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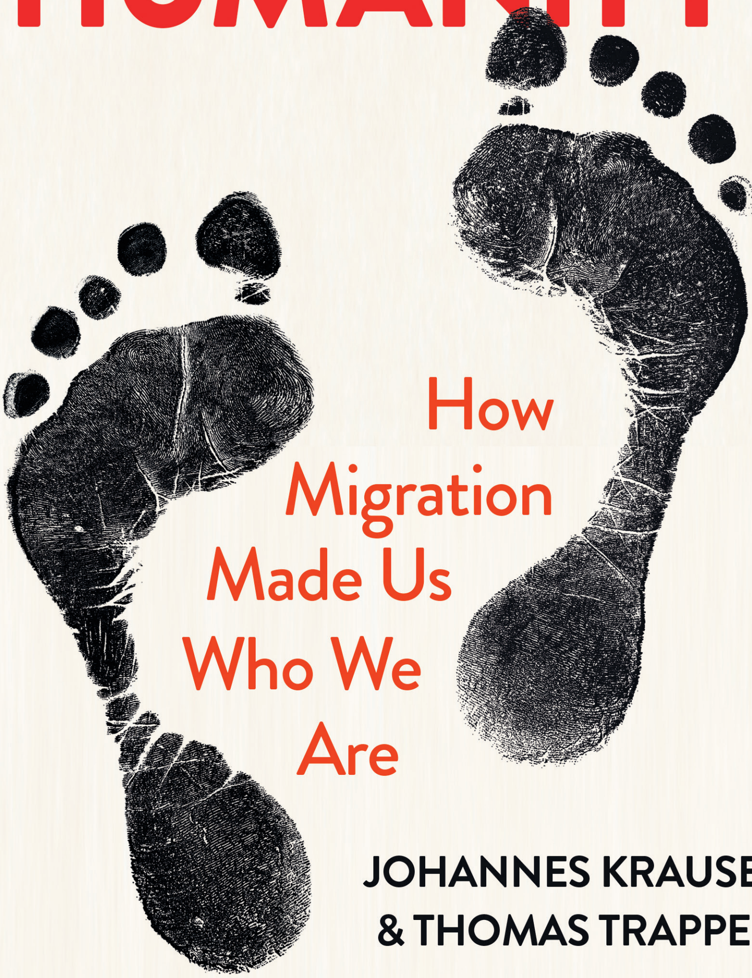
A SHORT HISTORY OF HUMANITY



How Migration Made Us Who We Are

JOHANNES KRAUSE
& THOMAS TRAPPE

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INTRODUCTION

After the pandemic, nothing will be as it was. A previously unknown illness has swept across Europe like a storm, and wherever it has raged, entire social systems have been utterly changed. Humanity has known the brutal power of pathogens before. Four thousand eight hundred years ago, a sickness that began in the East almost wholly transformed the genetic structure of people living in Europe; Eastern Europeans took control of the continent, ultimately ushering in the Bronze Age. This sickness was the plague. It ravaged Europe probably for the first time during the Stone Age, then repeatedly devastated the continent throughout its subsequent history, each attack worse than the last. Even then, people tried to curb the disease by closing borders, implementing quarantines, and reducing trade. Though they did not understand what caused it, they were able to observe its spread at close quarters. In Venice during the Middle Ages, for instance, which was in those days an economic powerhouse, trade almost ground to a halt. Countless people died in the streets, their numbers now revealed only by mass graves. Until recently, we had hoped the story would never be repeated. But in 2020, images were broadcast of trucks carrying the bodies of deceased COVID-19 victims to crematoriums and mass graves all over the world—in Bergamo, New York, and other cities and towns.

It would take nearly 5,000 years for us simply to discover the existence of the Stone Age plague. Armed with revolutionary technology, we ground ancient bones to dust and distilled from their DNA the stories told in this book. Archaeogenetics, a young branch of science, uses methods developed in the field of medicine to decode ancient genomes, some of which are hundreds of thousands of years old. The field is still only just taking off, yet already its contribution to our store of knowledge is vast. Using human bones from the distant past, we can uncover not only the genetic profiles of the dead but also how their genes spread across Europe—in other words, when our ancestors arrived and where they came from. Today we are also able to sift out DNA from bacteria that cause deadly diseases—not just the plague—from blood dried in teeth hundreds and thousands of years old. Thanks to archaeogenetics, history and the story of disease in Europe can be told in an entirely new way. And it turns out that two of the biggest issues the world is currently facing are constants in human history: deadly pandemics and constant migration.

When this book was first published in February 2019, the political discussion in Germany was still very much shaped by the "refugee crisis" of 2015. Readers and the press focused mainly on the passages that dealt with the archaeogenetic evidence of countless waves of past migration across the globe and constant genetic intermingling among our ancestors. A little more than a year later, as the entire planet reels from the ruthless SARS-CoV-2 virus, that particular crisis has fallen somewhat out of the spotlight despite the countless precarious journeys made by migrants every day. And although there's no real comparison between the far more lethal plague and the novel coronavirus, there is one parallel: invisible pathogens have always been capable of stopping a society in its tracks from one day to the next, jolting us out of our sense of unassailability into a paralyzing helplessness. What the consequences of the current pandemic will be for humankind, no one is currently in a position to say. In this book, however, we will show what impact such events had on the earliest denizens of Europe. It would be presumptuous to draw political conclusions from this and apply them to the present day—that is not the task of archaeogenetics—but we can help to clarify a few things. We can try to understand the world for what it undoubtedly is: a site of progress that has spanned millennia, progress that without migration and human mobility would have been impossible. Time and time again populations have been ultimately strengthened by adversity, even after catastrophic pandemics. In this sense, at least, we should make no secret of hoping that history will repeat itself.

The initial pages of this book explore the great waves of migration that have shaped Europe since its earliest times, as well as those that began there and founded the Western world. We are concerned, among other things, with the ever-present route through the Balkans and the conflicts that have accompanied migration since time immemorial. We will explain why the first Europeans had dark skin, and why we can use DNA analyses to pinpoint individual Europeans on a map but not to draw sharp genetic lines around ethnic groups—and certainly not nationalities. We trace an arc from the Ice Age, when Europeans' genetic journey began, to the present day, where we are on the verge of taking evolution into our own hands. Our book seeks to address not only political controversies but also the contributions of archaeogenetics to our understanding of the history of Europe.

This new information does not provide black-and-white answers. It's clear that migrants shaped Europe, and there's no question the resulting upheavals caused a good deal of suffering—for hunter-gatherers, for instance, who were displaced by Anatolian farmers. It's also true that the history of migration has always also been the history of deadly diseases. We know that people open to migration will find arguments in this book to support their beliefs, as will those in favor of stricter border control. Instead, our hope is that after reading our book no reader will dispute mobility's integral part of human nature. Ideally, you will be persuaded that a global approach to society—an approach that has been field-tested for thousands of years—will also be the key to progress in the future. The times we are living in have placed human mobility—with all its complications and side effects—under a powerful magnifying glass. On the one hand, the spread of COVID-19 would be unthinkable without it. On the other, placing large-scale limitations on migration for only a few weeks led to social upheaval and economic collapse, the worldwide effects of which will be felt in our everyday lives for years to come.

Two authors have contributed to this book. The first is Johannes Krause, who assumes the role of first-person narrator from the next chapter onward. He is one of the most established international experts in the field of archaeogenetics (for reasons of modesty this passage was written by the second author) and is director of the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany. His co-author, Thomas Trappe, was tasked not only with compressing Krause's knowledge into a compact narrative but also with placing it in a contemporary context and framing it within ongoing political debates. Trappe has previously collaborated with Krause several times; he has also reported on nationalism and contemporary populist ideas. Over the course of many conversations, both authors realized they wanted to write a book that would bring together science and up-to-the-minute debates.

We would like to start with a whistle-stop tour of the field of archaeogenetics—and with a finger bone that altered the course of scientific understanding as well as Krause's own scientific career. Quite unexpectedly, the bone revealed a new type of hominin, indirectly revealing the affinity between early Europeans and Neanderthals. This unlikely discovery is where we choose to begin our short history of humanity.

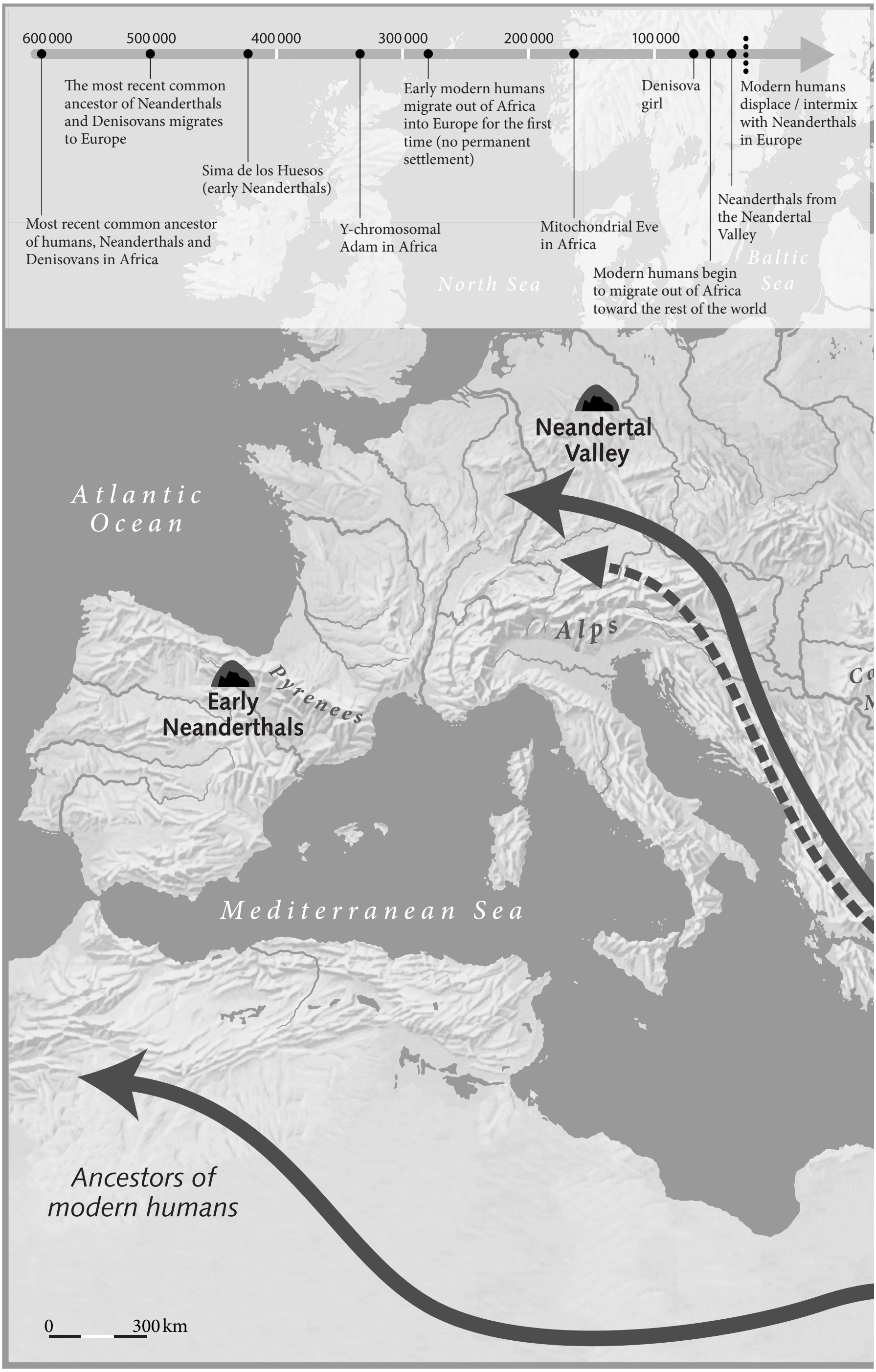
A SHORT HISTORY OF HUMANITY

CHAPTER

I

A New Science Is Born

A SIBERIAN FINGER POINTS US TO *a new archaic human. Archaeogenetics comes alive. Geneticists are feeling the gold rush with their shiny new toys.* Jurassic Park *makes everybody go nuts. Yes, we're all related to Charlemagne. Adam and Eve didn't live together. The Neanderthal reveals an error.*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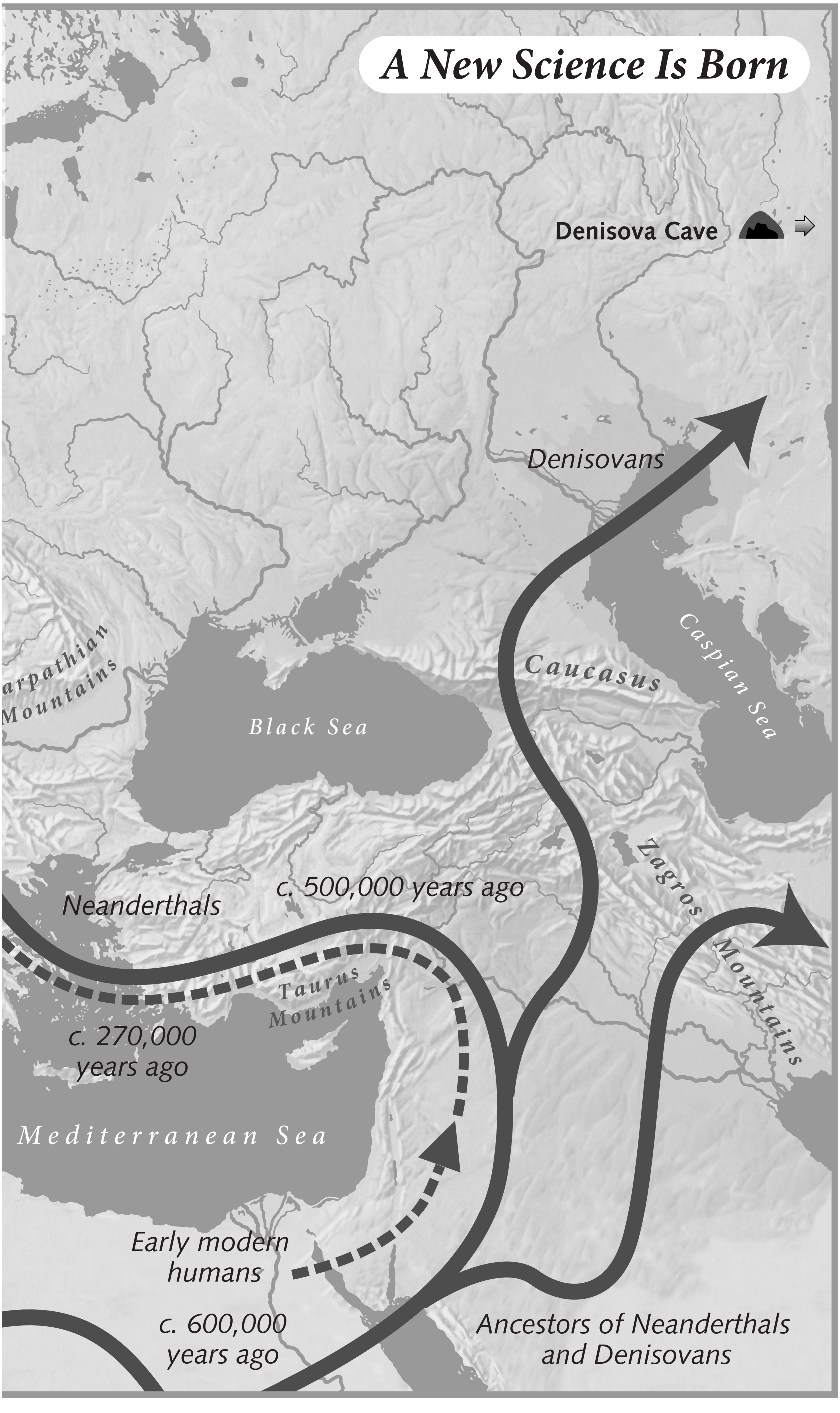
The most recent common ancestor of Neanderthals and Denisovans migrates to Europe
Sima de los Huesos (early Neanderthals)
Most recent common ancestor of humans, Neanderthals and Denisovans in Africa
Y-chromosomal Adam in Africa
Early modern humans migrate out of Africa into Europe for the first time (no permanent settlement)
Mitochondrial Eve in Africa
Denisova girl
Modern humans begin to migrate out of Africa toward the rest of the world
Neanderthals from the Neandertal Valley
Modern humans displace / intermix with Neanderthals in Europe
North Sea
Baltic Sea
Neandertal Valley
Atlantic Ocean
Alps
Early Neanderthals
Pyrenees
Mediterranean Sea
Ancestors of modern humans
0 300 km


A New Science Is Born
Denisova Cave
Denisovans
Carpathian Mountains
Black Sea
Caucasus
Caspian Sea
Zagros Mountains
c. 500,000 years ago
Neanderthals
Taurus Mountains
c. 270,000 years ago
Mediterranean Sea
Early modern humans
c. 600,000 years ago
Ancestors of Neanderthals and Denisovans

A BONE ON MY DESK

THE FINGERTIP I FOUND ON MY DESK ONE WINTER'S morning in 2009 was really only the last sad remnant of a finger. The nail was missing, and so was the skin; it was the very end of the outermost bone, no bigger than a cherry stone. It belonged, as I later discovered, to a girl between the ages of five and seven. The fingertip was nestled in the customary padded envelope and had come a long way, from Novosibirsk. Not everyone would be pleased to find a severed digit from Russia on their desk before they'd had their morning coffee—but I was.

Almost a decade earlier, in 2000, the American president Bill Clinton had given a press conference at the White House in which he announced that, after years of work and billions of dollars invested in the Human Genome Project, our genes had at last been decoded. The project, which began ten years before, in 1990, was the first-ever international scientific research attempt to sequence all of the genes of our own species—otherwise known as the human genome. It remains one of the most ambitious and groundbreaking moments in scientific history. DNA was instantly headline news across the world: one of Germany's biggest newspapers cleared its features section to print the sequence of the human genome, an endless series of the base pairs A, T, C, and G, which constitute DNA. Many people were struck by the new significance of genetics, believing DNA would allow them to read human beings as though from a blueprint.

In 2009, science was already much closer to this goal. I was working as a postdoctoral researcher at the Max Planck Institute for Evolutionary Anthropology in Leipzig (MPI-

EVA). The institute was the world's most important research hub for scientists wanting to sequence DNA from old bones, providing them with cutting-edge technology. More than a decade of laborious genetic research had already been conducted there, research without which the finger bone on my desk could never have been used to alter our understanding of the history of human evolution. The bone, discovered in Siberia, represented the 70,000-year-old remains of a girl who belonged to a previously unknown kind of archaic hominin. It took only a few milligrams of bone powder—and a highly complex sequencing machine—to reveal this fact. Just a few years earlier it would have been technologically inconceivable to determine from such a tiny fragment whom it belonged to. Yet the bone had more to tell us. Not only did we learn what made the girl similar to human beings alive today, we learned how she was different.

ONE TRILLION A DAY

THE NOTION THAT DNA IS LIFE'S BLUEPRINT HAS BEEN around for more than a hundred years. In 1953, using pioneering work by British chemist Rosalind Franklin, American biologist James Watson and British physicist Francis Crick discovered the structure of DNA. Nine years later the two men were both awarded the Nobel Prize in Physiology or Medicine (by that point Franklin had died, passing away at the young age of thirty-seven). Ever since then, the medical community had put in the work on DNA that ultimately heralded the Human Genome Project.

In the 1980s, another milestone along the road toward decoding, or reading, DNA was reached with the development of the polymerase chain reaction.[1] This process allows us to determine the order of base pairs within a DNA molecule, and it is indispensable to sequencers today. Since the turn of the century, sequencing technology has been advancing apace. If you compare the old Commodore 64 computer with a smartphone today, you'll have an idea of how swiftly technology has progressed in the field of genetics.

Let me give you a few statistics to illustrate the scale of what we're discussing when we talk about decoding DNA. The human genome consists of 3.3 billion base pairs.[2] In 2003, when the Human Genome Project came to an end, it would have taken more than ten years to unravel the genetic code of a particular individual.[3] Today our laboratory can process a trillion base pairs every day. The throughput of these machines has increased by a factor of 100 million over the past fifteen years: currently, one sequencer can decode an extraordinary 300 human genomes in a single day. In ten years the genome of a billion people worldwide will have been decoded with some degree of certainty, and so far we've systematically underestimated the rate of technological development. DNA sequencing is becoming quicker and cheaper all the time and will soon be an option for almost everybody. Mapping out someone's DNA currently costs less than a full blood panel, so it will hardly be surprising if young parents start routinely requesting the decoded genome of their newborns. DNA sequencing offers undreamed-of possibilities—catching genetic predispositions to certain illnesses early, for example—and this potential continues to grow.[4]

While the medical community tries to improve their understanding of disease and develop new therapies and drugs

Johannes Krause extracts a DNA sample from the upper-arm bone of a Neanderthal from the Neandertal Valley, which gave the Neanderthals their name.

The biggest risk in DNA analysis is contamination. In order to prevent this, the bone samples are extracted while wearing protective clothing and in air-tight, isolated rooms.

by decoding the genomes of living people, archaeogeneticists are harnessing this technology to analyze archaeological finds. Old bones, teeth, or even soil samples can help archaeogeneticists to draw conclusions about the origins and genetic relationships of people long dead. This work has opened up entirely new avenues for the field of archaeology. We no longer have to rely solely on theories and interpretation; rather, genetic analyses allow us to pin down, say, migration patterns more precisely than ever before. The ability to decode ancient DNA has proved as momentous for archaeology as another technological revolution that dates back to the 1950s, when the radiocarbon method transformed the way archaeological finds were dated. Carbon dating was the first tool that enabled scientists to reliably date human remains, albeit not to the precise year.[5] DNA technology allows archaeogeneticists to read skeletal fragments and identify connections that would have been unknown even to the people to whom the bones once belonged. The remains of human beings who have lain in the earth, sometimes for tens of thousands of years, have thus become valuable messengers from the past. In these fragments the stories of our ancestors are written, stories we will tell—some of them for the first time—in this book.

HUMANS MUTANTS

ONE OF ARCHAEOGENETICS' MOST IMPORTANT PIONEERS is Svante Pääbo, who has been director of the MPI-EVA in Leipzig since 1999. Originally from a medical background, in 1984 Pääbo extracted DNA from an Egyptian mummy as part of his PhD research at Uppsala University in Sweden, working more or less secretly at night in the lab. In 2003, Pääbo accepted me as a graduate student in Leipzig. When, two years later, I was casting about for a topic for my doctoral thesis, he suggested I work with him to help decode the Neanderthal genome. Frankly, the idea sounded nuts: such an undertaking would have taken decades with the technology available at the time, not to mention that we'd have to grind to dust dozens of kilograms of precious Neanderthal bones. Still, I trusted Pääbo and his judgment; if he said the project was feasible, then I believed him. I took the offer. This turned out to be the right decision. Sequencing technology developed at breakneck speed, and we were able to conclude our work in five years—and with minimal destruction to the bones. It was during this period that, examining the piece of finger from the Altai Mountains, I discovered a new relative of modern humans—the Denisovans—which fundamentally revised our story of human history (you can read more about my discovery in the box at the end of this chapter, "Working Our Fingers to the Bone"). Bones like these are the storage media of archaeogenetics, and they can tell us all sorts of things. Was the archaic human to whom this bone belonged one of our ancestors, or did their line die out? How is their genetic makeup different from ours?

In archaeogenetics, we use the genome of archaic humans as a kind of template and compare it to our own, contemporary DNA. As researchers, we're interested in the places where the DNA doesn't line up, because these are the places where it has changed, or mutated. The word "mutation" holds unpleasant connotations for many people, but mutations are the engine of evolution; they're the reason human beings and chimpanzees stand on different sides of the fence at the zoo. Mutations are the milestones of human history.

In the time it takes you to read this chapter, the DNA in millions of your cells will undergo chemical changes—in your skin, in your gut, everywhere. Usually these changes are immediately corrected by the body, but not always. When this process goes awry, it's called a mutation. If mutations appear during the formation of germ cells—that is, in sperm or egg cells—they can be passed on to the next generation. The body has mechanisms to prevent this; as a result, fertilized germ cells with mutations that cause serious illnesses usually die. But smaller mutations often slip through the net, and a genetic change can thus, under certain circumstances, become hereditary.[6]

Genetic changes that result in more offspring tend to spread more rapidly through a population, because they're more frequently passed on. There were probably several mutations, for instance, that led to our relative hairlessness compared to apes, our distant cousins. We developed sweat glands, a more effective cooling system that allowed less hairy archaic hominins to run farther, hunt better, and escape from predators more effectively, meaning they lived longer and had better odds of reproducing. Archaic humans with genes predisposing them to hairiness, on the other hand, less able to compete for resources and outrun prey, died out.

Of course, most mutations aren't adapted to any particular purpose. Either they have no effect on the organism at all or they damage it and are therefore negatively selected, or weeded out. In the rare cases where they prove useful to survival and reproduction, they're positively selected and propagate throughout the gene pool, driving evolution permanently forward. We can thus describe evolution as interplay of random accidents during an ongoing field trial, the field trial that is humanity's life on earth.

HALF JUNK, HALF BLUEPRINT

Anyone keen to understand their genetic blueprint should remember that of the 3.3 billion base pairs in our genome, most are considered junk—only 2 percent are genes. That 2 percent codes for proteins, the building blocks of our bodies, representing the blueprint for roughly 30 trillion cells.[7] A human being has only around 19,000 genes in total, a remarkably small number. An amoeba, a tiny single-celled organism, has 30,000 genes, while some ordinary beetles have more than 50,000. By itself, the number of genes in an organism does, therefore, not dictate its complexity. In an organism with cell nuclei, information from a single gene can be combined into a wide variety of building blocks; the gene is not necessarily responsible for only one function in the body. In more primitive organisms—bacteria, for instance—one gene can usually be turned into only one building block, which usually undertakes only one task. Another way of putting this is that human genes, and the genes of most animals, are a very small team that shows outstanding teamwork.

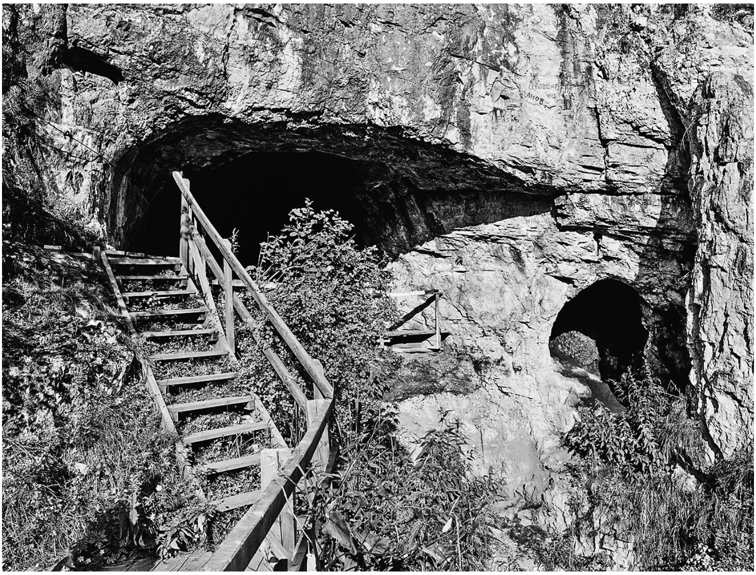
Fifty percent of the human genome is littered with junk, much like a computer hard drive that's far too big. By "junk" I mean DNA sequences that serve no discernible purpose. Besides genes, molecular "switches" play an important role, constituting approximately 10 percent of our immensely complex genetic structure. These switches are activated and deactivated by transcription factors, ensuring that every part of the body is producing the right protein—that the cells in your fingertip, for example, don't suddenly decide they're stomach cells and start producing acids. Fundamentally, all cells in the human body contain the same information; it's a question of discerning what information is relevant.

For archaeogeneticists, the useless parts of the genome are worth their weight in gold, because they allow us to establish what we call the molecular clock. Scientists measure mutations throughout the genome, drawing conclusions about, say, when two populations diverged—the further back this happened, the more new variants will have accumulated in the DNA or altered their frequency. If the entire genome consisted of genes, the number of variants—that is, mutations—would depend not on how long ago the split occurred but on how widely the two populations' environments differed. For example, sub-Saharan Africans have fewer changes in several of their genes than the descendants of people who migrated out of Africa. This is because the migrants' genes had to adapt to new conditions, while those of the people who remained in

Africa did not, or only to a lesser degree. Yet today the genome of sub-Saharan Africans contain even more mutations compared to people outside Africa. The reason? Mutations take place in the genome's junkyard, just as they do in genes, but are not as much subject to positive or negative selection. The same number of mutations has accumulated in all of us since our most recent common ancestor, so the molecular clock still works—no matter how far the actual genes of two comparable populations have diverged. Sub-Saharan African groups separated from each other much further back in time and therefore had more time to accumulate neutral mutations.

For archaeogeneticists, looking at the genetic material of old bones is like going back in time: using the DNA of ancestors who lived many thousands of years ago, we can learn which mutations have persisted till the present day and which have disappeared. But very few bones are suitable for sequencing, because the DNA must be well preserved. Radiation, heat, and moisture are among DNA's enemies, but its greatest enemy is time. The older the bone, the less likely it is that we can extract usable DNA. And then there is the problem of contamination. Modern DNA is as easily scattered as sand in a seaside vacation home: ceaselessly and into every nook and cranny. The DNA that Svante Pääbo extracted from his mummy in the eighties, for example, almost certainly came not from Egypt but from contemporary Sweden—in other words, from him.

Nonetheless, the nineties saw an explosion in DNA sequencing. The topic, which seemed a highly promising area of research, was a crowd-pleaser, especially since broad swaths of the public believed that dinosaurs could be brought to life from ancient mosquitos trapped in amber, as depicted in Steven Spielberg's *Jurassic Park*. Many of the sequencing studies carried out on ancient DNA weren't worth the paper they were printed on. Contamination of the fossils was a perpetual problem, and even the most careful testing couldn't exclude the possibility that the fossils had come into accidental contact with bacterial and researcher-related DNA. By the end of the 1980s, there were scientific criteria regarding the authenticity of ancient DNA, yet many researchers simply ignored them.



The Denisova Cave in the Siberian Altai Mountains, where the finger bone of the Denisova girl were found. Early modern humans and Neanderthals both lived in this cave.