is now completely outside of his activities, and is being administered by the Microsetta Initiative at UCSD with Rob Knight," Gilbert told *Science*. Knight says he no longer collaborates with Leach, and the project's website no longer mentions him.

Another project removed Leach's name from its website last week, after its leaders learned of the lawsuit. Until 5 February, the website of the Microbiota Vault, an international project to collect human microbiome samples, said Leach would "work to secure samples" from remote populations in Tanzania and Namibia. Maria Gloria Dominguez-Bello, a microbiome researcher at Rutgers University and a coordinator of the project, told *Science* she was surprised by the accusations and called the news "very disturbing and sad."

She does not, however, doubt the quality of the samples and data that Leach collected. She notes they are stored in the labs of Knight and microbiome researcher Justin Sonnenburg at Stanford, both of whom have co-authored papers with Leach. Sonnenburg, who is the corresponding author on three papers with Leach, including one in *Science* (25 August 2017, p. 802), said he has never met Leach in person and received the samples via Dominguez-Bello; he declined any further comment.

Research on the Hadza takes "training in ethnographic data collection and, ideally, bioethics.."

Alyssa Crittenden, University of Nevada, Las Vegas

The *Science* paper reported seasonal variation in the Hadza gut microbes, based on samples Leach collected. "It was neat, it was orderly, and the metadata all checked out: Poop was poop, and skin samples were from skin. And when you analyze the samples, they cluster by season," says Dominguez-Bello, a co-author. The paper concludes that the gut flora varies because of seasonal shifts in diet.

Some anthropologists who have worked extensively with the Hadza are skeptical of the paper. Alyssa Crittenden, an anthropologist at the University of Nevada, Las Vegas, says the *Science* paper's generalizations about seasonal foods are "inconsistent with nearly 60 years of data on Hadza diet." In a critique posted on bioRxiv in 2018, she and colleagues reported that they couldn't replicate the paper's results from the authors' open source data.

Dominguez-Bello says, "The discussion [of diet] could be all wrong, but that doesn't invalidate the paper. …[It] is claiming there are seasonal variations, that's all."

Crittenden says researchers who work with vulnerable groups such as the Hadza need "training in ethnographic data collection and, ideally, bioethics." As part of the case, Schwartz's lawyers submitted an affidavit by a Terlingua man who accompanied Leach to Tanzania in 2014. In it, he states that Leach smoked marijuana with study subjects in exchange for access to samples. In court filings, Leach's lawyers objected to the affidavit, saying the information it contains is not relevant to the defamation case. Leach wrote on his Human Food Project blog that "the Hadza are big pot smokers (they trade honey and meat for weed with the local Datoga)."

Tanzania's National Institute of Medical Research ethics board confirmed that it reviewed Leach's research proposal in 2011 or 2012, but could not say whether he currently has permits to work in the country. A member of the Hadza who is familiar with Leach but requested anonymity told *Science* that Leach's "work seems to be popular in the U.S., but my people don't really understand what it is for."

Daudi Peterson, co-founder of Dorobo Safaris in Tanzania, who works with the Hadza and has helped facilitate Leach's research, says Leach hasn't collected samples from the Hadza for more than a year, in part because he is waiting for permits. Peterson says Leach's relationships with the Hadza are "very good," and that Leach visited twice last year to connect with them. "Even today his name comes up," Peterson says. "He's fondly nicknamed the Hadza word for shit."

Epidemiologist Tim Spector of KCL, who went with Leach to Tanzania in 2017, says he saw no ethical issues with Leach's work. "I don't think he was doing anything others weren't doing."

Leach has had a colorful career. As part of the case, Schwartz's lawyers cited a 2003 civil case in Texas in which Leach was found to have violated laws against deceptive trade practices. The Texas attorney general alleged that Leach had sold subscriptions to magazines that had stopped publishing and had accepted more than $100,000 in payments for a tour in Egypt that was to feature the actor Omar Sharif, but was never organized. Leach failed to contest the claims and the court found them admitted and proven. Leifeste notes Leach has not admitted wrongdoing in this case and says it is not relevant to the lawsuit. Leach also co-launched a pizza chain and helped mount a search for Amelia Earhart's plane using a robotic submarine.

Leach says he plans to do his Ph.D. thesis on the Hadza. In 2018, he told a podcast he wanted to study the microbiome of Hadza children from birth, including collecting breast milk samples from mothers. ■

HUMAN EVOLUTION

Strange bedfellows for human ancestors

Homo erectus and other "super-archaics" may have interbred with ancient humans

By **Ann Gibbons**

The story of human evolution is full of ancient trysts. Genes from fossils have shown that the ancestors of many living people mated with Neanderthals and with Denisovans, a mysterious group of extinct humans who lived in Asia. Now, a flurry of papers suggests the ancestors of all three groups mixed at least twice with even older "ghost" lineages of unknown extinct hominins. One candidate partner: *Homo erectus*, an early human who left Africa by 1.8 million years ago, spread around the world, and could have mated with later waves of human ancestors.

The new genomic studies rely on complex models of inheritance and population mixing, and they have many uncertainties, not least the precise identities of our ancestors' strange bedfellows and when and where the encounters took place. But, taken together, they build a strong case that even before modern humans left Africa, it was not uncommon for different human ancestors to meet and mate. "It's now clear that interbreeding between different groups of humans goes all the way back," says computational biologist Murray Cox of Massey University of New Zealand, Turitea, who was not involved in the new studies.

The gold standard for detecting interbreeding with archaic humans is to sequence ancient DNA from fossils of the archaic group, then look for traces of it in modern genomes. Researchers have done just that with Neanderthal and Denisovan genomes up to 200,000 years old from Eurasia. But no one has been able to extract full genomes from more ancient human ancestors. So population geneticists have developed statistical tools to find unusually ancient DNA in genomes of living people. After almost a decade of tantalizing but unproven sightings, several teams now seem to be converging on at least two distinct episodes of very ancient interbreeding.

In *Science Advances* this week, Alan Rogers, a population geneticist at the University of Utah, Salt Lake City, and his team identified variations at matching sites in the genomes of different human populations, including Europeans, Asians, Neanderthals, and Denisovans. The team tested eight scenarios of how genes are distributed before and after mixing with another group, to see which scenario best simulated the observed patterns. They conclude that the ancestors of Neanderthals and Denisovans—whom they call Neandersovans—interbred with a "super-archaic" population that separated from other humans about 2 million years ago. Likely candidates include early members of our genus, such as *H. erectus* or one of its contemporaries. The mixing likely happened outside of Africa, because that's where both Neanderthals and Denisovans emerged, and it could have taken place at least 600,000 years ago.

"I think the super-archaics were in the first wave of hominids who left Africa," Rogers says. "They stayed in Eurasia, largely isolated from Africans, until 700,000 years ago when Neandersovans left Africa and interbred with them."

Occurring much earlier than encounters of modern humans with Neanderthals and Denisovans, the episode was "the earliest known interbreeding between ancient human populations and an expansion out of Africa," Rogers says. Other studies have hinted at such ancient mixing, Cox says, but Rogers's analysis is "particularly convincing."

Others, though, say Rogers's bold claim needs testing. One challenge is reconciling it with new results from other researchers that show modern human ancestors mixed with super-archaic groups more recently, in Africa. Just last week, for example, population geneticist Sriram Sankararaman and his student Arun Durvasula at the University of California (UC), Los Angeles, identified signs of a separate, more recent episode of mixing. The researchers analyzed the genomes of 405 people from four subpopulations in West Africa that were included in the 1000 Genomes Project, a catalog of genomes from around the world. They found numerous gene variants not seen in Neanderthals or Denisovans and concluded that the best explanation was that the variants came from an archaic, extinct human.

This ghost species may have been late *H. erectus*, *H. heidelbergensis,* or a close relative. One or more late-surviving members of this ancient group met and mated with the ancestors of living Africans sometime in the past 124,000 years, the modern genomes suggest.

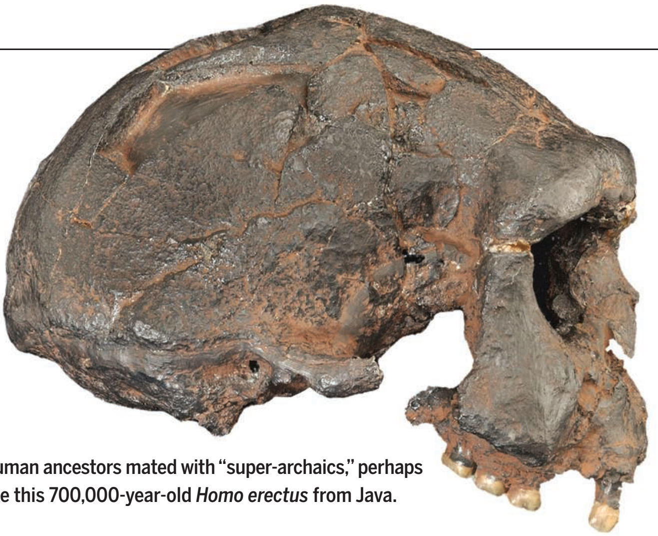
Another paper last month reported Neanderthal DNA in living Africans, likely from migrations back to Africa by early Europeans who bore Neanderthal DNA (*Science*, 31 January, p. 497). Sankararaman thinks some of the archaic DNA he detects in Africans may be from Neanderthals, but most is from the older ghost species. "I think the true picture is a combination of both an archaic population unrelated to Neanderthals as well as Neanderthal-related ancestry," he says.

In December 2019, yet another study found hints of an extinct ghost population in living Africans, although it was silent on the identity of the ghosts and when they bred with our ancestors. Population geneticist Jeff Wall at UC San Francisco and colleagues analyzed 1667 genomes from diverse populations in the GenomeAsia 100K consortium. They reported the strongest ghost signal in the Khoisan people and in Central African hunter-gatherers formerly known as pygmies.

But Wall and others warn their methods cannot rule out that the "ghosts" could be one or several groups of modern humans in Africa that were separated from other moderns for so long that their genes looked "archaic" when the groups finally came together again and mixed. "Our understanding of African population history in particular, is so far behind," says Joshua Akey of Princeton University.

Even if they differ on particulars, the studies emphasize that long after new lineages of humans emerge, they still can mix with others quite different from themselves. Other species, such as cave bears and mammoths, show the same pattern of divergence and later mixing, says population geneticist Pontus Skoglund of the Francis Crick Institute in London. "We are losing the idea that separation between populations is simple with instant isolation." Such mating between long isolated groups may quickly introduce valuable new genes (*Science*, 18 November 2016, p. 818). For example, some of the archaic alleles Sankararaman spotted in Africans were in genes that suppress tumors and regulate hormones.

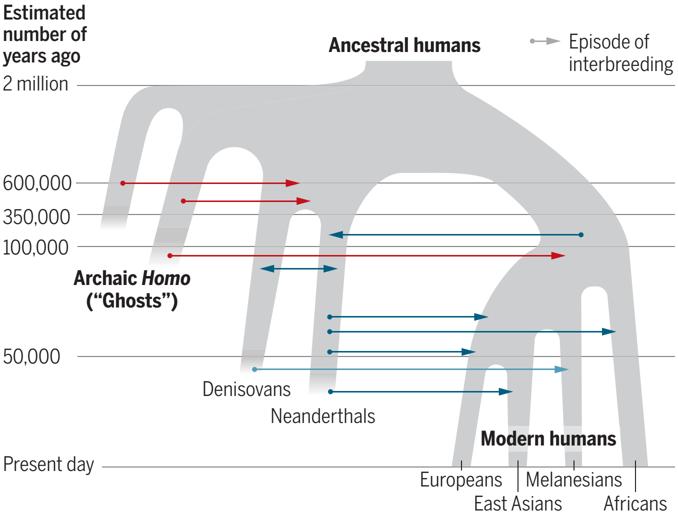
Today, *H. sapiens* doesn't have the possibility of quickly grabbing a load of diversity by mating with another group: For perhaps the first time in our history, we're the only humans on the planet. It's another reason to miss our extinct cousins, says population geneticist Carina Schlebusch of Uppsala University. "To have such a large densely spread species with … so little genetic diversity … is a dangerous situation," she says. ■



Human ancestors mated with "super-archaics," perhaps like this 700,000-year-old *Homo erectus* from Java.

Ghosts in the family tree

At least two super-archaic "ghost" hominins interbred with the ancestors of Neanderthals, Denisovans, and modern humans (red lines). Later, those three groups also met and mingled (blue lines), leaving complex traces in each other's genomes. (Split times are rough estimates; timeline is not drawn to scale).



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