Liste erstellt am 2017-06-03

References

Afrika

Breunig 1996

Peter Breunig, Katharina Neumann & Wim Van Neer, *New Research on the Holocene Settlement and Environment of the Chad Basin in Nigeria*. African Archaeological Review **13** (1996), 111–145.

Recent investigations of three archaeological sites in the Nigerian part of the Chad Basin during the Holocene reveal key stages in the cultural development and environmental history of that region. At Dufuna, a dugout boat was dated to around 6000 BQ making it the oldest known boat in Africa and one of the oldest in the world. Boats may thus have contributed to the mobility of the population of the southern edge of the Sahara 8000 years ago and, thereby, to the cultural homogeneity of this period. The pottery site at Konduga is around a thousand years younger than Dufuna but still belongs to the time of Mega-Chad. The site is on the Bama Ridge, an old shoreline. Its pottery, decorated in the Saharan tradition, belongs to the earliest ceramic phase of the West African Later Stone Age, long before the beginnings of food production. Although this site was probably settled by pioneers advancing into a largely flooded landscape along the slightly raised shoreline, the human occupation of the area previously covered by Mega-Chad began along a broad front around 2000 BC Archaeological and palaeoecological finds from two settlement mounds at Gajiganna are described as case studies for this phase, which predates the well-known site of Daima.

Keywords: Nigeria | Holocene | Later Stone Age | paleoenvironment | paleoeconomy.

Patin 2017

Etienne Patin et al., *Dispersals and genetic adaptation of Bantu-speaking populations in Africa and North America*. science **356** (2017), 543–546.

s356-0543-Supplement1.pdf, s356-0543-Supplement2.xlsx

Etienne Patin, Marie Lopez, Rebecca Grollemund, Paul Verdu, Christine Harmant, Hélène Quach, Guillaume Laval, George H. Perry, Luis B. Barreiro, Alain Froment, Evelyne Heyer, Achille Massougbodji, Cesar Fortes-Lima, Florence Migot-Nabias, Gil Bellis, Jean-Michel Dugoujon, Joana B. Pereira, Verónica Fernandes, Luisa Pereira, Lolke Van der Veen, Patrick Mouguiama-Daouda, Carlos D. Bustamante, Jean-Marie Hombert & Lluís Quintana-Murci

Bantu languages are spoken by about 310 million Africans, yet the genetic history of Bantu-speaking populations remains largely unexplored. We generated genomic data for 1318 individuals from 35 populations in western central Africa, where Bantu languages originated. We found that early Bantu speakers first moved southward, through the equatorial rainforest, before spreading toward eastern and southern Africa. We also found that genetic adaptation of Bantu speakers was facilitated by admixture with local populations, particularly for the HLA and LCT loci. Finally, we identified a major contribution of western central African Bantu speakers to the ancestry of African Americans, whose genomes present no strong signals of natural selection. Together, these results highlight the contribution of

Bantu-speaking peoples to the complex genetic history of Africans and African Americans.

SCHUENEMANN 2017

Verena J. Schuenemann et al., *Ancient Egyptian mummy genomes suggest an increase of Sub-Saharan African ancestry in post-Roman periods.* Nature Communications **8** (2017), 15694. DOI:10.1038/ncomms15694.

NatComm08-15694-Supplement.pdf

Verena J. Schuenemann, Alexander Peltzer, Beatrix Welte, W. Paul van Pelt, Martyna Molak, Chuan-Chao Wang, Anja Furtwängler, Christian Urban, Ella Reiter, Kay Nieselt, Barbara Teßmann, Michael Francken, Katerina Harvati, Wolfgang Haak, Stephan Schiffels & Johannes Krause

Egypt, located on the isthmus of Africa, is an ideal region to study historical population dynamics due to its geographic location and documented interactions with ancient civilizations in Africa, Asia and Europe. Particularly, in the first millennium BCE Egypt endured foreign domination leading to growing numbers of foreigners living within its borders possibly contributing genetically to the local population. Here we present 90 mitochondrial genomes as well as genome-wide data sets from three individuals obtained from Egyptian mummies. The samples recovered from Middle Egypt span around 1,300 years of ancient Egyptian history from the New Kingdom to the Roman Period. Our analyses reveal that ancient Egyptians shared more ancestry with Near Easterners than present-day Egyptians, who received additional sub-Saharan admixture in more recent times. This analysis establishes ancient Egyptian mummies as a genetic source to study ancient human history and offers the perspective of deciphering Egypt's past at a genome-wide level.

WATSON 2017

Traci Watson, *Mummy DNA unravels ancestry of ancient Egyptians.* nature **546** (2017), 17.

Genetic analysis reveals a close relationship with Middle Easterners, not central Africans.

The findings show that the mummies' closest kin were ancient farmers from a region that includes present-day Israel and Jordan. Modern Egyptians, by contrast, have inherited more of their DNA from central Africans.

The new data can't explain why the ancient Egyptians were so tightly aligned with people from the Middle East. Was it the result of migration, or were the Stone Age hunter-gatherers of northern Africa genetically similar to those of the Levant?

Aktuell

PENNISI 2017

Elizabeth Pennisi, *In a first, natural selection defeats a biocontrol insect.* science **356** (2017), 570.

Invasive weevil eludes parasitic wasp, shaking confidence in some uses of natural enemies to thwart pests.

Evolution is not known to have defeated biocontrol before, but a natural precedent indicates that hosts of an insect parasite can evolve resistance. In 2014, behavioral ecologist Sonia C. M. Pascoal at the University of Cambridge in the

United Kingdom showed that Hawaiian crickets had evolved a way to elude a fly that homes in on the crickets' mating calls. On two islands, crickets went silent within 24 generations of the parasite's appearance, Pascoal and her colleagues reported in Current Biology.

Stouthamer calls for introducing a second enemy for the weevil. Goldson notes, however, that finding the original wasp was so hard that identifying more biocontrols could be next to impossible. He's hoping that his team's studies will unearth new solutions. And he takes the weevil as a warning. “We can't take biocontrol for granted in New Zealand,” he says. “Just because it works, we don't know where it will go.”

Yehia 2017

Lamis Yehia, *Lucking into science.* science **356** (2017), 654.

Before I embarked on my Ph.D. journey in cancer genomics, I had never thought of a career as a scientist. I had dreamed of becoming a physician for as long as I could remember. But the Fulbright scholarship I won to pursue Ph.D. training in the United States was the chance of a lifetime to continue my education beyond what would have been possible in my home country of Lebanon. I couldn't say no. In retrospect, I was clueless about what it really means to be a scientist. If I had known, I might have hesitated. But now I see that scholarship as a stroke of good fortune, which sent me along a path that helped me find my life's purpose.

Amerika

Watson 2017

Traci Watson, *Is theory about peopling of the Americas a bridge too far?* PNAS **114** (2017), 5554–5557.

Some argue that humans flourished for thousands of years on a fertile intercontinental land bridge until melting glaciers opened the route to the Americas. But major gaps in the evidence remain.

The sparse archaeological record is particularly troubling. Bluefish Caves provides some of the only archeological evidence for human occupation of Beringia during the glacial maximum. But that timing provokes skepticism, and if it's correct, it places humans at a spot in Beringia close to the ice sheet, which was much more barren than the land bridge. “For people to be that far north at Last Glacial Maximum times you would need a lot of compelling evidence to demonstrate that,” says Ben Potter of the University of Alaska Fairbanks. “I'm not convinced.”

It also seems likely that the standstill site was within striking distance of North America. The models show that people entered the Americas from wherever they were waiting as soon as the glaciers began to pull back. Either they were on the doorstep of the Americas at that time, or the instant the ice sheets retreated they sprinted “very, very fast,” Kitchen says.

Anthropologie

Gibbons 2017

Ann Gibbons, *Newest member of human family is surprisingly young, Archaic species may have coexisted with our ancestors.* science **356** (2017), 571.

That means a creature reminiscent of much earlier human ancestors such as H. habilis lived at the same time as modern humans were emerging in Africa and

Neandertals were evolving in Europe. “This is astonishingly young for a species that still displays primitive characteristics found in fossils about 2 million years old,” says paleoanthropologist Chris Stringer of the Natural History Museum in London.

McGann 2017

John P. McGann, *Poor human olfaction is a 19th-century myth.* science **356** (2017), 597, 1–6.

It is commonly believed that humans have a poor sense of smell compared to other mammalian species. However, this idea derives not from empirical studies of human olfaction but from a famous 19th-century anatomist’s hypothesis that the evolution of human free will required a reduction in the proportional size of the brain’s olfactory bulb. The human olfactory bulb is actually quite large in absolute terms and contains a similar number of neurons to that of other mammals. Moreover, humans have excellent olfactory abilities. We can detect and discriminate an extraordinary range of odors, we are more sensitive than rodents and dogs for some odors, we are capable of tracking odor trails, and our behavioral and affective states are influenced by our sense of smell.

Slon 2017

Viviane Slon et al., *Neandertal and Denisovan DNA from Pleistocene sediments.* science **356** (2017), 605–608.

s356-0605-Supplement.pdf

Viviane Slon, Charlotte Hopfe, Clemens L. Weiß, Fabrizio Mafessoni, Marco de la Rasilla, Carles Lalueza-Fox, Antonio Rosas, Marie Soressi, Monika V. Knul, Rebecca Miller, John R. Stewart, Anatoly P. Derevianko, Zenobia Jacobs, Bo Li, Richard G. Roberts, Michael V. Shunkov, Henry de Lumley, Christian Perrenoud, Ivan Gušiæ, Äeljko Kuæan, Pavao Rudan, Ayinuer Aximu-Petri, Elena Essel, Sarah Nagel, Birgit Nickel, Anna Schmidt, Kay Prüfer, Janet Kelso, Hernán A. Burbano, Svante Pääbo & Matthias Meyer

Although a rich record of Pleistocene human-associated archaeological assemblages exists, the scarcity of hominin fossils often impedes the understanding of which hominins occupied a site. Using targeted enrichment of mitochondrial DNA, we show that cave sediments represent a rich source of ancient mammalian DNA that often includes traces of hominin DNA, even at sites and in layers where no hominin remains have been discovered. By automation-assisted screening of numerous sediment samples, we detected Neandertal DNA in eight archaeological layers from four caves in Eurasia. In Denisova Cave, we retrieved Denisovan DNA in a Middle Pleistocene layer near the bottom of the stratigraphy. Our work opens the possibility of detecting the presence of hominin groups at sites and in areas where no skeletal remains are found.

Judentum

Seager 1972

Andrew R. Seager, *The Building History of the Sardis Synagogue.* American Journal of Archaeology **76** (1972), 425–435.

Shiloh 1968

Y. Shiloh, *Torah Scrolls and the Menorah Plaque from Sardis.* Israel Exploration Journal **18** (1968), 54–57.

Thus, the appearance of this motif on the three plaques from Sardis, and Naveh enables us to append the Torah scroll to the list of menorah, shofar, lulab and ethrog, all usually appearing together.

Mathematatik

NOWAK 2017

Martin A. Nowak, Alex McAvoy, Benjamin Allen & Edward O. Wilson, *The general form of Hamilton's rule makes no predictions and cannot be tested empirically*. PNAS **114** (2017), 5665–5670.

Hamilton's rule asserts that a trait is favored by natural selection if the benefit to others, B, multiplied by relatedness, R, exceeds the cost to self, C. Specifically, Hamilton's rule states that the change in average trait value in a population is proportional to BR-C. This rule is commonly believed to be a natural law making important predictions in biology, and its influence has spread from evolutionary biology to other fields including the social sciences. Whereas many feel that Hamilton's rule provides valuable intuition, there is disagreement even among experts as to how the quantities B, R, and C should be defined for a given system. Here, we investigate a widely endorsed formulation of Hamilton's rule, which is said to be as general as natural selection itself. We show that, in this formulation, Hamilton's rule does not make predictions and cannot be tested empirically. It turns out that the parameters B and C depend on the change in average trait value and therefore cannot predict that change. In this formulation, which has been called "exact and general" by its proponents, Hamilton's rule can "predict" only the data that have already been given.

Keywords: evolution | cooperation | kin selection | sociobiology

Significance: Hamilton's rule is a well-known concept in evolutionary biology. It is usually perceived as a statement that makes predictions about natural selection in situations where interactions occur between genetic relatives. Here, we examine what has been called the "exact and general" formulation of Hamilton's rule. We show that in this formulation, which is widely endorsed by proponents of inclusive fitness theory, Hamilton's rule does not make any prediction and cannot be tested empirically. This formulation of Hamilton's rule is not a consequence of natural selection and not even a statement specifically about biology. We give simple and transparent expressions for the quantities of benefit, cost, and relatedness that appear in Hamilton's rule, which reveal that these quantities depend on the data that are to be predicted.

Neolithikum

GONZÁLEZ-FORTES 2017

Gloria González-Fortes et al., *Paleogenomic Evidence for Multi-generational Mixing between Neolithic Farmers and Mesolithic Hunter-Gatherers in the Lower Danube Basin*. Current Biology (2017), preprint, 1–10. DOI:10.1016/j.cub.2017.05.023.

Gloria González-Fortes, Eppie R. Jones, Emma Lightfoot, Clive Bonsall, Catalin Lazar, Aurora Grandal-d'Anglade, María Dolores Garralda, Labib Drak, Veronika Siska, Angela Simalcsik, Adina Boroneanté, Juan Ramón Vidal Romaní, Marcos Vaqueiro Rodríguez, Pablo Arias, Ron Pinhasi, Andrea Manica, & Michael Hofreiter

The transition from hunting and gathering to farming involved profound cultural and technological changes. In Western and Central Europe, these changes occurred rapidly and synchronously after the arrival of early farmers of Anatolian origin [1–3], who largely replaced the local Mesolithic huntergatherers [1, 4–6]. Further east, in the Baltic region, the transition was gradual, with little or no genetic input from incoming farmers [7]. Here we use ancient DNA to investigate the relationship between huntergatherers and farmers in the Lower Danube basin, a geographically intermediate area that is characterized by a rapid Neolithic transition but also by the presence of archaeological evidence that points to cultural exchange, and thus possible admixture, between hunter-gatherers and farmers. We recovered four human paleogenomes (1.13 to 4.13 coverage) from Romania spanning a time transect between 8.8 thousand years ago (kya) and 5.4 kya and supplemented them with two Mesolithic genomes (1.73and 5.33) from Spain to provide further context on the genetic background of Mesolithic Europe. Our results show major Western hunter-gatherer (WHG) ancestry in a Romanian Eneolithic sample with a minor, but sizeable, contribution from Anatolian farmers, suggesting multiple admixture events between hunter-gatherers and farmers. Dietary stableisotope analysis of this sample suggests a mixed terrestrial/aquatic diet. Our results provide support for complex interactions among hunter-gatherers and farmers in the Danube basin, demonstrating that in some regions, demic and cultural diffusion were not mutually exclusive, but merely the ends of a continuum for the process of Neolithization.

Highlights:

- Demic and cultural diffusions underlie the Neolithic period in the Danube basin
- A large WHG genome component was present in Eneolithic communities in this region
- The further east in Europe, the weaker the genetic component of Anatolian farmers
- Environmental factors may account for a demic diffusion breakdown in these regions

In Brief: A key question in archaeological research is whether the transition from hunting and gathering was more reliant on the movement of people or ideas. Gonza’ lezFortes et al. show, based on genomes of several ancient humans, that in parts of Romania, it was actually a mix of both processes that took place during this socalled Neolithization process.