



RAUSCHER.XYZ

OCTOBER 3, 2026

AI GENERATED

RAUSCHER.XYZ

GHOST DNA AND WHAT WE CANNOT KNOW ABOUT WHERE WE COME FROM

About a group of humans of whom not a single bone exists, yet whose genetic material is in every one of us; about regions of our genome that we thought held the heart of humanity and do not; and about the uncomfortable fact that three scientific models explain the same data and nobody can say which one is finally right

was sitting in my car in a parking lot off the highway again, because my back had once again decided it was time for a break and the pain was forcing me to take one. These days my back makes decisions like that on its own, without consulting me, with the authority of a boss you do not argue with. So I did what I always do at times like these, and read. On the screen was an article from the country's biggest tabloid, and it promised nothing less than ghosts in our blood. As always, that forces me to check what possible misinformation this rag is once again spreading among the people of this country.

“Only the shadow in the blood” was the exact wording, the poetic closing line of a paragraph about unknown ancestors. The forensic scientist in me corrected it before the rest of me could finish reading the sentence. Mature human red blood cells have no nucleus, and therefore no genetic material, so if the shadow is in the blood, it is in the white blood cells, which does sound considerably less frightening as a headline. Nobody is afraid of leukocytes. But the hacks at this paper need clicks and paying readers :xD.

I finished the article anyway, because beneath the tabloid language was a real study, published in one of the world's most important scientific journals, and it touches on the very question I have been working on for over a decade without ever being able to settle it. Where do we actually come from, and how much of that do we really know? We know absolutely nothing...

The honest answer is uncomfortable, and I will give it to you right at the beginning so nobody has to wait until the end. We know less than the textbooks claim, and every new method that looks deeper opens up more gaps than it closes, as always. That is the argument of this piece, and everything that follows is the examination of evidence my brain has been trained for over decades.

SO, ONE AND A HALF PERCENT AND A Y CHROMOSOME FROM FAR AWAY

I had my own DNA analyzed in 2022, and I know that will surprise some people who have read my article What DNA Actually Is. In it, I strongly warn against sending saliva samples to commercial US laboratories, because doing so means making a decision not only for yourself, but for your children and third cousins who were never asked. I expressly stand by that warning, and I am emphasizing it again here. I took the test anyway, and because I know both sides, I know how to read a result like this and how not to, and as a scientist, curiosity comes before everything else.

The result says that 1.5 percent of my genetic material comes from Neanderthals. I spent a long time wondering whether that one and a half percent might explain my deep dislike of small talk, but after much deliberation I concluded that the evidence was insufficient. The same analysis identifies me as 15.2 percent Italian, which gives my longing for that country a scientific veneer without explaining it in the slightest. And for Africa, it gives a flat 0.0 percent.

At the same time, that very report says my paternal line belongs to Y haplogroup E. Haplogroup E is the most common Y-chromosomal lineage in Africa; that is well established in the scientific literature. Africa: zero percent, says one line. Paternal line: a group now found predominantly in Africa, says the other. If you sense a contradiction here, you are both right and wrong, and this is exactly where the real subject of this article begins. Because all the research in this field is still full of contradictions that scientists regularly throw in one another's faces.

Here is what you need to know: the percentages in these tests do not measure where you come from. They measure how similar your genetic material is to the reference groups the provider has in its database, and they do so over a period of a few hundred to a few thousand years. The Y chromosome, by contrast, is a single line, from father to son, unbroken over tens of thousands of years, and it tells the story of one ancestor among thousands. Both results can be correct at the same time because they answer different questions. The mistake only arises when you forget which question was asked. And that is one of the main sources of distortion in this field.

And here is the punch line, which amuses me as a scientist more than any percentage. Nobody knows for certain where haplogroup E originated in the first place, nobody has a clue, and that keeps making me chuckle. A large analysis by Beniamino Trombetta's team places its history in Africa. David Poznik's team, on the other hand, proposed in Nature Genetics in 2016, based on 1,244 Y chromosomes, that E might have originated outside Africa and migrated back there around 58,000 years ago. My own Y chromosome, the smallest and most boring chromosome a man possesses, is an unsolved case too. I carry an open case file in every cell, and I did not even open it.

A BUILDING BLOCK WITH NO INSTRUCTIONS

Before I get to the study, I need to put something on record that some readers will not want to hear at this point. I am writing it anyway, because a piece about gaps would be dishonest if it left out the biggest gap of all.

We do not know how the building block that all of this is built from came into being. According to a major analysis from 2024, the last universal common ancestor of all life on Earth, known technically as LUCA, lived around 4.2 billion years ago and already possessed a genome encoding roughly 2,600 proteins. That is no little drop of primordial soup, that is a finished machine, appearing on a planet that had only just cooled down. I have written about this at length in The Constructors and in Probability Zero, and I will not repeat it here. Nothing can come from nothing, and that is a scientific “fact,” which many scientists are rather fond of forgetting now and then.

So I expressly stand by my thesis about our origins, and I know how controversial it is. The building block of life had a creator, and that creator was not chance in a warm pond. I call those creators the Constructors. We are too ingeniously built, the genetic code is too elegant,

and the starting complexity too high for me to accept the explanation that chemistry did it all on its own in a few hundred million years. I am nailing that down here, for centuries to come, and anyone who finds this text in 300 years is welcome to check who was right.

But I will also tell you where the evidence ends and opinion begins, because that is the difference between an expert report and a sermon. The Constructors are my conviction, supported by probabilities I have set out in the articles mentioned above. The study I am about to discuss says nothing about the Constructors, for or against. It is not about the origin of the code, but about what has happened to it over the past 2 million years. And that is precisely why it matters so much to me, because it shows how thin the ice is even where science feels most sure of itself.

WHAT THE NEWSPAPER SAID AND WHAT THE PAPER SAYS

On July 30, 2026, a paper appeared in Science that the tabloids summarized roughly like this: researchers find ghost DNA, two unknown human lineages, a shadow in the blood. That is not wrong, but it is so abbreviated that the interesting part gets lost, as always somewhere between the headline and the ads.

The study is by Yulin Zhang and Arjun Biddanda, listed as equal first authors, together with Sarah A. Johnson, Colm O'Dushlaine, and geneticist Priya Moorjani, who led the work at the University of California, Berkeley. Biddanda is now a postdoctoral researcher at Johns Hopkins University, something the tabloid version left out even though he shares equal first authorship with Zhang on the paper.

The team built a method it calls “TRACE,” short for TRacking Archaic Contributions via ARG Estimation. The researchers used it to search the genomes of 503 people alive today from the international 1000 Genomes Project: British people, Han Chinese from Beijing, Telugu from India, Yoruba from Nigeria, and Luhya from Kenya. They added 92 people from Oceania, 25 from Papua New Guinea and 67 from Vanuatu and the Santa Cruz Islands.

What they found can be said in three sentences, and I am deliberately starting with those three sentences, without elaboration. Every living person they studied carries genetic material from a group of humans that was neither Neanderthal nor Denisovan. This group interbred with our ancestors before modern humans left Africa. And a second, much older lineage also left traces, but only by way of the Denisovans and only in small amounts.

I need the rest of this piece to explain why those three sentences are true, why they are nevertheless not true in quite the way they sound, and what that tells us about our knowledge of ourselves. I will proceed as I do in one of my expert reports: first the measuring instrument, then its margins of error, then the findings, and finally the question of what those findings actually prove and what they merely suggest.

HOW TO FIND A HUMAN WHEN NOTHING IS LEFT

Until now, the search for archaic genetic material has essentially worked in two ways, and both have a blind spot you need to understand to see why TRACE is new at all.

The first approach assumes you have the source genome, a sequenced Neanderthal or Denisovan, and then directly compares which sections of the modern genome resemble it. That works extremely well, but only for groups of humans whose bones we have found with well-preserved DNA. For a group for which not a single genome exists, this approach is useless, because you cannot find what you cannot look for.

The second approach works without an archaic genome, but instead needs a comparison group assumed to carry no archaic genetic material. For Neanderthal DNA, researchers mostly used people from sub-Saharan Africa, because Neanderthals never lived there. That assumption is reasonably defensible for Neanderthals, but for the oldest layers of human history it is the weakest of all, because Africa is precisely where the lineages reach furthest back.

TRACE takes a different, third approach. From the genomes of people alive today, it reconstructs what is known as an “ancestral recombination graph,” or ARG. You can think of this as a complete family tree for every individual section of the genome. Because recombination reshuffles chromosomes in every generation, each short section has its own history of descent, and the ARG is ultimately the sum of all those histories, a forest of millions of little trees that change slightly at every recombination point.

In this forest, introgression from a deeply divergent lineage leaves two signatures. The first is unusually long branches, because a segment from a foreign lineage finds its common ancestor with the rest of humanity only far back in the past. The second is unusually long continuous stretches, because the introgression is much more recent than the divergence and recombination has not yet had enough time to tear the foreign segment into tiny scraps. Only the combination of the two distinguishes genuine introgression from variants that happen to be old and have simply persisted in the population for a long time.

A statistical model, a “hidden Markov model” with two states, archaic and modern, then runs along the graph and estimates which world each segment comes from. For computer scientists, this is an old acquaintance: speech recognition uses the same mathematics to identify which word is being spoken even when the signal is noisy. My favorite word for this: arithmetic, a term I use often in almost everything I write.

I need to make a distinction here that is missing from almost every press report, and it matters more than it appears to. Detecting the foreign segments really does work without an archaic reference genome and without an unadmixed comparison group. Assigning them, however, deciding whether a segment comes from Neanderthals, Denisovans, or an unknown group, very much does use the four archaic genomes we have. In this study, then, ghost means: found, but not similar enough to any known genome. That is a diagnosis of exclusion, and anyone who works with dead bodies knows the principle from everyday practice.

HOW WELL DOES THE TOOL MEASURE?

Before you trust a measuring instrument, you test it, and the authors have done that. Their own numbers deserve attention because they are what let us put the result in context, and because the tabloid version does not mention them at all.

In simulations where the true history is known because you programmed it yourself, TRACE achieves a precision of around 92 percent and a false discovery rate below 0.25 percent with perfect family trees. With family trees that have to be estimated from real data, which is the real-world situation, precision still stays at around 90 percent. But recall, the proportion of genuine archaic segments that are found at all, drops to about 50 percent, and to around 30 percent with more complex population models. People should know these numbers, because ignorance always leads to misinterpretation.

Translated into the language of an expert report, that means the following. What TRACE reports is very likely to be real, but TRACE misses a great deal. All the percentages that follow are therefore lower bounds rather than measurements in the strict sense. Incidentally, that explains why the study finds just under 1 percent Neanderthal ancestry in Europeans, while other methods give higher values and my own test reports 1.5 percent, even though I am actually a rather handsome man. The tool is strict, but it is not exhaustive, and the authors say so quite openly, something people are often happy to overlook.

For a forensic scientist, it is more reassuring to err in that direction. I would always rather have an expert report that makes few claims and gets them right than one that finds everything and invents half of it. Most of the miscarriages of justice I have seen in my decades of work arose from reports of the second kind, not the first.

THE FIRST GHOST IS IN EVERY ONE OF US

According to TRACE, the first unknown lineage accounts for between 0.49 and 1.1 percent of the genome, averaged across the people in a population. That is on the same order as the amount of Neanderthal ancestry the method finds in Europeans. And this inheritance is present in all the groups studied, in Yoruba and Luhya just as in British, Chinese, and Indian people.

“We were able to show that this ghost ancestry is present in all modern humans, not just Africans,” Yulin Zhang says in her university's announcement, in my translation here. This is the part that corrects earlier work, and it matters because it changes the story from an African peculiarity into a shared history of all humans.

In 2020, Arun Durvasula and Sriram Sankararaman reported evidence of a ghost lineage in West Africans in *Science Advances*. This lineage was estimated to have diverged between 360,000 and 1.02 million years ago, with an estimated contribution of 2 to 19 percent and introgression sometime within the past 124,000 years. TRACE contradicts that work on two

points. The inheritance is not West African but shared across humanity, and the interbreeding occurred before the departure from Africa; otherwise, we would not find it so evenly distributed outside Africa.

So when did this group split from our ancestors? The tabloid version says it was about 800,000 years ago, which sounds like a fixed date, the kind you carve into a gravestone. But the underlying study says something more cautious. The average time at which the ghost segments and modern segments trace back to a common ancestor is around 830,000 years, with a confidence interval of 610,000 to 1.27 million years. That is a coalescence time, not a divergence time, and it depends on two assumptions worth knowing: a mutation rate of 1.25 times 10^{-8} per base per generation, and a generation time of 28 years. The authors themselves are cautious too: they say the lineage diverged more than 500,000 years ago.

Those 28 years per generation distracted me for a moment, I admit. I was born in 1970, and by that calculation I would have two generations behind me, which is exactly how it feels some mornings, especially the ones when my back takes command with “pain.” In population genetics, however, generation time is not a measure of lived experience but an average over millennia, and shifting it by a few years shifts all the dates by tens of thousands of years. For such a harmless-sounding number, it carries a lot of weight in this case.

For context, and this is where I really start to pay attention: the ghost divergence falls roughly at the time when the Neanderthal and Denisovan lineage also split from ours. The ghost segments resemble Neanderthals and Denisovans equally, neither more than the other. So we are not dealing with some distant aunt of the Neanderthals, but rather with a sister who stayed in Africa while the other siblings moved to Eurasia.

So who was this group of humans? Chris Stringer of the Natural History Museum in London considers African *Homo heidelbergensis* a plausible candidate, a human form still living in Africa around 300,000 years ago. The authors themselves point to Middle Pleistocene finds from Africa. That is a plausible fit in time, but it is not an identification, and cannot be one until someone recovers genetic material from one of those bones, which may yet happen in the future.

That is exactly where things have stalled for decades. The oldest ancient DNA recovered in Africa is less than 20,000 years old. Heat and moisture break DNA down faster than science can recover it, and tropical soils are about as friendly to a genome as a shredder is to one of my manuscripts. The continent where human history reaches deepest is genetically the darkest, and that is not some irony of fate but simple chemistry.

THE DESERTS WERE NOT EMPTY

Now comes the finding that occupies my thoughts the most. The tabloid version mentions it in a single sentence without saying what it means. It is also the finding that fits most directly

with my argument that we know less than we think. Because we still know absolutely nothing.

For a little over a decade, geneticists have known about what are called archaic deserts. These are long stretches of the human genome where people alive today carry no or almost no Neanderthal and Denisovan genetic material. The obvious interpretation was that this is where what makes us human resides, because selection removed all foreign material incompatible with our biology from these regions. One of these deserts lies on chromosome 7 in the region around FOXP2, a gene associated with language. No screenwriter could have invented a more symbolic place for what is distinctly human.

TRACE found ghost ancestry in all five deserts examined. In the desert around FOXP2, one ghost segment reaches a frequency of 13.3 percent.

That sentence means more to me than it seems to say at first glance. The regions we thought were exclusively human are not. They are free of Neanderthal and Denisovan material, but they are not free of foreign material. The authors interpret this as showing that the deserts reflect selection specifically against the genetic material of those two groups, perhaps because their variants were disadvantageous in combination with ours, rather than a region that belongs to us alone.

But I need to qualify that immediately, or I will be making exactly the mistake I accuse the press of making. This is purely an interpretation, not proof. The clustering of high-frequency ghost segments in certain gene regions, such as around CSMD1 and RBFOX1 or in the immune system, has weak statistical support. Anyone who builds a story about a ghost language or a ghost immune system out of that is writing fiction, and should please call the book that, not “science.”

What is robust can be said in two simple sentences. Ghost ancestry is less common near functional elements and in regions with little recombination, which is the same pattern seen in Neanderthal ancestry. It suggests that natural selection removed some of this inheritance again over the generations because, where function matters, it did more harm than good.

And then there is a number I cannot get out of my head. Taken together across all the people studied, the ghost segments cover 71.5 percent of the accessible genome. Each individual carries only fragments, half a percent here, a percent there, but together we carry a large part of the genetic material of people of whom not a single bone exists. You carry a piece of it in you, I carry a piece of it in me, and only all of us together give us the picture of an ancestor nobody has ever seen.

For someone who has spent decades identifying people from fragments, it is a familiar situation on an entirely unfamiliar scale. In an identification, you piece together a picture from a tooth, a vertebra, and a fragment of skullcap, and here science is piecing together an ancestor who has not existed for hundreds of thousands of years from billions of base pairs scattered across thousands of people.

THE SECOND GHOST REACHED OCEANIA BY A ROUNDABOUT ROUTE

The second lineage is even older, and it is the part of the story whose scale is completely missing from the tabloid version, because the hack has no idea and probably used Chat-GPT to write the article by now anyway. So I will take this particularly slowly.

In the 92 genomes from Oceania, the researchers found that particularly deep lineages occur significantly more often in Denisovan segments than in Neanderthal segments. Their common ancestry with the rest of humanity reaches back an average of 1.77 million years, with a confidence interval of 1.13 to 3.98 million years. Researchers always call this super-archaic.

The interpretation goes like this: an ancient group of humans interbred with the ancestors of the Denisovans, and later, when the Denisovans encountered modern humans, they passed on some of that inheritance. That is why it is found mainly where Denisovan ancestry is strongest today, in Papua New Guinea and on the islands of Melanesia. Fiji, which the tabloid version specifically named, was not in the sample at all, incidentally.

The idea is not new, and that matters to me, because otherwise it sounds as though a sensational discovery has appeared out of nowhere. Back in 2014, while analyzing a Neanderthal genome, Kay Prüfer and colleagues estimated that 2.7 to 5.8 percent of the Denisovan genome came from a lineage that had diverged between 0.9 and 4 million years ago. In 2020, Alan Rogers and colleagues put the divergence at around 2 million years ago. What is new is that TRACE finds this lineage for the first time as identifiable segments in the genomes of people alive today.

And now comes the number that was in none of the headlines. This super-archaic contribution makes up about 0.3 percent of the Denisovan segments identified. That does not mean 0.3 percent of the genome, but 0.3 percent of a fraction that is itself below 1 percent. The classifier that distinguishes super-archaic from ordinary Denisovan ancestry achieves an accuracy of 70.2 percent in simulations. That is a signal, but not a strong one, and in an expert report I would describe it only as consistent with the proposed explanation, never as scientifically proven.

The findings are still exciting, though, and this is where I feel at home. Among the genes whose segments are more than 70 percent super-archaic are RNF39, PPP1R11, and POLR1H in the major histocompatibility complex, right at the center of immune recognition, and CYP24A1, an enzyme involved in breaking down vitamin D (my favorite vitamin, incidentally). Anyone who knows immunology knows why this particular complex keeps appearing as a harbor for ancient, foreign genetic material. Diversity is an advantage there, not a risk, because the more different variants a population carries, the harder it is for a pathogen to outwit everyone at once.

So who was this second, even older group? In my view, the most obvious candidate is “Homo erectus,” the first human form to leave Africa and spread across Asia. And since May 2026,

there has been a clue from a completely different direction that particularly fascinates me as someone who works with teeth a great deal.

Qiaomei Fu and her team in Beijing recovered proteins from the tooth enamel of six *Homo erectus* individuals from China, from Zhoukoudian, Hexian, and Sunjiadong, five males and one female, an astonishing 400,000 years old. In all six teeth they found two variants of the enamel protein “ameloblastin.” One, AMBN A253G, was previously completely unknown and could be a marker of these East Asian *erectus* groups. The other, AMBN M273V, had until then been considered characteristic of Denisovans and also occurs in some present-day humans. The authors suspect it entered the Denisovan lineage through populations related to this *Homo erectus*.

Tooth enamel endures where DNA has long since broken down. It is the hardest tissue the human body produces, and it preserves information over stretches of time in which any genetic material would have given up long ago. That is why I like using a tooth for carbon-14 dating. The possibility that teeth, of all things, could now bridge the gap between a statistical shadow in the genome and an actual fossil has a certain logic to it for me. But the sober rule applies here too: a single protein variant is a clue, not an identification. I would not, however, identify a person on that basis, and I am not identifying a human species on that basis either.

THREE MODELS EXPLAIN THE SAME DATA

Up to this point, it all sounds like clear progress. We now have a new tool, it finds two unknown lineages, and the human story gets richer. That is true, but it is only half the truth, and the other half is the real reason I am writing this piece.

For several years now, population genetics has had a dispute that barely reaches the public because it cannot be squeezed into a headline. It turns on a seemingly simple question: what actually are these deep, foreign-looking segments in the human genome?

The first answer is introgression. There was a separate group of humans, it was cut off from our ancestors for a very long time, and then its members reproduced with our ancestors. This is the ghost model, put forward by Durvasula and Sankararaman in 2020 and now, using a new method, by TRACE.

The second answer is structure. In 2023, Aaron Ragsdale and colleagues published a model in *Nature* in which the ancestors of modern humans in Africa were not a single uniform population but a weakly structured stem made up of several groups that remained in loose contact over hundreds of thousands of years. There is then no need for a foreign human form, because the deep lineages would simply be the inheritance of old subgroups within the same network. In this model, the earliest populations still distinguishable today split only 120,000 to 135,000 years ago. Ragsdale and colleagues explicitly criticized earlier ghost studies for choosing only between a single ancestral population and archaic introgression, without even testing structure as a third possibility.

The third answer is deep divergence and reunion. In 2015, Trevor Cousins, Aylwyn Scally, and Richard Durbin of the University of Cambridge introduced a method called “cobraa” in Nature Genetics. According to their analysis, the human ancestral population split into two groups around 1.5 million years ago, and those groups came back together about 300,000 years ago in a ratio of roughly 80 to 20. According to Scally, the larger of the two groups was also the population from which Neanderthals and Denisovans later emerged. We would therefore all be a mixture of two ancestral lineages separated for a long time, well before anyone ever encountered a Neanderthal.

Three different models, one kind of data, and each explains a good part of the patterns. I have seen many disputes between experts in my professional life, but rarely one where three experts stand before the same piece of evidence with three theories and all three make a genuinely sound case.

Where does TRACE stand in this dispute? The authors argue that their ghost lineage diverged at about the same time as the Neanderthals, making it a younger, separate event that could coexist with the deep structure described by Cousins and colleagues. But that is a claim of coexistence, and a claim of coexistence is not a test.

I will phrase the next point cautiously, because I could not fully examine the supplementary material for the final version. From everything I have read, the null model against which TRACE tests its ghost lineage is a world without ghost introgression, not a world with a weakly structured stem. The method's length filters also discard segments shorter than 50,000 bases, systematically excluding very old admixture. A reunion 300,000 years ago would have left mostly shorter stretches, so the three models are partly looking at different time windows.

Then there is a pattern that really makes me think. A signal of similar strength in Africans and non-Africans, collectively covering 71.5 percent of the genome and associated with selection and recombination rate, is exactly what an ancient structured stem followed by selection would also produce. The finding fits the ghost model, but it also fits the structure model, and a finding that fits two explanations decides nothing.

Patrick Reilly of Yale University put it soberly to a major American science magazine: “As with any method, there will always be false positives.” He calls for a second, independent line of evidence, and I agree, because in my field that goes without saying. No court convicts on the basis of a single method when a second one would be available.

And then there is the sample. Five populations from the 1000 Genomes Project, plus Oceania, but no Khoe-San from southern Africa and no central African hunter-gatherers such as the Mbuti or the BaAka. The very groups whose lineages reach furthest into the past are missing. The statement that ghost ancestry is present in all modern humans rests empirically on seven populations. It is plausible, but it has been demonstrated for exactly those seven.

I do not want to play this down now, and I do not want to make it bigger than it is either. TRACE is a real methodological advance because it locates deep lineages in the genome,

segment by segment, without a single fossil. What it cannot do, and what no method can currently do, is decide whether those lineages came from a separate group of humans that joined us at some point or from parts of a network that was always us.

That is the real gap, and it is not just in the fossil record. It is methodological, and it will not disappear just because a newspaper has found a catchy headline.

WHAT A FORENSIC SCIENTIST'S Y CHROMOSOME HAS TO DO WITH IT

I will return once more to my own test result, because it shows on a small scale the gap the study describes on a large one.

My report gives zero percent for Africa and haplogroup E for my paternal line. Both are correct, but neither tells me where I come from. The percentages measure similarity against a database of reference groups selected by the provider. If a group is missing from the database, it cannot appear in the result, however much of it a person carries. This is the same problem the classical methods had when looking for archaic genetic material, only at the level of an individual customer instead of an entire species.

What a database does not know does not exist for it. That applies to my test, it applied for decades to the ghosts in our genetic material, and in forensics it applies to every DNA trace whose donor is not registered in any database. A match proves similarity; the absence of a match proves absolutely nothing. The 0.0 in my report is not a statement about my ancestors but a statement about the limits of the method used to look for them.

Haplogroup E, in turn, is a single thread in a carpet of thousands. If I trace my paternal line back, father, grandfather, great-grandfather, and so on, at some point tens of thousands of years ago it reaches one man whose Y chromosome I still carry today. All the other ancestors from that time, and mathematically there are more ancestral slots in a family tree of that depth than there were people alive back then, because the lines cross countless times, have left no trace on my Y chromosome. Reading a Y chromosome and drawing conclusions about your own origins from it is rather like reconstructing an entire crime from a single witness statement.

And where this haplogroup itself comes from is, as I said, disputed. Africa or a migration back from Eurasia, both hypotheses have prominent proponents and solid data. So in every one of my cells, I carry proof that even the origin of one well-studied lineage remains unresolved to this day. I do not find that unsettling, I find it honest.

WHAT A FORENSIC SCIENTIST READS IN ALL OF THIS

In my profession, I have learned to distinguish between three kinds of statements: what a finding shows, what it suggests, and what someone would like it to show. Most of the wrong

judgments I have seen arose at the boundary between the second and third categories, where an expert stopped measuring and started wishing.

This study shows that present-day genomes contain segments whose family trees reach unusually far back and that do not resemble any known archaic genome. It shows that such segments also occur where we had previously assumed there was only human material. And in Oceania, it shows an enrichment of ancient lineages in Denisovan ancestry.

It suggests that, before leaving Africa, our ancestors interbred with a group that branched off more than 500,000 years ago. It also suggests that Denisovans carried an inheritance from an even older lineage, possibly *Homo erectus*, for which the tooth enamel proteins from China provide a second, independent clue.

What it does not show is just as important. It does not show that there were two new human species. It does not show what these people looked like, where exactly they lived, or how many there were. And it does not show whether they were separate groups at all or threads in a fabric that we can now recognize only statistically.

Priya Moorjani has found a way of describing the overall picture that I expressly agree with. To paraphrase her, we often imagine human evolution as a branching tree, but new genomic data show a far more interconnected history, more like a complex network of populations linked by repeated episodes of migration and interbreeding. That is not a poetic image for a press release, that is the current state of the data.

In my article *From Africa to the World*, I wrote about Jebel Irhoud, the roughly 315,000-year-old finds from Morocco that had already dismantled the picture of a single East African cradle back in 2017. Ghost DNA takes that movement further. First, human origins were a place, then they became a continent, and now they are a network whose nodes we can partly infer only through statistics.

Our “Otto Sapiens” will tell all of this differently, by the next barbecue at the latest. He has read the headline, he now knows he is a little over one percent ghost, and he will present that information with the same certainty he used last year to explain why his audiobook on the Stone Age diet disproves all of medicine. He will leave out the confidence interval, and the coalescence time too, and he does not know about the recall of 30 to 50 percent. Incidentally, that puts him in very good company with a large share of the reporting.

AND WHAT ABOUT THE CONSTRUCTORS?

At the beginning I promised to be fair, so I will return to my thesis and test it against what we now know.

Ghost DNA does not prove the Constructors, and it does not disprove them either. It operates on a different timescale. My thesis concerns the origin of the building block, the moment around 4.2 billion years ago when a complete replication system with a universal code appeared on this planet. What happened after that, diversification, divergence, admixture,

selection, is evolution, and I do not doubt it. The ghosts in our genetic material are evolution in its purest form, proof of how wild and interconnected this process has been.

But this study reinforces an attitude underlying my thesis. It shows how much of what is considered established rests on model assumptions that you only see if you deliberately look for them. A generation time of 28 years here, a mutation rate there, a length filter, a null model, a sample without humanity's oldest lineages. Change one of those settings, and the dates shift by hundreds of thousands of years, and what looked like introgression may turn out to be structure.

If we cannot even say with certainty, for the last 2 million years, whether we come from a tree, a network, or two merged lineages, then the self-assurance with which some people explain the first billions of years of life is not scientific. It is habit, and habit is the most convenient tool there is, because you never have to check it.

So I stand by my thesis. The building block had a creator, and to me, the gaps every new study opens up are no argument against that. They are more of a warning to everyone who thinks the question has long since been answered. It has not, and it will take centuries before we are in a position to answer it.

WHAT REMAINS OPEN, AND WHY THAT IS GOOD

So this piece does not fall into the very trap it describes, I will once more summarize the open questions as soberly as I can.

The study is the work of a single research group, and independent replication on other datasets, for example genomes from southern and central Africa, is still outstanding. Because recall is limited, all the percentages are lower bounds and cannot be compared directly with values from other methods. All the dates depend on mutation rate and generation time, and both are estimates. The distinction between introgression and ancient population structure remains unresolved, and none of the three main schools of thought has yet disproved the others. Until someone recovers genetic material or sufficiently informative proteins from an African Middle Pleistocene fossil, the first ghost will remain a ghost.

That is not a flaw in the study but the honest state of the science. It is more honest than most textbooks admit, and more exciting than any certainty we were taught at school.

A BENCH, EIGHT IN THE MORNING

I am sitting with my laptop on a bench outside my house, it is eight in the morning, and I am typing the final sentences of this piece. The highway parking lot is behind me, and on the screen is an article that began with a tabloid headline and ended up asking who we actually are.

As I type, I think about how much I learn from the way I live. I live and think by Murphy's law, I go through everything that could go wrong, and even as a child I applied the same method to every subject that interested me: take it apart until you can see where the construction holds and where it only pretends to. With an engine, that is how you find the fault; with an expert report, the error in reasoning; and with a study of ghost DNA, the point where an actual measurement becomes a simple story. Is it not remarkable that the same habit that makes me read a newspaper article in a highway parking lot more carefully than it was written ultimately leads me to an ancestor of whom no bone exists?

You carry him in you too, this human with no name, half a percent here, a percent there. Nobody knows who he was, and nobody knows whether he was even part of a distinct people or just a thread in the network that was always us. The next method will answer part of that and raise three new questions, and I will take it apart again, in some parking lot, on some bench, until my back demands another break.

DISCLAIMER

This article is provided for general information and commentary only. It does not constitute medical, genetic, or genealogical advice and is not a substitute for genetic counseling by a qualified professional. The scientific findings described reflect the publications and press reports available as of the editorial date. Some figures are taken from the preprint version of the study discussed and may differ in detail from the final published version, and the interpretation of these findings remains the subject of ongoing scientific debate. Statements expressly identified as the author's personal conviction, in particular the thesis of the Constructors, reflect opinion rather than established scientific consensus. The author's own DNA test result is reported as an individual finding without a control group and permits no conclusions about other people. The mention of commercial DNA testing constitutes neither a recommendation nor a warning regarding any specific provider, and the author has no business relationship with any such provider. Liability for decisions readers make on the basis of this text is excluded to the extent permitted by law.

REFERENCES

Cousins, T., Scally, A., & Durbin, R. (2025). A structured coalescent model reveals deep ancestral structure shared by all modern humans. *Nature Genetics*, 57, 856–864. <https://doi.org/10.1038/s41588-025-02117-1>

Durvasula, A., & Sankararaman, S. (2020). Recovering signals of ghost archaic introgression in African populations. *Science Advances*, 6, eaax5097. <https://doi.org/10.1126/sciadv.aax5097>

Fu, Q., et al. (2026). Enamel proteins from six *Homo erectus* specimens across China. *Nature*, 655(8121), 141. <https://doi.org/10.1038/s41586-026-10478-8>

Hublin, J.-J., Ben-Ncer, A., Bailey, S. E., et al. (2017). New fossils from Jebel Irhoud, Morocco and the pan-African origin of *Homo sapiens*. *Nature*, 546, 289–292. <https://doi.org/10.1038/nature22336>

Krywko, J. (2026, July 30). Everyone alive may carry DNA from a “ghost lineage” of human ancestors. *Scientific American*. <https://www.scientificamerican.com/article/everyone-alive-may-carry-dna-from-a-ghost-lineage-of-human-ancestors/>

Moody, E. R. R., Alvarez-Carretero, S., Mahendrarajah, T. A., et al. (2024). The nature of the last universal common ancestor and its impact on the early Earth system. *Nature Ecology and Evolution*, 8, 1654–1666. <https://doi.org/10.1038/s41559-024-02461-1>

- Poznik, G. D., Xue, Y., Mendez, F. L., et al. (2016). Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. *Nature Genetics*, 48(6), 593–599. <https://doi.org/10.1038/ng.3559>
- Prüfer, K., Racimo, F., Patterson, N., et al. (2014). The complete genome sequence of a Neanderthal from the Altai Mountains. *Nature*, 505, 43–49. <https://doi.org/10.1038/nature12886>
- Ragsdale, A. P., Weaver, T. D., Atkinson, E. G., et al. (2023). A weakly structured stem for human origins in Africa. *Nature*, 617, 755–763. <https://doi.org/10.1038/s41586-023-06055-y>
- Rogers, A. R., Harris, N. S., & Achenbach, A. A. (2020). Neanderthal-Denisovan ancestors interbred with a distantly related hominin. *Science Advances*, 6, eaay5483. <https://doi.org/10.1126/sciadv.aay5483>
- Sanders, R. (2026, July 30). New technique pinpoints human DNA inherited from “ghost” ancestors. *Berkeley News*. <https://news.berkeley.edu/2026/07/30/new-technique-pinpoints-human-dna-inherited-from-ghost-ancestors/>
- Trombetta, B., D'Atanasio, E., Massaia, A., et al. (2015). Phylogeographic refinement and large scale genotyping of human Y chromosome haplogroup E provide new insights into the dispersal of early pastoralists in the African continent. *Genome Biology and Evolution*, 7(7), 1940–1950. <https://doi.org/10.1093/gbe/evv118>
- Zhang, Y., Biddanda, A., Johnson, S. A., O'Dushlaine, C., & Moorjani, P. (2026). Recovering signatures of archaic hominin introgression using ancestral recombination graphs. *Science*, 393(6814), eaef8874. <https://doi.org/10.1126/science.aef8874>

KEYWORDS: ghost DNA, archaic introgression, TRACE, ancestral recombination graph, Denisovan, Neanderthal, *Homo erectus*, haplogroup E, population structure, human history

IMPRINT

intelligent piXel GmbH
International Institute of Forensic Expertise (IIFE)
Enzianstraße 4a
82319 Starnberg, Germany

CONTACT

george@rauscher.xyz · Telegram @intelligentpixel

MANAGING DIRECTOR / AUTHORIZED SIGNATORY

Managing Director: George A. Rauscher
Authorized Signatory: Dr. Louise Morgott

RESPONSIBLE FOR JOURNALISTIC AND EDITORIAL CONTENT

Responsible for journalistic and editorial content pursuant to Section 18(2) of the German Interstate Media Treaty:
George A. Rauscher, c/o intelligent piXel GmbH, Enzianstraße 4a, 82319 Starnberg

VAT ID NO. / COMMERCIAL REGISTER

VAT ID No.: DE291416044
Commercial Register: HRB 207 679, Munich District Court