Liste erstellt am 2024-02-07

References

Afrika

FORTES-LIMA 2024

Cesar A. Fortes-Lima, Concetta Burgarella, Rickard Hammarén, Brigitte Pakendorf & Carina M. Schlebusch et al., *The genetic legacy of the expansion of Bantu-speaking peoples in Africa.* nature **625** (2024), 540–547.

n625-0540-Supplement.pdf

The expansion of people speaking Bantu languages is the most dramatic demographic event in Late Holocene Africa and fundamentally reshaped the linguistic, cultural and biological landscape of the continent1–7. With a comprehensive genomic dataset, including newly generated data of modern-day and ancient DNA from previously unsampled regions in Africa, we contribute insights into this expansion that started 6,000–4,000 years ago in western Africa. We genotyped 1,763 participants, including 1,526 Bantu speakers from 147 populations across 14 African countries, and generated whole-genome sequences from 12 Late Iron Age individuals8. We show that genetic diversity amongst Bantu-speaking populations declines with distance from western Africa, with current-day Zambia and the Democratic Republic of Congo as possible crossroads of interaction. Using spatially explicit methods9 and correlating genetic, linguistic and geographical data, we provide cross-disciplinary support for a serial-founder migration model. We further show that Bantu speakers received signiicant gene low from local groups in regions they expanded into. Our genetic dataset provides an exhaustive modern-day African comparative dataset for ancient DNA studies10 and will be important to a wide range of disciplines from science and humanities, as well as to the medical sector studying human genetic variation and health in African and African-descendant populations.

Cesar A. Fortes-Lima, Concetta Burgarella, Rickard Hammarén, Anders Eriksson, Mário Vicente, Cecile Jolly, Armando Semo, Hilde Gunnink, Sara Pacchiarotti, Leon Mundeke, Igor Matonda, Joseph Koni Muluwa, Peter Coutros, Terry S. Nyambe, Justin Cirhuza Cikomola, Vinet Coetzee, Minique de Castro, Peter Ebbesen, Joris Delanghe, Mark Stoneking, Lawrence Barham, Marlize Lombard, Anja Meyer, Maryna Steyn, Helena Malmström, Jorge Rocha, Himla Soodyall, Brigitte Pakendorf, Koen Bostoen & Carina M. Schlebusch

Anthropologie

ALLENTOFT 2024

Morten E. Allentoft et al., *Population genomics of post-glacial western Eurasia.* nature **625** (2024), 301–311.

n625-0301-Supplement.pdf

Western Eurasia witnessed several large-scale human migrations during the Holocene1–5. Here, to investigate the cross-continental efects of these migrations, we shotgun-sequenced 317 genomes—mainly from the Mesolithic and Neolithic periods—from across northern and western Eurasia. These were imputed alongside published data to obtain diploid genotypes from more than 1,600 ancient humans. Our analyses revealed a 'great divide' genomic boundary extending from the Black Sea to the Baltic. Mesolithic hunter-gatherers were highly genetically diferentiated east and west of this zone, and the efect of the neolithization was equally disparate. Large-scale ancestry shifts occurred in the west as farming was introduced, including near-total replacement of hunter-gatherers in many areas, whereas no substantial ancestry shifts happened east of the zone during the same period. Similarly, relatedness decreased in the west from the Neolithic transition onwards, whereas, east of the Urals, relatedness remained high until around 4,000 bp, consistent with the persistence of localized groups of hunter-gatherers. The boundary dissolved when Yamnaya-related ancestry spread across western Eurasia around 5,000 bp, resulting in a second major turnover that reached most parts of Europe within a 1,000-year span. The genetic origin and fate of the Yamnaya have remained elusive, but we show that hunter-gatherers from the Middle Don region contributed ancestry to them. Yamnaya groups later admixed with individuals associated with the Globular Amphora culture before expanding into Europe. Similar turnovers occurred in western Siberia, where we report new genomic data from a 'Neolithic steppe' cline spanning the Siberian forest steppe to Lake Baikal. These prehistoric migrations had profound and lasting efects on the genetic diversity of Eurasian populations.

ALLENTOFT 2024

Morten E. Allentoft, Martin Sikora & Anders Fischer et al., *100 ancient genomes show repeated population turnovers in Neolithic Denmark.* nature **625** (2024), 329–337.

n625-0329-Supplement.docx

Major migration events in Holocene Eurasia have been characterized genetically at broad regional scales1–4. However, insights into the population dynamics in the contact zones are hampered by a lack of ancient genomic data sampled at high spatiotemporal resolution5–7. Here, to address this, we analysed shotgun-sequenced genomes from 100 skeletons spanning 7,300 years of the Mesolithic period, Neolithic period and Early Bronze Age in Denmark and integrated these with proxies for diet (13C and 15N content), mobility (87Sr/86Sr ratio) and vegetation cover (pollen). We observe that Danish Mesolithic individuals of the Maglemose, Kongemose and Ertebølle cultures form a distinct genetic cluster related to other Western European hunter-gatherers. Despite shifts in material culture they displayed genetic homogeneity from around 10,500 to 5,900 calibrated years before present, when Neolithic farmers with Anatolian-derived ancestry arrived. Although the Neolithic transition was delayed by more than a millennium relative to Central Europe, it was very abrupt and resulted in a population turnover with limited genetic contribution from local hunter-gatherers. The succeeding Neolithic population, associated with the Funnel Beaker culture, persisted for only about 1,000 years before immigrants with eastern Steppe-derived ancestry arrived. This second and equally rapid population replacement gave rise to the Single Grave culture with an ancestry proile more similar to present-day Danes. In our multiproxy dataset, these major demographic events are manifested as parallel shifts in genotype, phenotype, diet and land use.

CURRY 2024

Andrew Curry, *In Europe, an early, cold dawn for modern humans.* science **383** (2024), 468–469.

Moderns made mysterious ice age artifacts—implying overlap with Neanderthals.

Though they apparently managed to make a go of it for millennia, ultimately the Ranis people and their contemporaries “weren’t entirely successful,” Hublin says. “They didn’t replace the Neanderthals living farther south, and at least when we try to trace the descendants of people of this time, from Bacho Kiro, it seems we have very little of their genome in later populations.” About 40,000 years ago, a new wave of modern humans arrived and proliferated on a much larger scale. It was those people who soon pushed Neanderthals to the margins, and then to extinction.

IRVING-PEASE 2024

Evan K. Irving-Pease, Alba Refoyo-Martínez, William Barrie, Andrés Ingason, Alice Pearson & Anders Fischer et al., *The selection landscape and genetic legacy of ancient Eurasians.* nature **625** (2024), 312–320.

n625-0312-Supplement.pdf

The Holocene (beginning around 12,000 years ago) encompassed some of the most significant changes in human evolution, with far-reaching consequences for the dietary, physical and mental health of present-day populations. Using a dataset of more than 1,600 imputed ancient genomes1, we modelled the selection landscape during the transition from hunting and gathering, to farming and pastoralism across West Eurasia. We identify key selection signals related to metabolism, including that selection at the FADS cluster began earlier than previously reported and that selection near the LCT locus predates the emergence of the lactase persistence allele by thousands of years. We also find strong selection in the HLA region, possibly due to increased exposure to pathogens during the Bronze Age. Using ancient individuals to infer local ancestry tracts in over 400,000 samples from the UK Biobank, we identify widespread differences in the distribution of Mesolithic, Neolithic and Bronze Age ancestries across Eurasia. By calculating ancestry-specific polygenic risk scores, we show that height differences between Northern and Southern Europe are associated with differential Steppe ancestry, rather than selection, and that risk alleles for mood-related phenotypes are enriched for Neolithic farmer ancestry, whereas risk alleles for diabetes and Alzheimer’s disease are enriched for Western hunter-gatherer ancestry. Our results indicate that ancient selection and migration were large contributors to the distribution of phenotypic diversity in present-day Europeans.

Evan K. Irving-Pease, Alba Refoyo-Martínez, William Barrie, Andrés Ingason, Alice Pearson, Anders Fischer, Karl-Göran Sjögren, Alma S. Halgren, Ruairidh Macleod, Fabrice Demeter, Rasmus A. Henriksen, Tharsika Vimala, Hugh McColl, Andrew H. Vaughn, Leo Speidel, Aaron J. Stern, Gabriele Scorrano, Abigail Ramsøe, Andrew J. Schork, Anders Rosengren, Lei Zhao, Kristian Kristiansen, Astrid K. N. Iversen, Lars Fugger, Peter H. Sudmant, Daniel J. Lawson, Richard Durbin, Thorfinn Korneliussen, Thomas Werge, Morten E. Allentoft, Martin Sikora, Rasmus Nielsen, Fernando Racimo & Eske Willerslev

NOGRADY 2024

Bianca Nogrady, *Australian indigenous genomes are highly diverse and unique.* nature **625** (2024), 15–16.

Scientists hope to expand knowledge of human genetic diversity and improve health for this group.

Bibel

Luciani 2023

Marta Luciani, *Excavating the Qurayyah Oasis, Archaeology in the Land of Midian.* Biblical Archaeology Review **49** (2023), iv, 32–39.

Our excavations at Qurayyah, although not yet revealing the identity of the biblical Midianites, have nonetheless shown the sophistication, ingenuity, and resilience of the ancient North Arabian people who harnessed their desert landscape to its full potential. They created a walled urban oasis that flourished in the middle of the desert for more than three millennia, while at the same time developing their own cultural and religious traditions that were distinctive yet deeply connected and engaged with the peoples of the southern Levant and the wider Near East.

Biologie

Asgari 2024

Samira Asgari & Lionel A. Pousaz, *Multiple sclerosis rooted in European prehistory.* nature **625** (2024), 247–249.

An exploration of more than 1,600 ancient Eurasian genomes suggests that genetic changes that increase autoimmune-disease risk in modern Europeans could have protected ancient Europeans from pathogens.

Barrie 2024

William Barrie, Yaoling Yang, Evan K. Irving-Pease, Kathrine E. Attfield, Gabriele Scorrano & Lise Torp Jensen et al., *Elevated genetic risk for multiple sclerosis emerged in steppe pastoralist populations.* nature **625** (2024), 321–328.

n625-0321-Supplement.pdf

Multiple sclerosis (MS) is a neuro-inlammatory and neurodegenerative disease that is most prevalent in Northern Europe. Although it is known that inherited risk for MS is located within or in close proximity to immune-related genes, it is unknown when, where and how this genetic risk originated1. Here, by using a large ancient genome dataset from the Mesolithic period to the Bronze Age2, along with new Medieval and post-Medieval genomes, we show that the genetic risk for MS rose among pastoralists from the Pontic steppe and was brought into Europe by the Yamnaya-related migration approximately 5,000 years ago. We further show that these MS-associated immunogenetic variants underwent positive selection both within the steppe population and later in Europe, probably driven by pathogenic challenges coinciding with changes in diet, lifestyle and population density. This study Highlights the critical importance of the Neolithic period and Bronze Age as determinants of modern immune responses and their subsequent efect on the risk of developing MS in a changing environment.

William Barrie, Yaoling Yang, Evan K. Irving-Pease, Kathrine E. Attfield, Gabriele Scorrano, Lise Torp Jensen, Angelos P. Armen, Evangelos Antonios Dimopoulos, Aaron Stern, Alba Refoyo-Martinez, Alice Pearson, Abigail Ramsøe, Charleen Gaunitz, Fabrice Demeter, Marie Louise S. Jørkov, Stig Bermann Møller, Bente Springborg, Lutz Klassen, Inger Marie Hyldgård, Niels Wickmann, Lasse Vinner, Thorfinn Sand Korneliussen, Morten E. Allentoft, Martin Sikora, Kristian Kristiansen, Santiago Rodriguez, Rasmus Nielsen, Astrid K. N. Iversen, Daniel J. Lawson, Lars Fugger & Eske Willerslev

Curry 2024

Andrew Curry, *Ancient DNA ties modern diseases to ancestry*. science **383** (2024), 138–139.

Among Europeans, risk of multiple sclerosis rises with genes from Bronze Age Yamnaya herders.

A recent preprint by members of the same team suggests a reason: Many diseases themselves were latecomers. Analysis of pathogen DNA in the ancient bones suggests the incidence of diseases passing from animals to humans, such as the bubonic plague and leptospirosis, did not rise until the time of the first Yamnaya migrations, even though animals had been domesticated thousands of years earlier.

A gene variant that today brings a higher risk of diabetes and high cholesterol appears more frequently in samples from about 12,000 years ago and may have helped ice age hunter-gatherers weather famine.

Price 2024

Michael Price, *A mammoth's life story, written in tusk*. science **383** (2024), 249.

The travels of "Elma" show she faced twin pressures—climate change and human hunting.

Datierung

di Chiara 2024

Anita Di Chiara, Lisa Tauxe, Helen Gries, Barbara Helwing, Matthew D. Howland & E. Ben-Yosef, *An archaeomagnetic study of the Ishtar Gate, Babylon*. PLoS ONE **19** (2024), e293014. DOI:10.1371/journal.pone.0293014.

Data from the marriage of paleomagnetism and archaeology (archaeomagnetism) are the backbone of attempts to create geomagnetic field models for ancient times. Paleointensity experimental design has been the focus of intensive efforts and the requirements and shortcomings are increasingly well understood. Some archaeological materials have excellent age control from inscriptions, which can be tied to a given decade or even a specific year in some cases. In this study, we analyzed fired mud bricks used for the construction of the Ishtar Gate, the entrance complex to the ancient city of Babylon in Southern Mesopotamia. We were able to extract reliable intensity data from all three phases of the gate, the earliest of which includes bricks inscribed with the name of King Nebuchadnezzar II (605 to 562 BCE). These results (1) add high quality intensity data to a region relatively unexplored so far (Southern Mesopotamia), (2) contribute to a better understanding of paleosecular variation in this region, and the development of an archaeomagnetic dating reference for one of the key regions in the history of human civilizations; (3) demonstrate the potential of inscribed bricks (glazed and unglazed), a common material in ancient Mesopotamia, to archaeomagnetic studies; and (4) suggest that the gate complex was constructed some time after the Babylonian conquest of Jerusalem, and that there were no substantial chronological gaps in the construction of each consecutive phase. The best fit of our data (averaging 136 ± 2.1 ZAm2) with those of the reference curve (the Levantine Archaeomagnetic Curve) is 569 BCE.

Islam

NOTLEY 2023

R. Steven Notley, *The House of Peter, Capernaum or Bethsaida?* Biblical Archaeology Review **49** (2023), iv, 40–47.

Klima

GOTTLIEB 2024

Alexander R. Gottlieb & Justin S. Mankin, *Evidence of human influence on Northern Hemisphere snow loss.* nature **625** (2024), 293–300.

n625-0293-Supplement.pdf

Documenting the rate, magnitude and causes of snow loss is essential to benchmark the pace of climate change and to manage the diferential water security risks of snowpack declines1–4. So far, however, observational uncertainties in snow mass5,6 have made the detection and attribution of human-forced snow losses elusive, undermining societal preparedness. Here we show that human-caused warming has caused declines in Northern Hemisphere-scale March snowpack over the 1981–2020 period. Using an ensemble of snowpack reconstructions, we identify robust snow trends in 82 out of 169 major Northern Hemisphere river basins, 31 of which we can conidently attribute to human inluence. Most crucially, we show a generalizable and highly nonlinear temperature sensitivity of snowpack, in which snow becomes marginally more sensitive to one degree Celsius of warming as climatological winter temperatures exceed minus eight degrees Celsius. Such nonlinearity explains the lack of widespread snow loss so far and augurs much sharper declines and water security risks in the most populous basins. Together, our results emphasize that human-forced snow losses and their water consequences are attributable—even absent their clear detection in individual snow products—and will accelerate and homogenize with near-term warming, posing risks to water resources in the absence of substantial climate mitigation.

HAMILTON 2024

Rebecca Hamilton et al., *Forest mosaics, not savanna corridors, dominated in Southeast Asia during the Last Glacial Maximum.* PNAS **121** (2024), e2311280120.

pnas121-e2311280120-Supplement.pdf

The dominant paradigm is that large tracts of Southeast Asia's lowland rainforests were replaced with a "savanna corridor" during the cooler, more seasonal climates of the Last Glacial Maximum (LGM) (23,000 to 19,000 y ago). This interpretation has implications for understanding the resilience of Asia's tropical forests to projected climate change, implying a vulnerability to "savannization". A savanna corridor is also an important foundation for archaeological interpretations of how humans moved through and settled insular Southeast Asia and Australia. Yet an up-to-date, multiproxy, and empirical examination of the palaeoecological evidence for this corridor is lacking. We conducted qualitative and statistical analyses of 59 palaeoecological records across Southeast Asia to test the evidence for LGM savannization and clarify the relationships between methods, biogeography, and ecological change in the region from the start of Late Glacial Period (119,000 y ago) to the present. The pollen records typically show montane forest persistence during the LGM, while d13C biomarker proxies indicate the expansion of C4-rich grasslands. We reconcile this discrepancy by hypothesizing the expansion of montane forest in the uplands and replacement of rainforest with seasonally dry tropical

forest in the lowlands. We also find that smooth forest transitions between 34,000 and 2,000 y ago point to the capacity of Southeast Asia's ecosystems both to resist and recover from climate stressors, suggesting resilience to savannization. Finally, the timing of ecological change observed in our combined datasets indicates an ‘early’ onset of the LGM in Southeast Asia from ≈30,000 y ago.

Keywords: grassland | palaeoenvironmental change | ecological regime shift | monsoon forest

Rebecca Hamilton, Noel Amano, Corey J. A. Bradshaw, Frédérik Saltré, Robert Patalano, Dan Penny, Janelle Stevenson, Jesse Wolfhagen & Patrick Roberts

Significance: We present new qualitative and statistical analyses of 59 palaeoecological records across Southeast Asia to show that, instead of swings between open savanna and dense rainforest ecosystems, the climatic changes of the Last Glacial Period (119–11.7 ka) and particularly the Last Glacial Maximum (conventionally ≈23–19 ka) involved fluid transitions between lowland rainforest, more open canopy seasonally dry forest, and tropical montane forest. This “hybrid” open forest biome provides an alternative to the currently accepted binary ecologies for the region and yields new insights into ecological resilience for tropical forests in Southeast Asia and beyond. Additionally, it points to diversified rather than overturned resource availability for humans that were occupying and migrating through the region.

Sprachlehre

Joosten 2024

Jan Joosten, *Delocutive Nouns in Biblical Hebrew.* unknown (2024), preprint, 1–18. .

Delocutives are words derived from locutions. An English example is the verb “to tut-tut” as in: “We all spent a lot of time tut-tutting about Angie and her lifestyle.” “To tut-tut” means “to say ‘tut-tut”’—or rather: “to pronounce the peculiar sound which is transcribed as ‘tut-tut”’—in a situation where saying this is meaningful. An alternative lexical definition is: “to express disapproval by the exclamation of ‘tut-tut’.” In fact, “tut-tutting” does not necessarily imply saying “tut-tut”; expressing mild disapproval in a situation where one might say tut-tut would suffice.

Many of the “delocutive” meanings defended here have been considered in the history of exegesis, often as one of several possibilities. In an ancient language, represented by a relatively small corpus, defining meaning and usage of words is difficult. Some of the examples discussed in this paper remain open to discussion. Even so, it would seem to be useful to have a theoretical framework within which the phenomenon can be more clearly understood.