterisation of the mitochondrial gene pool of African pig breeds has revealed a very low frequency of Near Eastern alleles, suggesting that, if Fertile Crescent pigs played a part in the foundation of African breeds, their genetic signature has been substantially erased. Interestingly, genetic analysis of western and eastern African pig breeds has revealed a strong phylogeographic pattern, with the latter harbouring Far Eastern alleles at high frequencies. This finding is consistent with data obtained for chickens and confirms that livestock was transported in ancient times, from the Far East to Africa as a consequence of the Indian Ocean trade. European colonisation of Africa also involved the introduction of exotic swine breeds such as Iberian pigs. The confluence of the highly divergent European and Far Eastern Sus scrofa gene pools contributed to significantly enrich the genetic reservoir of African swine breeds, favouring their adaptation to environmental conditions that are often harsh. Conservation of this genetic legacy will be of utmost importance to ensure the prosperity of current resource-based subsistence farming systems in Africa.

BELEZA 2005

Sandra Beleza, Leonor Gusmão, António Amorim, Angel Carracedo & Antonio Salas, *The genetic legacy of western Bantu migrations*. Human Genetics **117** (2005), 366–375.

MolBiolEvol24-2180-Supplement1.pdf, MolBiolEvol24-2180-Supplement2.doc, MolBiolEvol24-2180-Supplement3.xls

There is little knowledge on the demographic impact of the western wave of the Bantu expansion. Only some predictions could be made based mainly on indirect archaeological, linguistic, and genetic evidences. Apart from the very limited available data on the mitochondrial DNA (mtDNA) side, there are not, however, Y-chromosome studies revealing–if any–the male contribution of western Bantu-farmers. To elucidate the still poorly characterized western Bantu expansion, we analyzed Y-chromosome (25 biallelic polymorphisms and 15 microsatellite markers) and mtDNA (hypervariable control regions I and II and selected coding region RFLPs) variation in a population of 110 individuals from southwest Africa, and compared it with a database of 2,708 Y-chromosome profiles and of 2,565 mtDNAs from all other regions of Africa. This study reveals (1) a dramatic displacement of male and female Khoisan-speaking groups in the southwest, since both the maternal and the paternal genetic pools were composed exclusively by types carried by Bantu-speakers; (2) a clear bias in the admixture process towards the mating of male Europeans with female Sub-Saharan Africans; (3) the assimilation of east

African lineages by the southwest (mainly mtDNA-L3f and Y-chromosome-B2a lineages); and (4) signatures of recent male and female gene flow from the southeast into the southwest. The data also indicate that the western stream of the Bantu expansion was a more gradual process than the eastern counterpart, which likely involved multiple short dispersals.

CAMPANA 2013

Michael G. Campana, Mim A. Bower & Pam J. Crabtree, *Ancient DNA for the Archaeologist*, *The Future of African Research*. African Archaeological Review **30** (2013), 21–37.

Ancient DNA analyses are increasingly popular in archaeology. With the exception of Egypt, the African continent has been grossly understudied using these techniques. We review the state of ancient DNA research on Africa, ancient DNA analysis techniques, and common pitfalls in these studies. We provide recommendations for archaeologists interested in collecting and interpreting ancient DNA data.

GIFFORD-GONZALEZ 2013

Diane Gifford-Gonzalez, *Animal Genetics and African Archaeology*, *Why It Matters*. African Archaeological Review **30** (2013), 1–20.

This article introduces the special issue of African Archaeological Review on the relevance of African livestock genetics to archaeology on the continent. It shows how modern and ancient animal genetic research in Eurasia has substantially revised archaeological scenarios for the origins and spread of food production there. It argues that, in contrast to colleagues in Europe and Asia, Africanist archaeologists have generally been slow to engage in truly collaborative research with archaeogeneticists, with some notable exceptions. It builds a case that animal introductions and domestication are as much social, cultural, and economic processes as they are ecological in nature. Through examples, it outlines some profound selective effects that animal keeping has had on humans themselves. Building on the concepts of taste and embodied practice in Stahl's (2002) discussion of artifacts and differently scaled encounters with non-local commerce, it develops suggestions for archaeologically studying genetically distinctive domestic animals as part of local and long-distance economic systems. Finally, it comments on the issue's review articles and offers suggestions for ways to encourage stronger collaboration between archaeologists and genetic researchers.

KIMURA 2013

Birgitta Kimura, Fiona Marshall & Albano Beja-Pereira & Connie Mulligan, *Donkey Domestication*. African Archaeological Review **30** (2013), 83–95.

Donkeys are one of the least studied large domestic animals, even though they are economically important in many regions of the world. They are predominantly used as transport animals. Consequently, they are not kept in large numbers and this limits the number of archaeological specimens available for study. The donkey's closest relative is the African wild ass, and genetic studies and zooarchaeological analyses of early donkeys indicate domestication of two genetically separate groups of wild asses in Africa. Maternal relationships revealed by mitochondrial DNA show that one group of donkeys was derived from the Nubian wild ass and that one was derived from an unknown ancestor distinct from the Somali wild ass.

MacEachern 2000

Scott MacEachern, *Genes, Tribes, and African History.* Current Anthropology **41** (2000), 257–384.

Over the past 40 years, traditional perspectives on the constitution of human groups have been subjected to stringent critique within anthropology. This began with the dismantling of accepted "race" divisions after World War II and continued with analyses of the meaning and reality of African "tribal" distinctions from the 1960s until the present. Archaeologists, ethnographers, linguists, and historians of Africa now work within a research milieu where social interactions, cultural exchange, and the dynamic nature of group identifications are accepted as a normal part of the human experience. At the same time, new techniques have been developed for the examination of human history, techniques based upon an expanding repertoire of tools for the analysis of genetic variability in human populations. Perhaps the most striking result of this research has been Cavalli-Sforza, Menozzi, and Piazza's The History and Geography of Human Genes. Rather less attention has been paid, however, to the conceptual relationships between the human groups defined through such analyses, in Africa and elsewhere, and those defined through other kinds of research. This paper is a preliminary examination of the fit between genetic, archaeological, and ethnographic data on the African past.

Muigai 2013

Anne W. T. Muigai & Olivier Hanotte, *The Origin of African Sheep, Archaeological and Genetic Perspectives.* African Archaeological Review **30** (2013), 39–50.

Indigenous African sheep genetic resources have been classified into two main groups, fat-tailed and thin-tailed sheep. The fat-tailed sheep are the most widely distributed, being found in a large part of North Africa (from Egypt to Algeria) and in Eastern and Southern Africa (from Eritrea to South Africa). The thin-tailed sheep are present mainly in Morocco, Sudan and in West Africa. African sheep were domesticated outside Africa. They share a common ancestry with European and Asian sheep. Archaeological information supports separate introductions and dispersion histories for the African thin-tailed and fat-tailed sheep. The first sheep entered Africa via the Isthmus of Suez and/or the southern Sinai Peninsula, between 7500 and 7000 BP. They were likely of the thin-tailed type. Fat-tailed sheep entered Africa through its northeastern part and the Horn of Africa. Mitochondrial DNA analysis supports a common maternal ancestral origin for all African sheep, while autosomal and Y chromosome DNA analysis indicates a distinct genetic history for African thintailed and sub-Saharan fat-tailed sheep. The main ancestral population of southern African fat-tailed sheep likely originated in East Africa. Further work is needed to assess the possible dispersion of sheep from western Africa to the southern African regions.

Mwacharo 2013

J. M. Mwacharo, G. Bjørnstad, J. L. Han & O. Hanotte, *The History of African Village Chickens, An Archaeological and Molecular Perspective.* African Archaeological Review **30** (2013), 97–114.

The history of the introduction and dispersal of village chickens across the African continent is a subject of intense debate and speculation among scholars. Here, we synthesize and summarise the current scientific genetic and nongenetic knowledge in relation to the history of the species on the continent. Sociocultural, linguistic, archaeological and historic data all suggest a complex history for the species in Africa, characterized by multiple maritime and/or terrestrial introductions over time and several dispersal routes towards and within Africa. Molecular genetics information supports these observations and in addition suggests possible Asian centers of origin for African domestic chickens, including South Asia and Island Southeast Asia. However, both sets of data were until now too limited in their geographic scope, both within Africa and in comparison with chickens from Asia, to unravel the history of the species in detail. We anticipate that further continent-wide studies combining archaeological, ancient and/or modern genetic information may shed new insights on the history of the species. These will contribute to a deeper understanding of the history of trading networks and human interactions within Africa and between African and Asian societies, at the root of the development and expansion of African civilizations.

OUMAR 2008

Ibrahima Oumar, Cédric Mariac, Jean-Louis Pham & Yves Vigouroux, *Phylogeny and origin of pearl millet (Pennisetum glaucum [L.] R. Br) as revealed by microsatellite loci*. Theoretical and Applied Genetics **117** (2008), 489–497.

During the last 12,000 years, different cultures around the world have domesticated cereal crops. Several studies investigated the evolutionary history and domestication of cereals such as wheat in the Middle East, rice in Asia or maize in America. The domestication process in Africa has led to the emergence of important cereal crops like pearl millet in Sahelian Africa. In this study, we used 27 microsatellite loci to analyze 84 wild accessions and 355 cultivated accessions originating from the whole pearl millet distribution area in Africa and Asia. We found significantly higher diversity in the wild pearl millet group. The cultivated pearl millet sample possessed 81 % of the alleles and 83 % of the genetic diversity of the wild pearl millet sample. Using Bayesian approaches, we identified intermediate genotypes between the cultivated and wild groups. We then analyzed the phylogenetic relationship among accessions not showing introgression and found that a monophyletic origin of cultivated pearl millet in West Africa is the most likely scenario supported by our data set.

PAGANI 2012

Luca Pagani et al., *Ethiopian Genetic Diversity Reveals Linguistic Stratification and Complex Influences on the Ethiopian Gene Pool*. American Journal of Human Genetics **91** (2012), 83–96.

AmJHumGen91-0083-Supplement1.pdf, AmJHumGen91-0083-Supplement2.xls
Luca Pagani, Toomas Kivisild, Ayele Tarekegn, Rosemary Ekong, Chris Plaster, Irene Gallego Romero, Qasim Ayub, S. Qasim Mehdi, Mark G. Thomas, Donata Luiselli, Endashaw Bekele, Neil Bradman, David J. Balding & Chris Tyler-Smith
Humans and their ancestors have traversed the Ethiopian landscape for millions of years, and present-day Ethiopians show great cultural, linguistic, and historical diversity, which makes them essential for understanding African variability and human origins. We genotyped 235 individuals from ten Ethiopian and two neighboring (South Sudanese and Somali) populations on an Illumina Omni 1M chip. Genotypes were compared with published data from several African and non-African populations. Principal-component and STRUCTURE-like analyses confirmed substantial genetic diversity both within and between populations, and revealed a match between genetic data and linguistic affiliation. Using comparisons with African and non-African reference samples in 40-SNP genomic windows, we identified "African" and "non-African" haplotypic components for each Ethiopian individual. The non-African component, which includes the SLC24A5 allele

associated with light skin pigmentation in Europeans, may represent gene flow into Africa, which we estimate to have occurred ≈3 thousand years ago (kya). The non-African component was found to be more similar to populations inhabiting the Levant rather than the Arabian Peninsula, but the principal route for the expansion out of Africa ≈60 kya remains unresolved. Linkage-disequilibrium decay with genomic distance was less rapid in both the whole genome and the African component than in southern African samples, suggesting a less ancient history for Ethiopian populations.

PATIN 2009

Etienne Patin et al., *Inferring the Demographic History of African Farmers and Pygmy Hunter–Gatherers Using a Multilocus Resequencing Data Set*. PLoS Genetics **5** (2009), e1000448. DOI:10.1371/journal.pgen.1000448.

Etienne Patin, Guillaume Laval, Luis B. Barreiro, Antonio Salas, Ornella Semino, Silvana Santachiara-Benerecetti, Kenneth K. Kidd, Judith R. Kidd, Lolke van der Veen, Jean-Marie Hombert, Antoine Gessain, Alain Froment, Serge Bahuchet, Evelyne Heyer & Lluís Quintana-Murci

The transition from hunting and gathering to farming involved a major cultural innovation that has spread rapidly over most of the globe in the last ten millennia. In sub-Saharan Africa, hunter–gatherers have begun to shift toward an agriculture-based lifestyle over the last 5,000 years. Only a few populations still base their mode of subsistence on hunting and gathering. The Pygmies are considered to be the largest group of mobile hunter–gatherers of Africa. They dwell in equatorial rainforests and are characterized by their short mean stature. However, little is known about the chronology of the demographic events—size changes, population splits, and gene flow—ultimately giving rise to contemporary Pygmy (Western and Eastern) groups and neighboring agricultural populations. We studied the branching history of Pygmy hunter–gatherers and agricultural populations from Africa and estimated separation times and gene flow between these populations. We resequenced 24 independent noncoding regions across the genome, corresponding to a total of ≈33 kb per individual, in 236 samples from seven Pygmy and five agricultural populations dispersed over the African continent. We used simulation-based inference to identify the historical model best fitting our data. The model identified included the early divergence of the ancestors of Pygmy hunter–gatherers and farming populations ≈60,000 years ago, followed by a split of the Pygmies' ancestors into the Western and Eastern Pygmy groups ≈20,000 years ago. Our findings increase knowledge of the history of the peopling of the African continent in a region lacking archaeological data. An appreciation of the demographic and adaptive history of African populations with different modes of subsistence should improve our understanding of the influence of human lifestyles on genome diversity.

SCHUSTER 2010

Stephan C. Schuster et al., *Complete Khoisan and Bantu genomes from southern Africa*. nature **463** (2010), 943–947.

n463-0943-Supplement.pdf

Stephan C. Schuster, Webb Miller, Aakrosh Ratan, Lynn P. Tomsho, Belinda Giardine, Lindsay R. Kasson, Robert S. Harris, Desiree C. Petersen, Fangqing Zhao, Ji Qi, Can Alkan, Jeffrey M. Kidd, Yazhou Sun, Daniela I. Drautz, Pascal Bouffard, Donna M. Muzny, Jeffrey G. Reid, Lynne V. Nazareth, Qingyu Wang, Richard Burhans, Cathy Riemer, Nicola E. Wittekindt, Priya Moorjani, Elizabeth A. Tindall, Charles G. Danko, Wee Siang Teo, Anne M. Buboltz, Zhenhai Zhang, Qianyi Ma, Arno Oosthuysen, Abraham W. Steenkamp, Hermann Oostuisen, Philippus

Venter, John Gajewski, Yu Zhang, B. Franklin Pugh, Kateryna D. Makova, Anton Nekrutenko, Elaine R. Mardis, Nick Patterson, Tom H. Pringle, Francesca Chiaromonte, James C. Mullikin, Evan E. Eichler, Ross C. Hardison, Richard A. Gibbs, Timothy T. Harkins & Vanessa M. Hayes

The genetic structure of the indigenous hunter-gatherer peoples of southern Africa, the oldest known lineage of modern human, is important for understanding human diversity. Studies based on mitochondrial1 and small sets of nuclear markers2 have shown that these hunter-gatherers, known as Khoisan, San, or Bushmen, are genetically divergent from other humans1,3. However, until now, fully sequenced human genomes have been limited to recently diverged populations4–8. Here we present the complete genome sequences of an indigenous hunter-gatherer from the Kalahari Desert and a Bantu from southern Africa, as well as protein-coding regions from an additional three hunter-gatherers from disparate regions of the Kalahari.Wecharacterize the extent ofwhole-genome and exome diversityamong the fivemen, reporting 1.3million novel DNA differences genome-wide, including 13,146 novel amino acid variants. In terms of nucleotide substitutions, the Bushmen seem to be, on average, more different from each other than, for example, a European and an Asian. Observed genomic differences between the hunter-gatherers and others may help to pinpoint genetic adaptations to an agricultural lifestyle. Adding the described variants to current databases will facilitate inclusion of southern Africans in medical research efforts, particularly when family and medical histories can be correlated with genome-wide data.

SOARES 2012

Pedro Soares et al., *The Expansion of mtDNA Haplogroup L3 within and out of Africa*. Molecular Biology and Evolution **29** (2012), 915–927.
MolBiolEvol29-0915-Supplement1.doc, MolBiolEvol29-0915-Supplement2.txt, MolBiolEvol29-0915-Supplement3.xls, MolBiolEvol29-0915-Supplement4.xls
Pedro Soares, Farida Alshamali, Joana B. Pereira, Verónica Fernandes, Nuno M. Silva, Carla Afonso, Marta D. Costa, Eliska Musilová, Vincent Macaulay, Martin B. Richards, Viktor Černý and Luísa Pereira

Although fossil remains show that anatomically modern humans dispersed out of Africa into the Near East ;100 to 130 ka, genetic evidence from extant populations has suggested that non-Africans descend primarily from a single successful later migration. Within the human mitochondrial DNA (mtDNA) tree, haplogroup L3 encompasses not only many sub-Saharan Africans but also all ancient non-African lineages, and its age therefore provides an upper bound for the dispersal out of Africa. An analysis of 369 complete African L3 sequences places this maximum at;70 ka, virtually ruling out a successful exit before 74 ka, the date of the Toba volcanic supereruption in Sumatra. The similarity of the age of L3 to its two non-African daughter haplogroups, M and N, suggests that the same process was likely responsible for both the L3 expansion in Eastern Africa and the dispersal of a small group of modern humans out of Africa to settle the rest of the world. The timing of the expansion of L3 suggests a link to improved climatic conditions after;70 ka in Eastern and Central Africa rather than to symbolically mediated behavior, which evidently arose considerably earlier. The L3 mtDNA pool within Africa suggests a migration from Eastern Africa to Central Africa ;60 to 35 ka and major migrations in the immediate postglacial again linked to climate. The largest population size increase seen in the L3 data is 3-4 ka in Central Africa, corresponding to Bantu expansions, leading diverse L3 lineages to spread into Eastern and Southern Africa in the last 3-2 ka.

Keywords: mtDNA, complete genomes, haplogroup L3, out of Africa, modern human expansions

STOCK 2013
Frauke Stock & Diane Gifford-Gonzalez, *Genetics and African Cattle Domestication*. African Archaeological Review **30** (2013), 51–72.
Whether cattle domestication occurred independently on the African continent is among the most controversial questions in the Holocene archaeology of northern Africa. One long-established scenario, based upon early archaeological evidence, suggested that Africa's earliest cattle derived from several introductions from Southwest Asia through the Nile Valley, or via the Horn of Africa. Based upon archaeofaunal remains retrieved in the late twentieth century, other archaeologists argued that an independent domestication of the African aurochs gave rise to Africa's earliest domestic cattle. Up to now, the genetic data have also been controversial. This paper reviews the archaeological evidence and the scope of debate, and then focuses on the recent contributions of genetic research to clarifying these issues.

TISHKOFF 2007
Sarah A. Tishkoff et al., *History of Click-Speaking Populations of Africa Inferred from mtDNA and Y Chromosome Genetic Variation*. Molecular Biology and Evolution **24** (2007), 2180–2195.
Sarah A. Tishkoff, Mary Katherine Gonder, Brenna M. Henn, Holly Mortensen, Alec Knight, Christopher Gignoux, Neil Fernandopulle, Godfrey Lema, Thomas B. Nyambo, Uma Ramakrishnan, Floyd A. Reed and Joanna L. Mountain
Little is known about the history of click-speaking populations in Africa. Prior genetic studies revealed that the clickspeaking Hadza of eastern Africa are as distantly related to click speakers of southern Africa as are most other African populations. The Sandawe, who currently live within 150 km of the Hadza, are the only other population in eastern Africa whose language has been classified as part of the Khoisan language family. Linguists disagree on whether there is any detectable relationship between the Hadza and Sandawe click languages. We characterized both mtDNA and Y chromosome variation of the Sandawe, Hadza, and neighboring Tanzanian populations. New genetic data show that the Sandawe and southern African click speakers share rare mtDNA and Y chromosome haplogroups; however, common ancestry of the 2 populations dates back .35,000 years. These data also indicate that common ancestry of the Hadza and Sandawe populations dates back .15,000 years. These findings suggest that at the time of the spread of agriculture and pastoralism, the click-speaking populations were already isolated from one another and are consistent with relatively deep linguistic divergence among the respective click languages.

Aktuell

BORJIGIN 2013
Jimo Borjigin, Michael M. Wang & George A. Mashour, *Near-death electrical brain activity in humans and animals requires additional studies, Reply to Chawla and Seneff*. PNAS **110** (2013), E4124.
Chawla and Seneff (1) state that our study "largely confirms" their hypothesis (3) that the "end-of-life electrical surges" (the term used by Chawla and Seneff) "could be responsible for near-death experiences." Although there are compelling similarities, we would like to clarify several points of distinction between their study and our recently published work (2).

CHAWLA 2013

Lakhmir Chawla & Michael G. Seneff, *End-of-life electrical surges*. PNAS **110** (2013), E4123.

Many would argue that studying death is not productive because, after all, the outcome is not changed. However, there are clear spiritual, religious, and existential questions about death that remain unanswered, and a better understanding of what happens to the brain at the time of death will help physicians address the many concerns that families and patients have regarding this event.

ELLINGSEN 2013

Dan-Mikael Ellingsen, Johan Wessberg, Marie Eikemo, Jaquette Liljencrantz, Tor Endestad, Håkan Olausson & Siri Leknes, *Placebo improves pleasure and pain through opposite modulation of sensory processing*. PNAS **110** (2013), 17993–17998.

Placebo analgesia is often conceptualized as a reward mechanism. However, by targeting only negative experiences, such as pain, placebo research may tell only half the story. We compared placebo improvement of painful touch (analgesia) with placebo improvement of pleasant touch (hyperhedonia) using functional MRI and a crossover design. Somatosensory processing was decreased during placebo analgesia and increased during placebo hyperhedonia. Both placebo responses were associated with similar patterns of activation increase in circuitry involved in emotion appraisal, including the pregenual anterior cingulate, medial orbitofrontal cortex, amygdala, accumbens, and midbrain structures. Importantly, placebo-induced coupling between the ventromedial prefrontal cortex and periaqueductal gray correlated with somatosensory decreases to painful touch and somatosensory increases to pleasant touch. These findings suggest that placebo analgesia and hyperhedonia are mediated by activation of shared emotion appraisal neurocircuitry, which down- or upregulates early sensory processing, depending on whether the expectation is reduced pain or increased pleasure.

expectancy | neuroimaging | hedonic feelings

FRENCH 2013

Scott French, Vedran Lekic & Barbara Romanowicz, *Waveform Tomography Reveals Channeled Flow at the Base of the Oceanic Asthenosphere*. science **342** (2013), 227–230.

s342-0227-Supplement1.pdf

Understanding the relationship between different scales of convection that drive plate motions and hotspot volcanism still eludes geophysicists. Using full-waveform seismic tomography, we imaged a pattern of horizontally elongated bands of low shear velocity, most prominent between 200 and 350 kilometers depth, which extends below the well-developed low-velocity zone. These quasi-periodic fingerlike structures of wavelength ≈2000 kilometers align parallel to the direction of absolute plate motion for thousands of kilometers. Below 400 kilometers depth, velocity structure is organized into fewer, undulating but vertically coherent, low-velocity plumelike features, which appear rooted in the lower mantle. This suggests the presence of a dynamic interplay between plate-driven flow in the low-velocity zone and active influx of low-rigidity material from deep mantle sources deflected horizontally beneath the moving top boundary layer.

FRITZ 2013

Thomas Hans Fritz et al., *Musical agency reduces perceived exertion during strenuous physical performance.* PNAS **110** (2013), 17784–17789.

Thomas Hans Fritz, Samyogita Hardikar, Matthias Demoucron, Margot Niessen, Michiel Demey, Olivier Giot, Yongming Li, John-Dylan Haynes, Arno Villringer & Marc Leman

Music is known to be capable of reducing perceived exertion during strenuous physical activity. The current interpretation of this modulating effect of music is that music may be perceived as a diversion from unpleasant proprioceptive sensations that go along with exhaustion. Here we investigated the effects of music on perceived exertion during a physically strenuous task, varying musical agency, a task that relies on the experience of body proprioception, rather than simply diverting from it. For this we measured psychologically indicated exertion during physical workout with and without musical agency while simultaneously acquiring metabolic values with spirometry. Results showed that musical agency significantly decreased perceived exertion during workout, indicating that musical agency may actually facilitate physically strenuous activities. This indicates that the positive effect of music on perceived exertion cannot always be explained by an effect of diversion from proprioceptive feedback. Furthermore, this finding suggests that the down-modulating effect of musical agency on perceived exertion may be a previously unacknowledged driving force for the development ofmusic in humans: making music makes strenuous physical activities less exhausting.

sport | civilization | emotional motor control | jymmin' | aesthetics

Amerika

FIEDEL 1999

Stuart J. Fiedel et al., *Monte Verde Revisited*, *Confusion and Contradictions.* Discovering Archaeology **1999**, Special Report, 1–23.

Stuart J. Fiedel, Tom D. Dillehay, Mario Pino, Jack Rossen, Carlos Ocampo, Pilar Rivas, David Pollack, Gwynn Henderson, Michael B. Collins, Frederick H. West, David J. Meltzer, Vance Haynes, David G. Anderson, J. M. Adovasio, Robson Bonnichsen & Ken B. Tankersley

Anthropologie

AIELLO 2001

Leslie C. Aiello & Mark Collard, *Our newest oldest ancestor?* nature **410** (2001), 526–527.

These are exciting times in the study of human origins. But excitement needs to be tempered with caution in assessing the claim of a six-million-year-old direct ancestor of modern humans.

The announcement of Orrorin has caused a considerable stir. The authors also argue that Orrorin is on the direct line leading to modern humans, whereas most of the members of the genus Australopithecus are not.

Most palaeoanthropologists do not recognize a major dichotomy in hominin locomotor ability before the evolution of Homo ergaster, around 1.9 million years ago, and recent analyses of the A. anamensis skeleton suggest that it was much like that of other members of the genus Australopithecus. Senut's claim for more modern walking for Orrorin, linking it with Praeanthropus and Homo, is based on detailed aspects of the anatomy of the upper part of the thigh-bone that are open to alternative explanations.

Arsuaga 2010

Juan Luis Arsuaga, *Terrestrial apes and phylogenetic trees.* PNAS **107** (2010), 8910–8917.

The image that best expresses Darwin's thinking is the tree of life. However, Darwin's human evolutionary tree lacked almost everything because only the Neanderthals were known at the time and they were considered one extreme expression of our own species. Darwin believed that the root of the human tree was very deep and in Africa. It was not until 1962 that the root was shown to be much more recent in time and definitively in Africa. On the other hand, some neo-Darwinians believed that our family tree was not a tree, because there were no branches, but, rather, a straight stem. The recent years have witnessed spectacular discoveries in Africa that take us close to the origin of the human tree and in Spain at Atapuerca that help us better understand the origin of the Neanderthals as well as our own species. The final form of the tree, and the number of branches, remains an object of passionate debate.

Darwin | modes of evolution | body size and shape | taxonomy of Homo | Atapuerca

Balter 2013

Michael Balter, *Farming's Tangled European Roots.* science **342** (2013), 181–182.

In the second event, beginning about 6000 years ago, central European farmers spread to Scandinavia, where they mixed with huntergatherers to give rise to the Funnel Beaker culture. These people were talented animal herders, but also continued to hunt and fish. And in a plot twist typical of the farming story, farmers carrying this mixture of farmer and hunter-gatherer genes then migrated from Scandinavia back into central Europe about a thousand years later, further complicating the genetic picture. Researchers are now busy on the next wave of studies: using ancient nuclear DNA to get an even crisper picture of what both men and women were doing during a revolution that apparently came in fits and starts.

Begun 2004

David R. Begun, *The Earliest Hominins, Is Less More?* science **303** (2004), 1478–1480.

Brandt 2013

Guido Brandt et al., *Ancient DNA Reveals Key Stages in the Formation of Central European Mitochondrial Genetic Diversity.* science **342** (2013), 257–261.

s342-0257-Supplement1.pdf, s342-0257-Supplement2.xls, s342-0257-Supplement3.mov

Guido Brandt, Wolfgang Haak, Christina J. Adler, Christina Roth, Anna Szécsényi-Nagy, Sarah Karimnia, Sabine Möller-Rieker, Harald Meller, Robert Ganslmeier, Susanne Friederich, Veit Dresely, Nicole Nicklisch, Joseph K. Pickrell, Frank Sirocko, David Reich, Alan Cooper, Kurt W. Alt & The Genographic Consortium

The processes that shaped modern European mitochondrial DNA (mtDNA) variation remain unclear. The initial peopling by Palaeolithic hunter-gatherers ≈42,000 years ago and the immigration of Neolithic farmers into Europe ≈8000 years ago appear to have played important roles but do not explain present-day mtDNA diversity. We generated mtDNA profiles of 364 individuals from prehistoric cultures in Central Europe to perform a chronological study, spanning the Early Neolithic to the Early Bronze Age (5500 to 1550 calibrated years before the common era). We used this transect through time to identify four marked shifts in genetic composition during the Neolithic period, revealing a key role for Late Neolithic cultures in shaping modern Central European genetic diversity.

BRUNET 2005

Michel Brunet et al., *New material of the earliest hominid from the Upper Miocene of Chad*. nature **434** (2005), 752–755.

Michel Brunet, Franck Guy, David Pilbeam, Daniel E. Lieberman, Andossa Likius, Hassane T. Mackaye, Marcia S. Ponce de León, Christoph P. E. Zollikofer & Patrick Vignaud

Discoveries in Chad by the Mission Paléoanthropologique Franco-Tchadienne have substantially changed our understanding of early human evolution in Africa. In particular, the TM 266 locality in the Toros-Menalla fossiliferous area yielded a nearly complete cranium (TM 266-01-60-1), a mandible, and several isolated teeth assigned to Sahelanthropus tchadensis3 and biochronologically dated to the late Miocene epoch (about 7 million years ago). Despite the relative completeness of the TM 266 cranium, there has been some controversy about its morphology and its status in the hominid clade. Here we describe new dental and mandibular specimens from three Toros-Menalla (Chad) fossiliferous localities (TM 247, TM 266 and TM 292) of the same age. This new material, including a lower canine consistent with a non-honing C/P3 complex, post-canine teeth with primitive root morphology and intermediate radial enamel thickness, is attributed to S. tchadensis. It expands the hypodigm of the species and provides additional anatomical characters that confirm the morphological differences between S. tchadensis and African apes. S. tchadensis presents several key derived features consistent with its position in the hominid clade close to the last common ancestor of chimpanzees and humans.

CELA-CONDE 2003

Camilo J. Cela-Conde & Francisco J. Ayala, *Genera of the human lineage*. PNAS **100** (2003), 7684–7689.

Human fossils dated between 3.5 and nearly 7 million years old discovered during the last 8 years have been assigned to as many as four new genera of the family Hominidae: Ardipithecus, Orrorin, Kenyanthropus, and Sahelanthropus. These specimens are described as having morphological traits that justify placing them in the family Hominidae while creating a new genus for the classification of each. The discovery of these fossils pushed backward by >2 million years the date of the oldest hominids known. Only two or three hominid genera, Australopithecus, Paranthropus, and Homo, had been previously accepted, with Paranthropus considered a subgenus of Australopithecus by some authors. Two questions arise from the classification of the newly discovered fossils: (i) Should each one of these specimens be placed in the family Hominidae? (ii) Are these specimens sufficiently distinct to justify the creation of four new genera? The answers depend, in turn, on the concepts of what is a hominid and how the genus category is defined. These specimens seem to possess a sufficient number of morphological traits to be placed in the Hominidae. However, the nature of the morphological evidence and the adaptation-rooted concept of what a genus is do not justify the establishment of four new genera. We propose a classification that includes four well defined genera: Praeanthropus, Ardipithecus, Australopithecus, and Homo, plus one tentative incertae sedis genus: Sahelanthropus.

Galik 2004

K. Galik, B. Senut, M. Pickford, D. Gommery, J. Treil, A. J. Kuperavage & R. B. Eckhardt, *External and Internal Morphology of the BAR 1002'00 Orrorin tugenensis Femur.* science **305** (2004), 1450–1453.

s305-1450-Supplement.pdf, s307-0845-Ohman.pdf

Late Miocene fossils from the Lukeino Formation in Kenya's Tugen Hills are assigned to Orrorin tugenensis. Of 20 fossils recovered there to date, 3are proximal femurs. One of these, BAR 1002'00, preserves an intact head connected to the proximal shaft by an elongated neck. Although this fossil is comparable in size to Pan troglodytes, computerized tomography scans of the neck-shaft junction of BAR 1002'00 reveal that the cortex is markedly thinner superiorly than inferiorly, differing from the approximately equal cortical thicknesses observed in extant African apes, approaching the condition in later hominids, and indicating that O. tugenensis was bipedal.

Gibbons 2005

Ann Gibbons, *Facelift Supports Skull's Status as Oldest Member of the Human Family.* science **308** (2005), 179–181.

Guy 2005

Franck Guy et al., *Morphological affinities of the Sahelanthropus tchadensis (Late Miocene hominid from Chad) cranium.* PNAS **102** (2005), 18836–18841.

pnas102-18836-Table2.xls, pnas102-18836-Table3.xls, pnas102-18836-Table4.xls, pnas102-18836-Table5.xls

Franck Guy, Daniel E. Lieberman, David Pilbeam, Marcia Ponce de León, Andossa Likius, Hassane T. Mackaye, Patrick Vignaud, Christoph Zollikofer & Michel Brunet

The recent reconstruction of the Sahelanthropus tchadensis cranium (TM 266-01-60-1) provides an opportunity to examine in detail differences in cranial shape between this earliest-known hominid, African apes, and other hominid taxa. Here we compare the reconstruction of TM 266-01-60-1 with crania of African apes, humans, and several Pliocene hominids. The results not only confirm that TM 266-01-60-1 is a hominid but also reveal a unique mosaic of characters. The TM 266-01-60-1 reconstruction shares many primitive features with chimpanzees but overall is most similar to Australopithecus, particularly in the basicranium. However, TM 266-01-60-1 is distinctive in having the combination of a short subnasal region associated with a vertical upper face that projects substantially in front of the neurocranium. Further research is needed to determine the evolutionary relationships between Sahelanthropus and the known Miocene and Pliocene hominids.

geometric morphometric | 3D reconstruction | Homo | Australopithecus | African apes

Haile-Selassie 2001

Yohannes Haile-Selassie, *Late Miocene hominids from the Middle Awash, Ethiopia.* nature **412** (2001), 178–181.

Molecular studies suggest that the lineages leading to humans and chimpanzees diverged approximately 6.5±5.5 million years (Myr) ago, in the Late Miocene. Hominid fossils from this interval, however, are fragmentary and of uncertain phylogenetic status, age, or both. Here I report new hominid specimens from the Middle Awash area of Ethiopia that date to 5.2±5.8Myr and are associated with a wooded palaeoenvironment. These Late Miocene fossils are assigned to the hominid genus Ardipithecus and represent the earliest definitive evidence of the hominid clade. Derived dental characters are shared exclusively with all younger hominids. This indicates that the fossils probably represent a hominid taxon that postdated the divergence of lineages leading to modern chimpanzees and humans. However, the persistence of primitive dental and postcranial characters in these new fossils indicates that Ardipithecus was phylogenetically close to the common ancestor of chimpanzees and humans. These new findings raise additional questions about the claimed hominid status of Orrorin tugenensis, recently described from Kenya and dated to ,6 Myr.

HAILE-SELASSIE 2004

Yohannes Haile-Selassie, Gen Suwa & Tim D. White, *Late Miocene Teeth from Middle Awash, Ethiopia, and Early Hominid Dental Evolution*. science **303** (2004), 1503–1505.

Late Miocene fossil hominid teeth recovered from Ethiopia's Middle Awash are assigned to Ardipithecus kadabba. Their primitive morphology and wear pattern demonstrate that A. kadabba is distinct from Ardipithecus ramidus. These fossils suggest that the last common ancestor of apes and humans had a functionally honing canine–third premolar complex. Comparison with teeth of Sahelanthropus and Orrorin, the two other named late Miocene hominid genera, implies that these putative taxa are very similar to A. kadabba. It is therefore premature to posit extensive late Miocene hominid diversity on the basis of currently available samples.

HAWKS 2012

John Hawks, *Longer time scale for human evolution*. PNAS **109** (2012), 15531–15532.

A mere 2 y ago, genomic evidence from Neanderthals suggested that they had originated within the past 270,000 to 440,000 y (12). This troublesome date excludes specimens that have appeared to be strong candidates for Neanderthal ancestors, including the large sample of skeletal remains from Sima de los Huesos, Atapuerca, Spain, possibly more than 530,000 y old. Now, the maximum value for Neanderthal–human common ancestry from 2010 seems instead closer to a minimum date. Langergraber et al. suggest a range from 420,000 to 780,000 y, bringing much of the Middle Pleistocene record of Europe into the scope of Neanderthal ancestry.

OHMAN 2005

James C.Ohman, C. Owen Lovejoy, Tim D. White, *Questions About Orrorin Femur*. science **307** (2005), 845.

Given the importance of the Lukeino femur, we urge its discoverers to make available evidence to support their assertions. The required evidence is (i) photographs, measurements, and drawings of its broken neck; (ii) conventional anteroposterior x-rays; and (iii) higher-resolution CT scans obtained with proper femoral orientation. Exceptional claims demand exceptional evidence; the adjustment of previously published data does not suffice.

PATTERSON 2006

Nick Patterson, Daniel J. Richter, Sante Gnerre, Eric S. Lander & David Reich, *Genetic evidence for complex speciation of humans and chimpanzees*. nature **441** (2006), 1103–1108.

n441-1103-Supplement.pdf

The genetic divergence time between two species varies substantially across the genome, conveying important information about the timing and process of speciation. Here we develop a framework for studying this variation and apply it to about 20 million base pairs of aligned sequence from humans, chimpanzees, gorillas and more distantly related primates. Human–chimpanzee genetic divergence varies from less than 84 % to more than 147 % of the average, a range of more than 4 million years. Our analysis also shows that human–chimpanzee speciation occurred less than 6.3 million years ago and probably more recently, conflicting with some interpretations of ancient fossils. Most strikingly, chromosome X shows an extremely young genetic divergence time, close to the genome minimum along nearly its entire length. These unexpected features would be explained if the human and chimpanzee lineages initially diverged, then later exchanged genes before separating permanently.

RICHMOND 2008

Brian G. Richmond & William L. Jungers, *Orrorin tugenensis Femoral Morphology and the Evolution of Hominin Bipedalism*. science **319** (2008), 1662–1665.

s319-1662-Supplement.pdf

Bipedalism is a key human adaptation and a defining feature of the hominin clade. Fossil femora discovered in Kenya and attributed to Orrorin tugenensis, at 6 million years ago, purportedly provide the earliest postcranial evidence of hominin bipedalism, but their functional and phylogenetic affinities are controversial. We show that the O. tugenensis femur differs from those of apes and Homo and most strongly resembles those of Australopithecus and Paranthropus, indicating that O. tugenensis was bipedal but is not more closely related to Homo than to Australopithecus. Femoral morphology indicates that O. tugenensis shared distinctive hip biomechanics with australopiths, suggesting that this complex evolved early in human evolution and persisted for almost 4 million years until modifications of the hip appeared in the late Pliocene in early Homo.

SPOOR 2013

Fred Spoor, *Small-brained and big-mouthed*. nature **502** (2013), 452–453.

A complete hominin cranium found at the archaeological site of Dmanisi shows remarkably primitive morphology, prompting its discoverers to propose that early forms of the genus Homo evolved as a single, highly variable lineage.

The radical proposal to subsume the well-established taxa H. habilis and H. rudolfensis into H. erectus warrants careful scrutiny, and in my view the presented evidence is weak. It is doubtful whether analyses of overall cranial shape have the diagnostic power to distinguish between closely related taxa. Finally, the authors make no reference to the available non-cranial fossil evidence, even though biomechanical analyses of specimens attributed to H. habilis and H. erectus indicate marked differences in locomotive behaviour.

SUWA 2007

Gen Suwa, Reiko T. Kono, Shigehiro Katoh, Berhane Asfaw & Yonas Beyene, *A new species of great ape from the late Miocene epoch in Ethiopia*. nature **448** (2007), 921–924.

n448-0921-Supplement.pdf

With the discovery of Ardipithecus, Orrorin and Sahelanthropus1–7, our knowledge of hominid evolution before the emergence of Pliocene species of Australopithecus8,9 has significantly increased, extending the hominid fossil record back to at least 6 million years (Myr) ago. However, because of the dearth of fossil hominoid remains in sub-Saharan Africa spanning the period 12–7 Myr ago, nothing is known of the actual timing and mode of divergence of the African ape and hominid lineages. Most genomic-based studies suggest a late divergence date—5–6 Myr ago and 6–8 Myr ago for the human–chimp andhuman–gorilla splits, respectively10–14—and some palaeontological and molecular analyses hypothesize a Eurasian origin of the African ape andhominid clade15,16.Wereport here the discovery and recognition of a new species of great ape, Chororapithecus abyssinicus, fromthe 10–10.5-Myr-old deposits of the Chorora Formation at the southern margin of the Afar rift. To the best of our knowledge, these are the first fossils of a largebodied Miocene ape from the African continent north of Kenya. They exhibit a gorilla-sized dentition that combines distinct shearing crests with thick enamel on its 'functional' side cusps. Visualization of the enamel–dentine junction by micro-computed tomography reveals shearing crest features that partly resemble the modern gorilla condition. These features represent genetically based structural modifications probably associated with an initial adaptation to a comparatively fibrous diet. The relatively flat cuspal enamel–dentine junction and thick enamel, however, suggest a concurrent adaptation to hard and/or abrasive food items. The combined evidence suggests that Chororapithecus may be a basal member of the gorilla clade, and that the latter exhibited some amount of adaptive and phyletic diversity at around 10–11 Myr ago.

Thorpe 2007

S. K. S. Thorpe, R. L. Holder & R. H. Crompton, *Origin of Human Bipedalism as an Adaptation for Locomotion on Flexible Branches.* science **316** (2007), 1328–1331.

s316-1328-Supplement.pdf

Human bipedalism is commonly thought to have evolved from a quadrupedal terrestrial precursor, yet some recent paleontological evidence suggests that adaptations for bipedalism arose in an arboreal context. However, the adaptive benefit of arboreal bipedalism has been unknown. Here we show that it allows the most arboreal great ape, the orangutan, to access supports too flexible to be negotiated otherwise. Orangutans react to branch flexibility like humans running on springy tracks, by increasing knee and hip extension, whereas all other primates do the reverse. Human bipedalism is thus less an innovation than an exploitation of a locomotor behavior retained from the common great ape ancestor.

Wood 2010

Bernard Wood, *Reconstructing human evolution: Achievements, challenges, and opportunities.* PNAS **107** (2010), 8902–8909.

This contribution reviews the evidence that has resolved the branching structure of the higher primate part of the tree of life and the substantial body of fossil evidence for human evolution. It considers some of the problems faced by those who try to interpret the taxonomy and systematics of the human fossil record. How do you to tell an early human taxon from one in a closely related clade? How do you determine the number of taxa represented in the human clade? How can homoplasy be recognized and factored into attempts to recover phylogeny?
history | hominin

Wood 2011

Bernard Wood & Terry Harrison, *The evolutionary context of the first hominins.* nature **470** (2011), 347–352.

The relationships among the living apes and modern humans have effectively been resolved, but it is much more difficult to locate fossil apes on the tree of life because shared skeletal morphology does not always mean shared recent evolutionary history. Sorting fossil taxa into those that belong on the branch of the tree of life that leads to modern humans from those that belong on other closely related branches is a considerable challenge.

ZOLLIKOFER 2005

Christoph P. E. Zollikofer et al., *Virtual cranial reconstruction of Sahelanthropus tchadensis.* nature **434** (2005), 755–759.

Christoph P. E. Zollikofer, Marcia S. Ponce de León, Daniel E. Lieberman, Franck Guy, David Pilbeam, Andossa Likius, Hassane T. Mackaye, Patrick Vignaud & Michel Brunet

Previous research in Chad at the Toros-Menalla 266 fossiliferous locality (about 7 million years old) uncovered a nearly complete cranium (TM 266-01-60-1), three mandibular fragments and several isolated teeth attributed to Sahelanthropus tchadensis. Of this material, the cranium is especially important for testing hypotheses about the systematics and behavioural characteristics of this species, but is partly distorted from fracturing, displacement and plastic deformation. Here we present a detailed virtual reconstruction of the TM 266 cranium that corrects these distortions. The reconstruction confirms that S. tchadensis is a hominid and is not more closely related to the African great apes. Analysis of the basicranium further indicates that S. tchadensis might have been an upright biped, suggesting that bipedalism was present in the earliest known hominids, and probably arose soon after the divergence of the chimpanzee and human lineages.

Energie

ALLEN 2013

David T. Allen et al., *Measurements of methane emissions at natural gas production sites in the United States.* PNAS **110** (2013), 17768–17773.

David T. Allen, Vincent M. Torres, James Thomas, David W. Sullivan, Matthew Harrison, Al Hendler, Scott C. Herndon, Charles E. Kolb, Matthew P. Fraser, A. Daniel Hill, Brian K. Lamb, Jennifer Miskimins, Robert F. Sawyer & John H. Seinfeld

Engineering estimates of methane emissions from natural gas production have led to varied projections of national emissions. This work reports direct measurements of methane emissions at 190 onshore natural gas sites in the United States (150 production sites, 27 well completion flowbacks, 9 well unloadings, and 4 workovers). For well completion flowbacks, which clear fractured wells of liquid to allow gas production, methane emissions ranged from 0.01 Mg to 17 Mg (mean = 1.7 Mg; 95 % confidence bounds of 0.67–3.3 Mg), compared with an average of 81 Mg per event in the 2011 EPA national emission inventory from April 2013. Emission factors for pneumatic pumps and controllers as well as equipment leaks were both comparable to and higher than estimates in the national inventory. Overall, if emission factors from this work for completion flowbacks, equipment leaks, and pneumatic pumps and controllers are assumed to be representative of national populations and are used to estimate national emissions, total annual emissions from these source categories are calculated to be 957 Gg of methane (with sampling and measurement uncertainties estimated at ±200 Gg). The estimate for comparable source categories in the EPA national inventory is ≈1,200 Gg. Additional

measurements of unloadings and workovers are needed to produce national emission estimates for these source categories. The 957 Gg in emissions for completion flowbacks, pneumatics, and equipment leaks, coupled with EPA national inventory estimates for other categories, leads to an estimated 2,300 Gg of methane emissions from natural gas production (0.42 % of gross gas production).
greenhouse gas emissions | hydraulic fracturing

Grundlagen

Gibbons 2002

Ann Gibbons, *One Scientist's Quest for The Origin of Our Species.* science **298** (2002), 1708–1711.

Years of effort in hostile territory finally pay off for French paleontologist Michel Brunet,who discovered a fossil that might be the first member of the human family.

Pluciennik 2006

Mark Pluciennik, *Clash of cultures? Archaeology and genetics.* Documenta Praehistorica **33** (2006), 39–49.

This paper examines the ways in which genetic data have been used to interpret the transition to agriculture in Europe over the past two decades, and the relationship of these interpretations to more strictly archaeological explanations. It is suggested that, until recently, those working within the two disciplines have been using not only different data sets and methodologies, but also working within different disciplinary traditions which have inhibited communication and collaboration, and the production of a genuinely integrated field of 'archaeogenetics'.

Story or Book

Beckwith 2013

Christopher I. Beckwith, *Science spun on the Silk Road.* nature **502** (2013), 445–446.

Christopher I. Beckwith assesses a study probing Central Asia's pivotal role in Islam's golden age.
Lost Enlightenment: Central Asia's Golden Age from the Arab Conquest to Tamerlane. S. Frederick Starr. Princeton University Press: 2013.
It is increasingly recognized that many of the greatest scientists, philosophers, poets and artists of the Islamic golden age were from Central Asia. A few of their works have been studied or translated, such as al-Biruni's famous ethnography of India. But Starr's book is the first to identify the leading lights of that age as Central Asians, place them squarely in Central Asia, and detail their accomplishments.
The dominant literary language was classical Arabic. However, this was not due to the Arabs destroying Khwarizm's libraries, a claim repeated by Starr but shown by Wilhelm Barthold in 1928 to be folklore.
He does, however, ignore recent work that explodes myths about Eurasian steppe peoples being aggressors, and even obliquely suggests that Chinggis Khan "attempted genocide" of Central Asians.
Starr shines in his core chapters, where he presents the great achievements of the Central Asian philosopher–scientists at a time when their homeland was the creative intellectual capital of the world.

Crease 2013

Robert P. Crease, *Science under the Nazis.* nature **502** (2013), 441–442.

Robert P. Crease applauds the story of three great physicists who struggled to maintain their integrity during the Third Reich.

Serving the Reich: The Struggle for the Soul of Physics Under Hitler. Philip Ball. Bodley Head: 2013.

Ball insists that, rather than simplistically condemning or absolving the German scientists, we should look at their moral behaviour as a perpetually open question. Most daringly, he suggests that the way they coped with entanglements of science, politics and life is still representative of scientists now. By the end of this book, careful readers will be left with the queasy feeling that our own moral high ground has disappeared, and that Ball has revealed the "soul" of physics to be no more intrinsically noble than any other.