

## References

### Aktuell

BORTOLINI 2017

Eugenio Bortolini et al., *Inferring patterns of folktale diffusion using genomic data*. *PNAS* **114** (2017), 9140–9145.

[pnas114-09140-Supplement.xlsx](#)

Eugenio Bortolini, Luca Pagani, Enrico R. Crema, Stefania Sarno, Chiara Barbieri, Alessio Boattini, Marco Sazzini, Sara Graça da Silva, Gessica Martini, Mait Metspalu, Davide Pettener, Donata Luiselli & Jamshid J. Tehrani

Observable patterns of cultural variation are consistently intertwined with demic movements, cultural diffusion, and adaptation to different ecological contexts [Cavalli-Sforza and Feldman (1981) *Cultural Transmission and Evolution: A Quantitative Approach*; Boyd and Richerson (1985) *Culture and the Evolutionary Process*]. The quantitative study of gene–culture coevolution has focused in particular on the mechanisms responsible for change in frequency and attributes of cultural traits, the spread of cultural information through demic and cultural diffusion, and detecting relationships between genetic and cultural lineages. Here, we make use of worldwide whole-genome sequences [Pagani et al. (2016) *Nature* 538:238–242] to assess the impact of processes involving population movement and replacement on cultural diversity, focusing on the variability observed in folktale traditions (n = 596) [Uther (2004) *The Types of International Folktales: A Classification and Bibliography*. Based on the System of Antti Aarne and Stith Thompson] in Eurasia. We find that a model of cultural diffusion predicted by isolation-by-distance alone is not sufficient to explain the observed patterns, especially at small spatial scales (up to  $\approx 4,000$  km). We also provide an empirical approach to infer presence and impact of ethnolinguistic barriers preventing the unbiased transmission of both genetic and cultural information. After correcting for the effect of ethnolinguistic boundaries, we show that, of the alternative models that we propose, the one entailing cultural diffusion biased by linguistic differences is the most plausible. Additionally, we identify 15 tales that are more likely to be predominantly transmitted through population movement and replacement and locate putative focal areas for a set of tales that are spread worldwide.

**Keywords:** cultural diffusion | demic diffusion | whole-genome sequences | folktales | Eurasia

**Significance:** This paper presents unprecedented evidence on the transmission mechanism underlying the spread of a broad cross-cultural assemblage of folktales in Eurasia and Africa. State-of-the-art genomic evidence is used to directly assess the relevance of demic diffusion processes, in particular on the distribution of Old World folktales at intermediate geographic scales, and identify individual stories that are more likely to be transmitted through population movement and replacement. The results provide an empirical solution to operate with linguistic barriers and highlight the impossibility of disentangling genetic from geographic relationships at a cross-continental scale, warning against the direct use of extant genetic variability to infer processes of long-range cultural transmission.

SOON LEE 2017

Mary Soon Lee, *Elemental haiku*. *science* **357** (2017), 461–463.

Author Mary Soon Lee (marysoonlee@gmail.com) provides this review of the periodic table composed of 119 science haiku, one for each element plus a closing haiku for element 119 (not yet synthesized). The haiku encompass astronomy, biology, chemistry, history, physics, and a bit of whimsical flair.

## STAR 2017

Bastiaan Star et al., *Ancient DNA reveals the Arctic origin of Viking Age cod from Haithabu, Germany*. *PNAS* **114** (2017), 9152–9157.

Bastiaan Star, Sanne Boessenkool, Agata T. Gondek, Elena A. Nikulina, Anne Karin Hufthammer, Christophe Pampoulie, Halvor Knutsen, Carl André, Heidi M. Nistelberger, Jan Dierking, Christoph Petereit, Dirk Heinrich, Kjetill S. Jakobsen, Nils Chr. Stenseth, Sissel Jentoft & James H. Barrett

Knowledge of the range and chronology of historic trade and long-distance transport of natural resources is essential for determining the impacts of past human activities on marine environments. However, the specific biological sources of imported fauna are often difficult to identify, in particular if species have a wide spatial distribution and lack clear osteological or isotopic differentiation between populations. Here, we report that ancient fishbone remains, despite being porous, brittle, and light, provide an excellent source of endogenous DNA (15–46 %) of sufficient quality for whole-genome reconstruction. By comparing ancient sequence data to that of modern specimens, we determine the biological origin of 15 Viking Age (800–1066 CE) and subsequent medieval (1066–1280 CE) Atlantic cod (*Gadus morhua*) specimens from excavation sites in Germany, Norway, and the United Kingdom. Archaeological context indicates that one of these sites was a fishing settlement for the procurement of local catches, whereas the other localities were centers of trade. Fish from the trade sites show a mixed ancestry and are statistically differentiated from local fish populations. Moreover, Viking Age samples from Haithabu, Germany, are traced back to the North East Arctic Atlantic cod population that has supported the Lofoten fisheries of Norway for centuries. Our results resolve a long-standing controversial hypothesis and indicate that the marine resources of the North Atlantic Ocean were used to sustain an international demand for protein as far back as the Viking Age.

**Keywords:** genomics | high-throughput sequencing | trade | chromosomal inversion | fish bone

**Significance:** A rich archaeological record of fish-bone remains testifies to the millennia-long human exploitation of the natural resources of the oceans. In Europe, historical evidence demonstrates that an extensive international industry developed during the Middle Ages that exported preserved cod from the Lofoten Archipelago, northern Norway, to expanding urban centers around the North and Baltic Sea regions. The early origins of this iconic exchange, however, have long been debated. We genetically trace the ancestry of Viking Age fish from mainland Europe to the North East Arctic cod population that supports the modern Lofoten fisheries. This application of genome-wide analyses from ancient fish bone reveals an early origin of what became an economically important trade, with implications for archaeology and environmental history.

## Amerika

## KENNETT 2017

Douglas J. Kennett et al., *High-precision chronology for Central American maize diversification from El Gigante rockshelter, Honduras*. *PNAS* **114** (2017), 9026–9031.

Douglas J. Kennett, Heather B. Thakar, Amber M. VanDerwarker, David L. Webster, Brendan J. Culleton, Thomas K. Harper, Logan Kistler, Timothy E. Scheffler & Kenneth Hirth

The first steps toward maize (*Zea mays* subspecies *mays*) domestication occurred in the Balsas region of Mexico by  $\approx 9,000$  calendar years B.P. (cal B.P.), but it remains unclear when maize was productive enough to be a staple grain in the Americas. Molecular and microbotanical data provide a partial picture of the timing and nature of morphological change, with genetic data indicating that alleles for some domestication traits were not yet fixed by 5,300 cal B.P. in the highlands of Mexico. Here, we report 88 radiocarbon dates on the botanical remains from El Gigante rockshelter (Honduras) to establish a Bayesian chronology over the past  $\approx 11,000$  y spanning the transition to maize-based food production. Botanical remains are remarkably well preserved and include over 10,000 maize macrofossils. We directly dated 37 maize cobs to establish the appearance and local change of maize at the site. Cobs are common in deposits dating between 4,340 and 4,020 cal B.P., and again between 2,350 and 980 cal B.P. The earliest cobs appear robustly domesticated, having 10–14 rows, suggesting strong selection for increased yield. The later cobs are comparable to these earliest ones, but show clear emergence of diverse traits, including increased cob width, rachis segment length, and cupule width. Our results indicate that domesticated landraces of maize productive enough to be a staple grain existed in Central America by 4,300 cal B.P.

**Keywords:** maize | teosinte | Central America | domestication | agriculture

**Significance:** Maize was initially domesticated in the Balsas region of Mexico  $\approx 9,000$  y ago, but it remains unclear when this globally important cultigen became a staple crop in the Americas. We demonstrate that highly productive maize varieties were present in Central America outside the natural distribution of ancestral teosinte populations [*Zea mays* subspecies (ssp.) *parviglumis*] by  $\approx 4,340$  calendar years B.P., and we hypothesize that reduced introgression with *Z. mays* ssp. *parviglumis* and *Z. mays* ssp. *mexicana* was instrumental in the development of more productive staple grain varieties.

## Anthropologie

VON CRAMON-TAUBADEL 2017

Noreen von Cramon-Taubadel, *Measuring the effects of farming on human skull morphology*. *PNAS* **114** (2017), 8917–8919.

First, it is important to point out, as Katz et al. do, that the effects of dietary changes are small when considered alongside other factors such as sexual dimorphism and population history (i.e., how groups are related). The majority of human cranial variation can be explained on the basis of a neutral (or stochastic) model of microevolutionary change. What this means is that most global human morphological diversity (irrespective of diet) was shaped by the past action of random mutations, population dispersals, and among-group gene flow. This basic pattern of human variation is then overlain by additional sources of variation, such as the effects of climatic selection to extreme cold climates and the effects of dietary changes related to the shift to agriculture. The study by Katz et al. is timely and important in explicitly quantifying the relative importance of having a soft versus a harder diet on overall cranial form.

KATZ 2017

David C. Katz, Mark N. Grote & Timothy D. Weaver, *Changes in human skull morphology across the agricultural transition are consistent*

*with softer diets in preindustrial farming groups.* [PNAS 114 \(2017\), 9050–9055.](#)

Agricultural foods and technologies are thought to have eased the mechanical demands of diet—how often or how hard one had to chew—in human populations worldwide. Some evidence suggests correspondingly worldwide changes in skull shape and form across the agricultural transition, although these changes have proved difficult to characterize at a global scale. Here, adapting a quantitative genetics mixed model for complex phenotypes, we quantify the influence of diet on global human skull shape and form. We detect modest directional differences between foragers and farmers. The effects are consistent with softer diets in preindustrial farming groups and are most pronounced and reliably directional when the farming class is limited to dairying populations. Diet effect magnitudes are relatively small, affirming the primary role of neutral evolutionary processes—genetic drift, mutation, and gene flow structured by population history and migrations—in shaping diversity in the human skull. The results also bring an additional perspective to the paradox of why *Homo sapiens*, particularly agriculturalists, appear to be relatively well suited to efficient (high-leverage) chewing.

**Keywords:** foragers | farmers | subsistence effects | human skull form | mastication

**Significance:** Agriculture changed not only human culture and lifeways, but human biology as well. Previous studies indicate that softer agricultural diets may have resulted in a less robust craniofacial morphology in early farmers. However, obtaining reliable estimates of worldwide subsistence effects has proved challenging. Here, we quantify changes in human skull shape and form across the agricultural transition at a global scale. Although modest, the effects are often reliably directional and most pronounced in craniofacial features that are directly involved in mastication.

## Anthropologie Kultur

BYERS-HEINLEIN 2017

Krista Byers-Heinlein, Elizabeth Morin-Lessard & Casey Lew-Williams, *Bilingual infants control their languages as they listen.* [PNAS 114 \(2017\), 9032–9037.](#)

Infants growing up in bilingual homes learn two languages simultaneously without apparent confusion or delay. However, the mechanisms that support this remarkable achievement remain unclear. Here, we demonstrate that infants use language-control mechanisms to preferentially activate the currently heard language during listening. In a naturalistic eye-tracking procedure, bilingual infants were more accurate at recognizing objects labeled in same-language sentences (“Find the dog!”) than in switched-language sentences (“Find the chien!”). Measurements of infants’ pupil size over time indicated that this resulted from increased cognitive load during language switches. However, language switches did not always engender processing difficulties: the switch cost was reduced or eliminated when the switch was from the nondominant to the dominant language, and when it crossed a sentence boundary. Adults showed the same patterns of performance as infants, even though target words were simple and highly familiar. Our results provide striking evidence from infancy to adulthood that bilinguals monitor their languages for efficient comprehension. Everyday practice controlling two languages during listening is likely to explain previously observed bilingual cognitive advantages across the lifespan.

Keywords: bilingualism | infancy | code switching | language control | language processing

Significance: Bilingual infants must manage two languages in a single developing mind. However, the mechanisms that enable young bilinguals to manage their languages over the course of learning remain unclear. Here, we demonstrate that bilingual infants monitor and control their languages during real-time language listening, and do so similarly to bilingual adults. This ability could help bilinguals' language learning to keep pace with that of their monolingual peers, and may underpin the cognitive advantages enjoyed by bilinguals in both infancy and adulthood.

## Biologie

HOOGSTRATEN 2017

Charles G. Hoogstraten, *Fighting through the darkness*. [science](#) **357** (2017), 522.

One of the worst mistakes I made was repeatedly assuming that, when I was feeling well and productive, I was home free—only to be caught flat-footed when my depression flared again. Staying ahead of the situation by keeping a support network in place, even across the frequent relocations that are part of an academic's life, is critical.

## Klima

HOPCROFT 2017

Peter Hopcroft, *Ancient ice and the global methane cycle*. [nature](#) **548** (2017), 403–404.

An analysis of 12,000-year-old Antarctic ice revises our understanding of natural methane emissions to the atmosphere, and constrains estimates of the sensitivity of natural methane sources to abrupt climate-warming events.

As the authors point out, if geological emissions today are indeed less than or equal to 15.4 Tg CH<sub>4</sub> yr<sup>-1</sup>, rather than 52 Tg CH<sub>4</sub> yr<sup>-1</sup>, then the difference of approximately 40 Tg CH<sub>4</sub> yr<sup>-1</sup> needs to be accommodated by revising our estimates of anthropogenic 14C-free emissions upward by about 25 % — a substantial correction to our view of the contemporary methane cycle. Such a revision would imply that there is more scope to reduce human influence on climate than was thought, by reducing methane emissions associated with human activities.

PETRENKO 2017

Vasilii V. Petrenko et al., *Minimal geological methane emissions during the Younger Dryas–Preboreal abrupt warming event*. [nature](#) **548** (2017), 443–446.

n548-0443-Supplement.pdf

Vasilii V. Petrenko, Andrew M. Smith, Hinrich Schaefer, Katja Riedel, Edward Brook, Daniel Baggenstos, Christina Harth, Quan Hua, Christo Buizert, Adrian Schilt, Xavier Fain, Logan Mitchell, Thomas Bauska, Anais Orsi, Ray F. Weiss & Jeffrey P. Severinghaus

Methane (CH<sub>4</sub>) is a powerful greenhouse gas and plays a key part in global atmospheric chemistry. Natural geological emissions (fossil methane vented naturally from marine and terrestrial seeps and mud volcanoes) are thought to contribute around 52 teragrams of methane per year to the global methane source, about 10

per cent of the total, but both bottom-up methods (measuring emissions)<sup>1</sup> and top-down approaches (measuring atmospheric mole fractions and isotopes)<sup>2</sup> for constraining these geological emissions have been associated with large uncertainties. Here we use ice core measurements to quantify the absolute amount of radiocarbon-containing methane ( $^{14}\text{CH}_4$ ) in the past atmosphere and show that geological methane emissions were no higher than 15.4 teragrams per year (95 per cent confidence), averaged over the abrupt warming event that occurred between the Younger Dryas and Preboreal intervals, approximately 11,600 years ago. Assuming that past geological methane emissions were no lower than today<sup>3,4</sup>, our results indicate that current estimates of today's natural geological methane emissions (about 52 teragrams per year)<sup>1,2</sup> are too high and, by extension, that current estimates of anthropogenic fossil methane emissions<sup>2</sup> are too low. Our results also improve on and confirm earlier findings<sup>5–7</sup> that the rapid increase of about 50 per cent in mole fraction of atmospheric methane at the Younger Dryas–Preboreal event was driven by contemporaneous methane from sources such as wetlands; our findings constrain the contribution from old carbon reservoirs (marine methane hydrates<sup>8</sup>, permafrost<sup>9</sup> and methane trapped under ice<sup>10</sup>) to 19 per cent or less (95 per cent confidence). To the extent that the characteristics of the most recent deglaciation and the Younger Dryas–Preboreal warming are comparable to those of the current anthropogenic warming, our measurements suggest that large future atmospheric releases of methane from old carbon sources are unlikely to occur.

## Methoden

KING 2017

Adam King, Terry G. Powis, Kong F. Cheong & Nilesh W. Gaikwad, *Cautionary tales on the identification of caffeinated beverages in North America*. [Journal of Archaeological Science](#) **85** (2017), 30–40.

In recent years several studies have attempted to understand the use of caffeinated beverages in North America before the coming of Europeans using absorbed residues. These studies have focused on the two key plant sources of caffeine in North America: *Theobroma cacao* (cacao) and *Ilex vomitoria* (yaupon holly). The authors initiated a study to explore the possibility that one or both plants were used at the Mississippian period (900–1600 CE) center of Etowah in northern Georgia. In the process, a series of problems with methodologies in use were revealed. Key among those were limitations on the methods used to identify ancient caffeinated beverage residues, distinguish them from modern contamination, and differentiate residues made by each plant. In this paper we explore what our data from the Etowah site reveal about methodologies currently in use and make suggestions for future studies of residues created by caffeinated beverages in North America.

Keywords: Absorbed residues | Cacao | Yaupon holly | Mass spectrometry | Ultra performance liquid chromatography

## Story or Book

SHABLOVSKY 2017

Suzanne Shablovsky, *The perils of permanence*. [science](#) **357** (2017), 459.

Hunters and foragers thrived while early agrarian societies struggled, argues an anthropologist.

Against the Grain. A Deep History of the Earliest States. James C. Scott. Yale University Press, 2017. 336 pp.

Tentatively, he argues that hunters and gatherers were peripheral peoples living outside the agrocenter who resisted permanent settlement and statehood. Here, Scott turns the idealized notion of domestication on its head. While hunters and gatherers could adapt to shortages by making use of a wider food net, settled peoples, he maintains, were vulnerable to drought, disease, and the crushing demands of a rising elite.

Although the decline of the early states allowed for some egalitarianism, it also triggered a comeback for hunters and gatherers. Scott argues that the attacks mounted by these pastoralists were the single greatest force opposing agrarian spread.