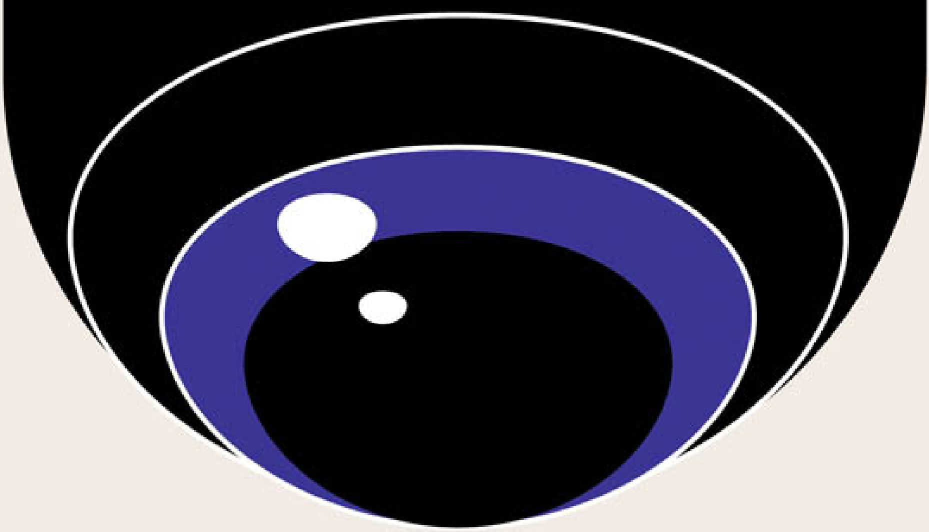
Critical Perspectives on Ancient DNA



Edited by
Daniel Strand,
Anna Källén, and
Charlotte Mulcare

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Critical Perspectives on Ancient DNA: An Introduction

Daniel Strand and Anna Källén

In recent years, an intense focus on DNA has had a major impact on archaeology and our general knowledge about the ancient past.[1] While ancient DNA, or aDNA, has been extracted and analyzed since the late 1980s, the use of bioinformatics and innovations such as next-generation sequencing has from 2015 onward resulted in a dramatic increase in the number of analyzed samples. Although high-profile research papers on female Viking warriors and black Neolithic Europeans have made archaeogenetics famous beyond the corridors of academia, the field can be said to have got its definite public breakthrough in the fall of 2022, when the Nobel Prize in Medicine was awarded to Swedish paleogeneticist Svante Pääbo.

The hard-science muscle of archaeogenetics has certainly brought new resources, much attention, and a renewed confidence to research and knowledge claims within archaeology. Conversely, one might argue that the allure of archaeology has endowed genetic research with a profitable aura of adventure and mystique. In this sense, the rapid development of the field has been a win-win enterprise for archaeology and genetics. But what are the broader consequences of this development when it comes to our understanding of the ancient past? What are the social and political effects of a genetic conceptualization of past people's identities and our present relations to them? What qualitative changes have the recent methodological developments in genomics brought to our knowledge of prehistory?

In *Critical Perspectives on Ancient DNA*, we dive deep into these issues, interrogating the practices, communications, and broader consequences of archaeogenetics. The seven chapters in this book present a critical perspective on this research field, exploring how, rather than simply revealing all-encompassing objective truths, it not only reifies old categories of identity and belonging but also creates new ones. The chapters assess to what extent archaeogenetics has contributed to a new and better version of historical knowledge, and they scrutinize the validity of bold claims about finding the real answers to questions of prehistoric events and ancient people's identities. Do these claims have any foundation, or are they, rather, reflections of an ambitious—but ultimately impossible—positivist effort to uncover historical truths by employing the methods of natural science?

The Study of DNA

DNA is a molecule, of which long strands—chromosomes—exist in the nucleus of human cells. Parts of the chromosomes (usually considered to be less than 2 percent in humans) contain coded instructions for the production of various proteins and thus influence the physical functions and appearance of the human body. These units are called genes. A human genome contains the chromosomes for an individual in their cell nuclei, as well as a separate, smaller body of maternally inherited DNA found in the mitochondria, the cell's "powerhouses." By extracting and analyzing DNA from the cell nucleus and the mitochondria, and comparing the DNA of different individuals, it is possible to detect close biological family relationships and estimate distant ones. It is also possible to diagnose some diseases (such as Huntington's disease and sickle-cell anemia) and trace some physical characteristics (such as waxy ears).

The iconic helix shape of the DNA molecule was officially presented by Francis Crick and James Watson in the early 1950s, a time of postwar optimism, when science and technological innovation were seen as leading the way to a prosperous future.[2] Crick and Watson became media celebrities, and DNA became publicly known as an objectively detectable code of life. It inspired widespread phantasms of DNA as a complete "blueprint" of an organism with the potential to bring the long-dead past back to real life, spicing up adventure fiction and archaeohorror films such as *The Mummy*.[3] In the 1980s, when DNA profiling was developed for forensic science, DNA became widely known as hard evidence of individual identity, valid in a judicial sense. Altogether, this created a solid, popular confidence in DNA as a source of indisputable truth providing a complete map of an individual's characteristics.

While it is easy to be seduced by the metaphor of DNA as a blueprint, this is not quite how genes works. As molecular anthropologist K. Ann Horsburgh puts it, “Blueprints share a one-to-one correspondence with the object they specify; they always produce the same results. This is certainly not the case with DNA.”[4] In reality, the relation between DNA (the so-called genotype) and the actual outcome (the so-called phenotype) is much more complicated than suggested by the blueprint metaphor. Human identity and family relations are, moreover, defined by so many factors other than biology. Hence, there is little congruence between the great popular trust in DNA and what DNA can actually say in a scientific analysis—especially when it comes to aDNA. While this divergence between DNA as popular image and genetics as science is well known, it has rarely been brought into serious conversation by researchers working in the field. When it has, the focus has tended to be on the risks of false claims, which are said to diminish the public’s trust in science.[5]

In this volume, we offer a slightly different perspective on this problem. Rather than dismissing the inflated public trust in DNA as unimportant just because it may be false or trivial, we point to its great importance for archaeogenetics.[6] In this vein, we recognize that knowledge about aDNA is not only created in science laboratories and at universities, but through complex meaning-making interactions between research and society at large. Throughout the volume, we maintain that the scientific discourse and practice of archaeogenetics have been formed in close, and continuous, interaction with popular imagination. Indeed, as Amade M’charek points out in her chapter in this book, archaeogenetics “invites a wide audience to project different kinds of aspirations, feelings, and vested ideas” on its subject. Popular phantasms and public expectations have played, and continue to play, prominent roles in the development of the field.

Ancient DNA, Archaeogenetics, and Archaeogenomics

Ancient DNA refers to the DNA of organic remains from the past. Since DNA molecules start to degrade as soon as the organism is dead—unless soft tissues are preserved as, for example, in the case of bog bodies or permafrost mummies—ancient DNA is in nearly every case more fragmentary than that of a living organism. Most attempts to extract and analyze aDNA are therefore ridden with problems of degradation. In analyses of ancient human DNA, there is also the risk of contamination from the abundance of DNA from living humans swirling around at archaeological excavations, in museums, and in the laboratory. For a long time, these problems seemed insurmountable, and it was not until the 1980s that the first studies of aDNA were published. In terms of knowledge structure and research questions, these studies built on earlier work in molecular anthropology, population genetics, and forensic science, but added the specific methodological challenges of working with degraded and potentially contaminated DNA, as well as questions and problems relating to archaeological and historical discourses.

The development of aDNA studies, or archaeogenetics, can be roughly divided into two phases. The first began in earnest in 1984, when scientists at a laboratory in Berkeley, California managed to sequence mitochondrial DNA from a stuffed quagga in a museum in Germany.[7] Around the same time, biologists in Silicon Valley developed a new technology for replicating fragments of DNA from different types of samples in order to visualize genetic diversity. Geneticists had previously been forced to sequence particular strands of interest by hand, involving a heavy investment of time and money, but polymerase chain reaction (PCR) made it possible to amplify small fragments of genetic material and visualize them far more easily. By the beginning of the 1990s, scientists had successfully applied PCR to amplify aDNA fragments not only from preserved soft tissue, but also from dry bones and fossilized remains of ancient plants and insects.[8]

The field of human archaeogenetics—with which this book is primarily concerned—grew rapidly in the following years. As geneticists and molecular anthropologists turned from skin and mummies to more common ancient human remains in the form of bone and teeth, they could start addressing questions about genetic relations between tentative ancient population groups, such as the Pacific Islanders and Native Americans, as well as investigating prehistoric "celebrities" such as Ötzi, the 5,000-year-old man found in a melting glacier in the Tyrolean Alps in 1991.[9] One particularly noted study during this period was a 1997 article in which geneticists in Germany presented the sequencing of mitochondrial DNA from the remains of an approximately 30,000-year-old Neanderthal individual. By demonstrating that the resulting sequence fell outside the variation of modern humans, the study indicated that Neanderthals went extinct without interbreeding with modern humans.[10]

In this first phase of archaeogenetics, the introduction of DNA to the toolkit of archaeological science also inspired discussions among archaeologists and molecular anthropologists regarding the methodological and epistemological challenges, and potential ethical issues, pertaining to this new line of research.[11]

The second phase of archaeogenetics came with the introduction of the technology known as next-generation sequencing.[12] Developed in the first decade of the new millennium, this technology made it possible for scientists to sequence multiple small fragments of DNA in parallel, with bioinformatic technology piecing together the fragments by mapping "reads" to a reference genome. In practical terms, this meant that the whole breadth of a human genome could be sequenced in a single day, in contrast to the technology used in the 1990s, with which it could take over a year.[13]

The possibility of sequencing larger parts of ancient human genomes allowed archaeogenetics to develop into archaeogenomics.[14] Published in 2010, the first genome-wide DNA studies of ancient humans included sequences from a 4,000-year-old individual from present-day Greenland and an archaic hominin individual from a Russian cave.[15] The same year, a paper presenting the first sequencing of a Neanderthal genome showed that modern humans indeed have traces of DNA shared with Neanderthals in their genomes.[16] This finding suggested that the two human subspecies, contrary to previous claims, not only lived at the same time but also interbred.

With next-generation sequencing, the number of sequenced samples from ancient human remains grew exponentially. While a handful of ancient genomes were sequenced in 2010, more than a hundred samples were sequenced every year between 2015 and 2018. By 2018, over 1,300 genome sequences had been produced from ancient human remains.[17] Meanwhile, the publications on ancient human DNA—from scientific papers in *Science* and *Nature* to popular science books and journalistic reports—skyrocketed. As noted by scholars covering the development of archaeogenetics, the field has become a "hype" buttressed by a steady stream of interviews, television documentaries, TED talks, and newspaper profiles featuring the leading scientists in the discipline.[18] According to philosopher of science Joyce Havstad, the unwavering media interest has turned archaeogenetics into a "sensational science" whose practitioners "can foreseeably expect to capture and sustain public interest . . . in a way that is likely to foster its development, and to amplify the publication and prestige of its results."[19] As Andreas Nyblom puts it in his contribution to this volume, archaeogenetics thrives in the media limelight.

The "aDNA Revolution"

The hype around archaeogenetics has not gone unnoticed by the scientists themselves. In the wake of next-generation sequencing and the steep publication curve of aDNA data and papers, researchers in the field have begun claiming that archaeogenetics constitutes a "revolution," and that the application of new molecular technologies marks a "paradigm shift" in the history of archaeology and anthropology.[20] The revolution trope has been reproduced not merely in academic settings but also in popular science, news media, and interviews with scientists involved in the field.[21]

While many have been eager to announce this "aDNA revolution," however, it is worth noting that few have sought to clarify why this is a revolution and against what or whom it is directed. In his classic 1962 book *The Structure of Scientific Revolutions*, historian of science Thomas Kuhn argues that a "scientific revolution" takes place when a discipline is confronted by a fundamental problem which threatens to devastate the entire scientific pursuit. With the establishment of a new "paradigm" designed to resolve the problem, Kuhn suggests, the discipline is saved, but at the expense of vast amounts of previously accepted knowledge, methodology, and terminology. As with a political revolution, Kuhn notes that the scientific revolution means that "the world itself changes."[22]

A critical question, however, is how all of this applies to aDNA research. What is the problem that threatens to undermine archaeology and anthropology, and to which genetic analysis promises a solution? What is the new paradigm established by archaeogenetics, and in what way(s) has it fundamentally transformed archaeological or anthropological research? What previously established archaeological knowledge has been ground by the mills of next-generation sequencing? And against whom or what is the revolution staged?

Since none of the proponents of the "aDNA revolution" have addressed any of these questions, it seems reasonable to suggest that the term does not purport to represent a scientific revolution in the traditional Kuhnian sense of the word. Rather, the "aDNA revolution" seems to be a somewhat hyperbolic euphemism for the past years' increasing number of sequenced ancient genomes and published scientific papers. Seen from this perspective, it is revealing that Harvard-based geneticist David Reich, who is perhaps the person most closely associated with the term "aDNA revolution," has described his main contribution to archaeogenetics as "to make ancient

DNA industrial—to build an American-style genomics factory."[23] As Reich boasts, his laboratory is "producing data so fast that the time lag between data production and publication is longer than the time it takes to double the data in the field."[24]

The most striking feature of this kind of rhetoric is the focus on numbers: more samples, more data, more papers. For Reich and his fellow aDNA revolutionaries, the revolution does not primarily seem to concern the quality of scientific results, but the quantitative leap in numbers of resources (ancient human genomes, next-generation sequencing technology, big data) and products (databases, scientific papers, books, conferences). While it is of course true that archaeogenetics has experienced a boom in the number of samples and publications, however, it is not apparent that this boom itself constitutes a "revolution" of archaeological or anthropological knowledge. Indeed, one could go as far as K. Ann Horsburgh in her concluding commentary to this volume and say that "despite grandiose claims to the contrary, aDNA data have not, and will not, revolutionize reconstructions of the past."

The Social Effects of Archaeogenetics

If empirical aDNA studies now abound, less attention has been paid to the cultural, social, and political aspects of archaeogenetics. The enthusiasm over technological advancements and the possibilities for cost-effective and hitherto unfeasible large-scale analyses has left little room for thorough critical inquiries into the wider effects of archaeogenetic research.[25] For sure, in the past years we have seen a number of publications presenting recommendations and best practices for archaeogenetics, often calling for a more genuine engagement with descendant communities and improved "collaboration" between geneticists, archaeologists, and custodians of human remains.[26] Moreover, several scientists in the field have published opinion pieces requesting a more cautious handling of ancient human remains and a greater sensitivity toward groups affected by archaeogenetic research.[27] The basic intention of such texts—to facilitate a more ethically attuned and politically informed approach among scientists in the field—is certainly important. One hopes a better understanding of the interests of different stakeholders would engender more socially responsible practices.[28]

Since most of these publications have been written by researchers with stakes in the current standing and future development of the field, however, they rarely address more profound epistemological, cultural, and political issues related to archaeogenetics. What happens to our understanding when archaeology and historical inquiries into the past are married to genetic science? How does the research field relate to earlier traditions of categorizing human subjects according to biological differences, and in what ways can it not only challenge but activate and reify ideas of identity, race, and nationality? What kinds of cultural or historical narratives are generated by archaeogenetics, and what sorts of politics might such narratives give rise to? How does the entanglement of research laboratories, popular media and funding agencies shape the production of archaeogenetic knowledge? And how does the genetic concept of "ancestry" promoted by archaeogenetics relate to nonbiological, much older, ideas of what it means to be related?

These are the kind of questions addressed in *Critical Perspectives on Ancient DNA*. A collection of essays written by renowned scholars in Europe and the United States, this book offers the first comprehensive and in-depth inquiry into the practices and effects of archaeogenetics. As a multidisciplinary venture, it features anthropologists, archaeologists, geneticists, media historians, cultural studies scholars, and researchers in science and technology studies. Although their objects of study and methodological approaches differ, all contributions come together in an effort to critically investigate how archaeogenetics appears in relation to, and in interaction with, society at large.

The Chapters

In the first chapter in this book, "Gained in Translation: Interdisciplinary Challenges in Ancient DNA," geneticists Charlotte Mulcare and Mélanie Pruvost delve into one of the most discussed problems of archaeogenetics, namely the interdisciplinary collaboration between geneticists and archaeologists. The challenges stemming from interdisciplinarity have been discussed many times before, and improved collaboration between geneticists and archaeologists has often been proposed as the silver bullet to solve most problems identified in the field. Arising from profound personal experiences of working in research teams with scholars from the humanities, Mulcare and Pruvost take a slightly different approach to the problem of interdisciplinarity. Rather than glossing over the differences between geneticists and archaeologists, they emphasize the importance of acknowledging the fundamental epistemological distinctions between genomic science and disciplines in the humanities. While disparities in technical knowledge and language may lead to misunderstanding and tension, Mulcare and Pruvost argue that there is good reason to avoid rushing to immediate consensus. Instead, they encourage researchers in the field of archaeogenetics to sit with conflicts, acknowledge differences, and engage in acts of translation.

In "Diagrams of Human Genetic Kinship and Diversity: From the Tree to the Mosaic and the Network?," cultural studies scholars Marianne Sommer and Ruth Amstutz home in on technologies of knowledge production and visualization in archaeogenetic research. By describing and comparing software programs employed for the statistical analyses of populations, as well as visual representations used to illustrate the resultant data, Sommer and Amstutz show that what may seem to be neutral or data-derived technologies are in fact creative, generating fundamentally different research results depending on choices made by programmers and researchers. Following the use of common visual metaphors such as the tree and the mosaic from early thinking on human evolution to current research on aDNA, they demonstrate how "tree thinking" lingers in software programs and how this legacy potentially reproduces notions about discrete and "pure" populations. Despite the persistent emphasis on "admixture" and "gene flow" between populations, Sommer and Amstutz argue that archaeogenetic research which rests on such technologies risks reproducing a tradition of scientific racism, to which it is often said to be antithetical.

In the third chapter, "Past Pathogens and Precarious Futures," science and technology studies scholar Venla Oikkonen explores cultural representations of ancient pathogens in permafrost. In the face of thawing due to climate change, there has been an increasing anxiety surrounding the capacity of pathogens to come alive and cause life-threatening infections. Focusing on two cases—the anthrax outbreak in Siberia 2016, and the reconstruction of the 1918 pandemic influenza virus—Oikkonen teases out the cultural imaginations and political narratives that take shape around these ancient pathogens. It is not only the past that matters when we deal with aDNA, she argues, but also the future. As Oikkonen's two cases demonstrate, the relations between past, present, and future engendered by aDNA are ambivalent, as it both threatens and promises future life.

In the fourth chapter, "Twisting Strings: Hopi Ancestors and Ancient DNA," Hopi tribe member Stewart B. Koyiyumptewa and anthropologist Chip Colwell discuss the problems inherent in uses of the concept of ancestry in archaeogenetics. Juxtaposing the strictly biological definition of ancestry in genetic science with Hopi notions of ancestry—conceived as a complex tapestry including humans and nonhumans, material objects, sites, and historical events—Koyiyumptewa and Colwell highlight the limitations of genetics in analyses of social identity. For archaeogeneticists to make valid contributions about cultures that do not share their specific concept of ancestry, they will have to adapt to other, extragenetical, definitions of what it means to be related. Reviewing the encounter between Indigenous tribes and archaeogenetics, the chapter points to an urgent need for a profound form of collaboration that does not merely aim to persuade Indigenous people to provide DNA samples for archaeogeneticists' databases but is also open to negotiation of key concepts in archaeogenetics.

In "Whitewashing the Neanderthal: Doing Time with Ancient DNA," anthropologist Amade M'charek scrutinizes cultural meaning making around concepts of race and identity by examining the influence of archaeogenetics on popular imaginations of the Neanderthal. If Neanderthals used to be depicted as brutal, dumb, dark-skinned, and apelike creatures, recent archaeogenomic research showing that Neanderthals interbred with *Homo sapiens sapiens* has engendered new representations of the Neanderthal as akin to the modern white European man, sporting business suits and talking on cell phones. This genre of representation, M'charek notes, inserts the Neanderthal as an object into a single story of origin where the European subject poses at the end as the crown of evolution. Weaving together personal memories and fieldnotes from her anthropological work in a leading lab working with Neanderthal DNA, along with close readings of museum displays and popular images of Neanderthals, she calls attention to the dangers of using aDNA to create a single story of evolution—in this case featuring a whitewashed version of the Neanderthal—with significance for racial politics in Europe and other parts of the world.

The relations between aDNA and popular culture are further explored in media historian Andreas Nyblom's chapter "The Lagertha Complex: Archaeogenomics and the Viking Stage." Presenting a close reading of the story about the "female Viking warrior"—a global media celebrity born out of a 2017 analysis of ancient human remains excavated from a Viking Age site in Sweden—Nyblom carefully unpacks the construction of individual identity based on aDNA. Contrary to the idea, promoted by the researchers and communicators, that the complex social identity of this individual from a thousand years ago was determined or “confirmed” by genomics, Nyblom demonstrates how the persona of the “female Viking warrior” was in fact constructed in convoluted interactions between archaeologists, academic journals, popular culture, news outlets, and social media. The main contribution of DNA to the story about the “female Viking warrior” was not analytical, Nyblom argues, but metaphorical. More than anything else, DNA was used as a sign of indisputable proof, stamped on creative interpretations inspired by archaeological findings, ancient mythology, and contemporary fiction.

In the final chapter, “Ancient DNA and the Politics of Ethnicity in Neo-Nationalist China,” anthropologist Magnus Fiskesjö offers a unique insight into the political potentials of aDNA. With historical overviews and current descriptions of the concept of ethnicity in national politics in China, Fiskesjö demonstrates how “the power of naming” in genetic mappings of past and present populations becomes complicit in political violations of human rights in contemporary China. He unfolds a deliberate political effort to establish the ethnic Han group as the deep-rooted origin of the Chinese nation, with subsequent programs of forced assimilation and erasure of targeted ethnic minorities. Official actors—from high-profile Chinese geneticists to president Xi Jinping himself—have emphasized the importance of DNA in this political pursuit. International researchers engaging in archaeogenetic research on Chinese material, Fiskesjö argues, often lack the cultural competence to understand the broader consequences of their research. As a warning example, the case of China points to the inherent potential of archaeogenetics to serve political ambitions with severe consequences.

In a concluding commentary arising from her own experiences of working with ancient DNA, molecular anthropologist K. Ann Horsburgh demonstrates how genetic data can become meaningful only by being articulated to other kinds of data, such as social and historical context. For the future of archaeogenetics, she makes a plea for broader interdisciplinary collaborations that can close the door to “molecular chauvinism,” in which genetic data are regarded as pure and privileged, and instead open up for a genuine appreciation of the epistemological complexity of aDNA studies. It will, Horsburgh implies, require a profound critical reflection that includes a halt in the hunt for flashy press releases, an engagement with Indigenous and descendant communities throughout the research processes, and a “recalibration of [the field’s] core mission and its core values.”

Critical Perspectives on Ancient DNA

As the title of this volume makes clear, these chapters offer critical perspectives on ancient DNA. But what exactly is the critique? What is meant by a genuinely critical perspective on archaeogenetics?

As noted above, the public perception of DNA has long tended to be characterized by the idea that our genes offer a source of absolute truth about who we "really" are. With aDNA, this idea has been projected onto the past. Researchers involved in archaeogenetic research have famously portrayed their enterprise as a "door to the past," or a means for attaining indisputable evidence of what actually happened in prehistoric times.[29] In a classic quote, Oxford geneticist and popular science personality Bryan Sykes has claimed that "our DNA does not fade like an ancient parchment; it does not rust in the ground like the sword of a warrior long dead. . . . It is the traveler from an antique land who lives within us all."[30]

From this point of view, DNA is a passive artifact of the past, just waiting to be uncovered by cutting-edge scientists. It is not, however, an accurate description of archaeogenetics. The compositions of DNA molecules in our genomes are indeed inherited as more or less randomly recombined versions of the molecular compositions in the genomes of our ancestors. But the molecules are our own. And molecules do not speak. To make meaning out of what is fundamentally a meaningless substance, scientists and others who create and communicate stories about aDNA have to use words, names, labels, categories, statistical models, and images. These discursive components do not emerge naturally and neutrally out of the DNA molecules. Instead, they are the product of culturally informed techniques of meaning making. Not only do they hinge on specific historical contexts and existing discourses, they also have social and political effects that extend beyond the sphere of genetic science itself.[31]

The chapters in this volume can be seen as a critique of the notion of aDNA as a petrified historical source that can be neutrally and objectively unveiled by genetic analysis. Rather than approaching DNA in this way, the chapters investigate the meaning-making techniques of archaeogenetics and explore how these are anchored both in the history of the research field itself and in cultural discourses pertaining to other parts of society. Here, we find reason to recall some of the debates that surrounded the Human Genome Diversity Project (HGDP) in the 1990s. Fronted by Stanford geneticist Luigi

Luca Cavalli-Sforza, and setting out to survey and map genetic relations between groups of people in order to reveal "who we are as a species and how we came to be,"[32] the HGDP was caught between an outspoken antiracist ethos and allegations of biocolonialism, biopiracy, and racialist exploitation.[33] After fierce debates that went on for years, the project was officially discontinued in 1997 when funding agents withdrew support. But the HGDP inspired new grand-scale endeavors with similar aims and ambitions, such as the Genographic and HapMap projects. Its legacy still lingers in current aDNA research—in terms of both methodology and ambition.[34]

In an influential study of the HGDP debate, sociologist Jenny Reardon argues that our understanding of the HGDP has been obscured by a flawed Enlightenment-based image of science as essentially pure and separate from politics.[35] This figure of purity was at the heart of the idea that the HGDP would be an antidote to racism, just by providing scientific facts about complicated genetic relations. When critics pointed out that the principles of sampling and the structures of the analytical models used to sort out and "map" genetic diversity actually reinforced old and murky ideas of primitivity and essential identity, proponents of the HGDP struggled to take it in. Taking refuge in the idea of a pure science, they were adamant that their project could not be contributing to racism, because of its high-quality scientific foundation. Any dangerous or unethical effects of the project must, according to this mindset, be due to "misuse" or popular misunderstandings of science.

As Reardon and others have demonstrated with much clarity, however, this is not a sustainable understanding of scientific practice, which in reality is always entangled in the society that it is part of.[36] In the words of science and technology studies scholar Kim TallBear, the molecular sequences that genetics draw on are not "simply uncovered in human genomes," but "conceived in ways shaped by key historical events and influential narratives."[37] As a meaning-making practice, archaeogenetics does not only intersect with prevailing cultural discourses about history, identity, and belonging, as becomes clear in Amade M'charek's chapter on the recent whitewashing of the Neanderthal. It also takes shape within prevailing power structures, such as those legacies of colonialism that inform the encounter between geneticists and Indigenous groups discussed in Stewart B. Koyiyumptewa and Chip Colwell's chapter. Whatever social or political consequences archaeogenetics might have, these cannot be seen as the unfortunate result of a "misuse" of science, sloppy media accounts, or mistakes by bold and attention-seeking researchers. As the essays in this volume make clear, they ultimately stem from the science itself.

This point is perhaps made most clearly in Marianne Sommer and Ruth Amstutz's chapter, which explores how archaeogenetics—and population genetics more broadly—is based on visual representations that render humanity as divided into discreet, separate "populations." In spite of the recurring insistence that research on aDNA undermines racism by demonstrating that human history has always been characterized by "admixture" between different groups, the very idea of "admixture" is, in fact, based on the notion of purity.[38] As Sommer and Amstutz suggest, archaeogenetics tends to reproduce notions about humanity as divided into different "races." Thus, while the political transgressions legitimized by aDNA that Magnus Fiskesjö discusses in his chapter are of course perpetrated by actors outside the realm of archaeogenetics itself, the very employment of aDNA to separate groups from each other is fully in line with the logic of a research field that, as we have noted elsewhere, is based on a methodology of differentiation.[39] As Fiskesjö's chapter demonstrates, it is not possible to make a clear distinction between geneticists who create such differentiations and political actors who put them to work. Indeed, as Andreas Nyblom shows in his chapter on the worldwide commotion around the "female Viking warrior," archaeogenetics is not an insulated, sealed-off laboratory enterprise, but a complex ecosystem in which geneticists and archaeologists operate alongside communicators, journalists, and actors in popular culture and the entertainment business. This ecosystem interconnects university departments, funding agencies, media actors, cultural institutions, and political movements.

All of this shows that the idea of a boundary between archaeogenetics and society cannot be upheld. If it could, aDNA research would not generate the immense public interest that we have seen during the past decade. It would not make any headlines, receive massive funding, or be awarded any Nobel Prizes. But archaeogenetics has always been a high-profile research field thriving by the attention from the public. Unlike most academic disciplines, it has repercussions far beyond the university. Not only does it have the power to unsettle the past and unleash political energies whose consequences it cannot control; not only can it untie groups from their histories and provoke conflicts about land, rights, and identities; as Venla Oikkonen argues in her chapter on the threats and promises of pathogens in the thawing permafrost, it has the capacity to alter our very perception of the future.

Rather than taking the claims of archaeogenetics at face value and submitting to the idea that ancient DNA holds the key to absolute historical truths, it is time that we subject this research field to critical scrutiny.

Notes

1. We want to thank our coeditor, Charlotte Mulcare, as well as Andreas Nyblom and two anonymous reviewers for their critical reading and important inputs to this introduction.

2. For a historic overview of the study of DNA, including the drama surrounding the double helix, which also included scientist Rosalind Franklin, see Siddharta Mukherjee, *The Gene: An Intimate History* (New York: Scribner, 2016).

3. Dorothy Nelkin and M. Susan Lindee, *The DNA Mystique: The Gene as a Cultural Icon* (Ann Arbor: University of Michigan Press, 2004).

4. K. Ann Horsburgh, "Molecular Anthropology: The Judicial Use of Genetic Data in Archaeology," *Journal of Archaeological Science* 56 (2015): 142.

5. Some examples are Mark Thomas, "To Claim Someone Has 'Viking Ancestors' Is No Better than Astrology," *The Guardian*, February 25, 2013; "Debunking Genetic Astrology," University College London, accessed December 19, 2021, https://www.ucl.ac.uk/biosciences/gee/molecular-and-cultural-evolution-lab/debunking-genetic-astrology; Jennifer Raff, "Genetic Astrology: When Ancient DNA Meets Ancestry Testing," *Forbes*, April 9, 2019, https://www.forbes.com/sites/jenniferraff/2019/04/09/genetic-astrology-when-ancient-dna-meets-ancestry-testing.

6. See also Nelkin and Lindee, *DNA Mystique*; Judith Roof, *The Poetics of DNA* (Minneapolis: University of Minnesota Press, 2007); Josie Gill, *Biofiction: Race, Genetics and the Contemporary Novel* (London: Bloomsbury Academic, 2020).

7. Russell Higuchi et al., "DNA Sequences from the Quagga, an Extinct Member of the Horse Family," *Nature* 312, no. 5991 (1984): 282–284.

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23. Reich, *Who We Are*, xix.

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29. See Bryan Sykes, *The Seven Daughters of Eve: The Science that Reveals Our Genetic Ancestry* (New York: Norton, 2001), x; Adam Rutherford, *A Brief History of Everyone Who Ever Lived: The Human Story Retold through Our Genes* (New York: The Experiment, 2017); Reich, *Who We Are*, xxvi;

30. Sykes, *Seven Daughters of Eve*, x.

31. See Kim TallBear, *Native American DNA: Tribal Belonging and the False Promise of Genetic Science* (Minneapolis: University of Minnesota Press, 2013), 4–5.

32. Luigi Luca Cavalli-Sforza et al., "Call for a Worldwide Survey of Human Genetic Diversity: A Vanishing Opportunity for the Human Genome Project," *Genomics* 11 (1991): 490–491.

33. Jenny Reardon, *Race to the Finish: Identity and Governance in an Age of Genomics* (Princeton, NJ: Princeton University Press, 2005); Amade M'charek, *The Human Genome Diversity Project: An Ethnography of Scientific Practice* (Cambridge: Cambridge University Press, 2005); Jonathan Marks, "'We're Going to Tell These People Who They Really Are': Science and Relatedness," in *Relative Values: Reconfiguring Kinship Studies*, ed. Sarah Franklin and Susan McKinnon (Durham, NC: Duke University Press, 2001), 355–383.

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35. Reardon, *Race to the Finish*.

36. Reardon, *Race to the Finish*; Elgabsi, "Ethic of Knowledge."

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1 Gained in Translation: Interdisciplinary Challenges in Ancient DNA

Charlotte Mulcare and Mélanie Pruvost

> The oldest cliché in the world is about "what's lost in translation," but you don't very often read much intelligent about what's gained by translation, and the answer is everything. Our language is a compendium of translation.
>
> —Sam Hamill, 2003[1]

An archaeologist, a media historian, a historian of ideas, and a geneticist walk into a bar. They begin an enjoyable discussion about the challenges of interdisciplinarity and conflict in current practice in ancient DNA (aDNA) research. The warm feeling of being in total agreement, amplifying arguments and completing each other's sentences, comes to an abrupt halt when the geneticist suddenly asks how the group's criticisms of archaeogenetics could be addressed by changes in working culture. As punchlines go, this one is not well received. In the deafening silence that follows, the geneticist argues that criticism without any attempt at resolution or roadmap to redress shortcomings is a little nihilistic. The archaeologist is, in turn, concerned that calls to improve practice along prescriptive guidelines can be a way to control criticism and, to some extent, avoid it by formulating a set of given solutions to all problems. The historian of ideas argues that the genre of best practices serves as a way of glossing over the more profound and structural issues in aDNA research. The media historian, finally, suggests that the purpose and value of humanities scholarship should not be reduced to its practical applicability. A critical analysis of practices in aDNA research would be compromised if it encompassed an interest in the furtherance of that particular field of research.

Over the following years, the Code Narrative History research team took part in many similar discussions in a variety of settings (cafés, libraries, Zoom), ranging in tone (muddled, bracing, catastrophic) but broadly following a similar trend: an optimism regarding the potential of the discipline and a desire to resolve issues set against the need to critique and unpick them. Equivalent discussions in the Ancestra team (also interdisciplinary) revealed some deep schisms in understandings of language, methodology, and practice.

The idea that conflict in the field of human aDNA research rests along disciplinary boundaries is not particularly controversial. Recent years have seen extensive conflict within the field of archaeogenetics,[2] and a common reaction in the literature posits best-practice publications and guidelines as a potential solution. These generally seek to address existing grievances and to provide a consensus for a new, more enlightened culture of effective collaboration across disciplines.[3]

At first glance, these are positive developments and often lauded as such. Yet our combined experiences of working in interdisciplinary environments have given us pause for thought. While admirable in intention and principle, best-practice publications do not address the deeper challenge of implementing their recommendations in a working environment where deep cultural schisms impede many of the advocated measures.[4] This avenue may also risk contributing to a culture in which researchers cannot articulate problems unless they believe there is a way to solve them. Furthermore, while improved communication is often welcomed as the silver bullet for successful collaborations, critical voices—particularly those of Indigenous communities and marginalized groups—are often absent from the generation of these guidelines, guidelines that are themselves a product of the environment they seek to regulate.[5]

However, it is also understandable that our colleagues (and reviewers) are reluctant to engage with lengthy articles that offer relentlessly negative criticism. As an alternative to both strategies, we suggest there is a value to articulating the fault-lines inherent in archaeogenetic discourse, without seeking to impose specific direction on research teams. In our own interdisciplinary teams, which included scientists and humanities scholars, we found that conflict could be a precursor to innovation, and it is this benefit that we seek to explore here. Through unpicking dialogues that have been marred by misunderstanding, and by identifying places where the axioms of different research areas collide, we believe individual projects can benefit by increasing awareness within a team. In this way, awareness itself becomes a driver for improved practice, increased respect and sensitivity to nuance. This type of reflection need not result in a tangible end product, such as an ethical roadmap or processual toolkit. In any case, the research questions, environments, and eccentricities of any given team are often so specific as to render a universal approach of limited use. Our proposed approach would instead be to use insights derived from conflict within a group as a means to enhance a specific research project.

In this chapter, we use our own experiences as geneticists to reflect on the sources and dynamics of misunderstandings that emerged during the course of our research. Despite differences in our projects' ambitions and aspirations, we were able to identify a series of key themes, or clusters, of common problems. In this reflection, we sit with conflict in order to understand fully what is being lost—and gained—in translation. Our hope is that this exercise, though challenging, may bring unforeseen benefits to other research projects open to this kind of experiment.

A Tale of Two Projects

Code Narrative History: Making Sense of Ancient DNA in Contemporary Society (2018–2021) was an interdisciplinary research project based at Stockholm University in Sweden. The project investigated how ancient genetic sequences are used to formulate meaningful historical narratives, which often include claims of identity and pertain to cultural and sociopolitical issues in contemporary society. A key component of the project was understanding how actors from diverse fields—researchers in science and the humanities, as well as museum curators, journalists, and academic editors—understand, interpret, and explain new scientific data through existing cultural frameworks and traditional historiographies.

Members of the project recognized that a prerequisite of archaeogenetics is the generation of genetic data, which often places a strong reliance on a laboratory team formed by a community of scientists. Collaborations may, therefore, involve a predominance of scientists relative to humanities researchers and archaeological scientists, with the influence of a lab-based culture at their core. This paradigm was subverted in Code Narrative History, as the team included an archaeologist as the principal investigator, a media historian, a historian of ideas, and only one member (Charlotte Mulcare) with a background in genetic science.

The focus and composition of the Ancestra project, of which Mélanie Pruvost is principal investigator, differed significantly from Code Narrative History. Despite France's substantial archaeological and historical wealth, few archaeogenetic data were available for France when the Ancestra project was initiated toward the end of 2015 with the support of Agence Nationale de la Recherche funding. The objective was to study the origins and dynamics of the settlement of France since the Neolithic period or, more precisely, of the territory corresponding to present-day France. The approach involved combining culture and genetics to focus on what archaeologists call "transition periods," and, in doing so, to inform an ongoing debate: To what extent are visible changes in material culture, evidenced through archaeological remains, reflective of changes at a population level—that is, the movement of groups of people—and to what extent are they the result of acculturation? The project covered the Mesolithic to the Early Middle Ages, a broad chronology during which profound technological, cultural, and social changes occurred, including the introduction of agriculture, the emergence of people following a sedentary lifestyle, and the mastery of metallurgy.

The Ancestra project reflects many of the core features in archaeogenetics, including a focus on identity, migration, and stories of national origin. In terms of methodology, the work was mobilized by technological advances linked to high-throughput sequencing, which made the mapping of ancient genomes technically feasible and affordable. The project also benefited from the discovery of an anatomical region that acts as a veritable "vault" for ancient DNA: the dense petrous part of the temporal bone.[6] Both these drivers—characteristic of archaeogenetics research after 2015—were complemented and ignited by the interest of the French archaeological community, enabling the establishment of a strong corpus for analyses and a dynamic interdisciplinary culture.

From our established standpoints as researchers with a genetic background in these two projects, we consider some of the issues that have caused friction and conflict in the field. While we are conscious that the field of archaeogenetics spans a wide remit, here we consider the five particular areas pertinent to aDNA from human remains.

Questions

The gap between the types of questions that researchers of the past may seek to answer and the types of questions that can be realistically addressed in analyses of aDNA burdens many collaborations, with a mismatch of expectations. This disconnect may undermine the first task of an interdisciplinary group—the generation of coherent, appropriate research questions.[7] Notably, the desire to push the data too far and to address “the big questions” was, in our experience, not necessarily limited to the archaeologists or humanities researchers on a team, who were less familiar with the scope of genetics research. The problem appears rather to be a product of interdisciplinarity.

Archaeologists in the Ancestra project were often interested in how the genetic identity of different cultural groups related to their respective origins. This line of inquiry rests, in turn, on whether or not the differences observed in the funerary treatment of certain individuals correspond with observable genetic differences. At the genetic level, variation between individual humans and human populations is relatively low: we need a certain amount of genetic data to see a meaningful resolution. In an ideal world, to make the kinds of inferences commonly discussed in archaeogenetics, we would need a good knowledge of the genetic diversity of ancient human populations. Unfortunately, this knowledge is lacking, due to scarcity of samples and the degradation of genetic material over time. This brings substantial uncertainty into the work. In the Ancestra project, there was a sense from the archaeologists that genetic data could be used to address a broader scope of questions, and with more confidence than was actually the case. In the Code Narrative History team, an interview-based research exercise found this same trend but among the scientists, suggesting that underinterrogation of material is not confined to either archaeologists or geneticists but is a phenomenon within the discipline.[8]

Inflating research questions beyond the scope of genetic data seems to be a particular (and oft-cited) concern in the world of archaeogenetics. Here, perhaps more so than in other branches of genetics, scientific and academic caution coexist with the drive to feed a diverse audience hungry for the fusion of romanticized ideas from the distant past with the clarifying authority of genetics. This may in part be driven by a certain fascination with key themes such as gender roles and origin stories[9] but may also be a product of interdisciplinarity itself, which amplifies the impact of its constituent knowledge components.[10]

The literature appears to be rich with titles seeking to answer the “big” questions that translate well to a broader public interest. A quick scan of recent literature supports this perception: out of sixty-four Medline indexed archaeogenetics papers scanned for relevance, focusing on humans and published over the last year, forty-one were data-driven publications in that they applied aDNA material to archaeological research (as opposed to guidelines, reflections, or methodology papers).[11] A scan of titles and abstracts found that, of these, ten sought to answer historical questions pertinent to entire continents, nine covered time frames of over 10,000 years, and seven claimed to solve the question of origins for various ethnic groups.

This scan—albeit fairly rudimentary—indicates an ambitious scale of intention. It is not our intention to critique the science or rationale for these research questions, and it is important to note that it is the minority of research groups that run the gamut of solving such epic riddles. Instead, we want to draw attention to the trend for “soundbite titles” that suggests that archaeogenetics has assumed a center-stage position in an increasingly mediatized landscape. This is a truism that the Code Narrative History team witnessed during discussions with journalists and media specialists, who noted that the more bounded aspects of scientific inquiry were often pared back in favor of “big stories.” In this respect, groundbreaking conclusions and enticing prospects satisfy the requirements of popular science consumption and provide headline-generating research results.[12] The idea that mediatized research may be stimulating a cultural shift in the structure and formulation of research questions is far from new, and may reflect a more general trend in academia. An emerging body of literature has postulated that academic outputs now seek to keep pace with a fast-moving attention economy which, increasingly, is linked to academic funding and tenure.[13]

As a relatively new discipline, archaeogenetics enters an arena already rich with context, content, and questions grounded in two very different research traditions. Research questions in the archaeogenetic field frequently reflect the broad historic lines of inquiry embedded within some strands of popular-scientific history or archaeology, but with genetic analyses they become distanced from the methodological frameworks that first conceived them. In the archaeological sciences and the humanities, multiple factors of inquiry intersect and this level of interaction remains in play throughout a research project. Genetic studies, in contrast, seek to identify controlled and distinct variables that can be used to address a focused avenue of interest. Critical inquiry in the humanities often seeks to "problematize"—that is, to increase complexity, search for discrepancy, elucidate and unpack meaningful messages that may cause conflict and confusion if they remain hidden. This is not to say that geneticists involved in collaborative projects with historians or archaeologists are unaware of the broader complexity. It is rather that they tend to avoid the open-ended analyses that are more commonplace in archaeological research. Instead, genetic research is orientated toward answering questions, even where the findings are speculative, negative, or puzzling. As a fusion of starkly different yet equally valid traditions, archaeogenetic research questions thus oscillate between these two ideals, and the attempt to develop a working hybrid can cause researchers to feel there have been "conceptual disagreements" that have yet to be resolved.[14]

Words

At the heart of many of the misunderstandings we witnessed in archaeogenetics was a disconnect in the way that our teams used language. This disconnect is perhaps an inevitable consequence of our natural assumption that a familiar, frequently used word has a shared meaning. If we take it for granted that the way individuals within interdisciplinary (and often multilingual) teams use language will vary, exploring a shared vocabulary might be a valuable first priority. This search for a common language has been explored in other areas of interdisciplinary studies, such as environmental science, engineering, economics, and ecology.[15]

Several words saw our own teams at cross purposes. As geneticists, we used the terms "population," "significance," and "hypothesis" with very precise statistical definitions, yet as these words are also used in common parlance, our colleagues from the humanities interpreted them differently. The understanding that conclusions reached through mathematical processes do not constitute "proof" in the literal sense is an accepted, yet not always articulated, part of scientific parlance. As the results of archaeogenetic research venture beyond a scientific readership, the risk that a statistical conclusion is given a heavier weighting than merited appears to be a hazard of archaeogenetics. This is a risk that can be negated or exacerbated, depending on the language used by researchers at write-up and in subsequent communication with popular media. Conversely, we also recognize that we as geneticists were sometimes wrong-footed by terms such as "gender," "kinship," and "ethnicity," which our humanities and archaeologist colleagues viewed as socially constructed, situated, and intersectional.

Speaking at cross-purposes can potentially derail a project: for example, the term "ancestry" in genetics assumes a basis of biological inheritance, yet as Stewart B. Koyiyumptewa and Chip Colwell show in their chapter in this volume, a community cocreating an archaeogenetics research project used a definition of ancestry based on much broader, and extragenetical, social kinship dynamics. In such a situation, a reductive insistence on a biological definition would have caused significant problems and led to incorrect conclusions.

For the Ancestra team, an initial challenge concerned the use of the word "France," as the work was country-specific. When referring to genetic populations or human remains, archaeogeneticists often attribute a country or location and time frame (such as the Neolithic or Mesolithic) as a convenient shorthand, yet clearly these descriptors would have been meaningless to the individuals to whose remains the terms are ascribed. We locate ancient people in the area that they were buried in (not necessarily the area of their birth, life, or personal identification) and anchor them using the language of our own time as the nomenclature of their own is unknown. For the archaeologists in a team, ascribing the terms of nation-state or time period to genetic data risks introducing notions of the cultural achievements associated with that nation or time into the analysis. And as geneticists, we may bring unconscious bias into our interpretation of genetic relatedness. Researchers can and do, to some extent, anonymize samples—this process can successfully divorce cultural associations and labels from samples, rendering aDNA into a more neutral framework. Yet, however we approach the naming of our genetic data sets, their reintegration into the full gamut of evidence from historical, archaeological, and even contemporary sources is an exercise that may require significant caution.[16]

For the nongeneticist researchers in the Code Narrative History team, the term "whole genome analysis" was initially thought to refer to the complete extraction and sequencing of the totality of an ancient genome. While it may be (more or less) possible to sequence the majority of a modern genome, ancient genomes are usually decayed or fragmented. In reality, while geneticists may seek to sequence an entire ancient genome, only a proportion—sometimes a very small proportion—of genetic material will be recovered. This misperception, common to most lay readers (and many journalists), tends to elevate expectations of the data. This misunderstanding can be exploited when research findings enter the public domain: here, media representations give a strong impression that when teams "sequence a whole genome," every letter of the genetic code from a historical individual has been captured with perfect confidence. It is not difficult to see how this happens: intuitively, the language is suggestive, and the hype surrounding findings lends itself to this interpretation. While we may consider the sequencing of any ancient genetic fragment to be an achievement worthy of excitement, it is not always evident in the outputs quite how small a proportion of this "whole" genome has, in reality, been decoded. Researchers bear some responsibility here for ensuring that communications signpost—for a lay audience—the coverage of ancient genomes and the relative proportion of material retrieved.

The divergence in the language used to describe ancient human remains is an area where the differences between archaeological and genetic sciences come starkly to the fore. For archaeologists, often with direct experience of excavation and presence at a burial site, the individual human to whom the DNA belongs is a tangible and real presence throughout the research. In work with the Code Narrative History team, Mulcare's colleagues talked about "human remains" and "individuals," and—when referring to a group of burials—the emphasis was on the "people" who were buried there. Conversely, she came to the project handling data labeled as from a "sample" rather than a person and thought of groups in terms of defined "populations." These discrepancies in the use of language are replicated across publications and informal dialogue. Ensuring the continuity between a person and their genetic code has broader repercussion in terms of ethics, respect, and provenance. It is, perhaps, a useful challenge for teams to strive for a balance between acknowledging the humanity inherent in a person's remains, while understanding that the universal language of genetics places the individual into a broader human story.

While these differences in terminology may be easy to clarify through discussion, the assumptions underpinning them frame our understanding of research in ways that are harder to navigate.[17] These profound differences are often downplayed in calls for best-practice consensus.[18] Such definitional impasses in the field—along with some of the difficulties they create in theoretical analyses—can be overcome by recognizing the fluidity of language and allowing different terminologies to coexist with equal weighting. For example, a "population" can simultaneously mean a statistically defined group or a culturally defined one, as long as differences are understood by all parties involved and made clear in popular outreach. This ambiguity can be respected for the lifespan of a research project. The risk of ignoring a discrepancy goes beyond mere confusion and/or unease. In an increasingly stark political world, the complexity behind words can even be dangerous, as Magnus Fiskesjö shows in his chapter in this volume. We could take the road less traveled: rather than a consensus approach that seeks to limit language to an agreed definition, we could sit with a plurality of meanings, no matter how uncomfortable that may be at times.

Numbers

If we consider the end of the Paleolithic in Europe, a period that covers 30,000 to 10,000 BCE, genetic data are available for only about twenty people. As numbers go, twenty is not much if we wish to understand the genetic makeup of ancient populations living across a 20,000-year time frame and distributed over an entire continent. The problem of numbers intensifies when we consider the amount of genetic material we are able to retrieve from these individuals: given degradation, our coverage of ancient genomes—that is, the amount of sequence we can retrieve and the confidence we have in this sequence—is inevitably far lower than it would be for their modern equivalents. Pragmatically, researchers must work with what they have, be it published aDNA libraries or incomplete sequences painstakingly obtained from a limited number of excavated remains. Controversy over numbers arises as genetic findings (taken from a few individuals) are used to hypothesize about the dynamics of multiple ancient populations (comprising many individuals). To put it crudely, what number of human burials and what number of genetic markers do we need before we can make meaningful inferences about the past?

An example from the Ancestra project illustrates that there is no easy answer to this question. To represent the genetic diversity of the Middle Neolithic in the northern half of France, archaeological and genetic data were obtained from multiple sites. The Pont-sur-Seine "Ferme de l'Île" site is located in the Aube in the Seine valley dating from 4,000-3,500 BCE and consists of a ditched enclosure, ditches, post structures, pits, and about fifty Neolithic burials. In terms of human remains, adults of both chromosomal sexes were represented along with twenty children. The Bergheim "Saulager" site located in Alsace, Haut-Rhin, revealed the existence of several protohistoric occupations, with sixty silos attributed to the Middle Neolithic. Of these, fourteen yielded human remains corresponding to complete individuals dated to 4,800–3,800 BCE. As a final example, we have the site of Escalles "Mont d'Hubert" in the Pas-de-Calais, a causewayed enclosure dating to around 4,000 BCE. Altogether, the human bones found here correspond to nine adults and eight children of various ages.

Intuitively, one might think that the first site, Ferme de l'Île, would show the most genetic diversity, given the comparatively large number of human burials found there. However, the genetic samples showed that all individuals found in this cemetery shared the same haplotype for mitochondrial DNA.[19] As the name suggests, mitochondrial DNA is found in the mitochondria, structures inside a human cell that generate the chemical energy needed to drive the biochemical reactions of that cell. Notably, mitochondrial DNA is inherited intact from mother to child, allowing the team to identify maternally inherited relatedness between individuals. In contrast, the findings from the two other Neolithic sites showed a much broader mitochondrial diversity, similar to that associated with other Neolithic sites across Europe. For understanding kinship in terms of matrilineal relatedness within each site, the genetic data were informative. Yet if only one of these sites had been chosen to represent populations for the Neolithic in Northern France, a very limited and misleading picture would have emerged.

In the example described above, the team explored one defining genetic marker transmitted intact from only one parent—the mother. What happens if we increase the number of markers we look at, and if we look at not one parent but both?

The Ancestra project initially planned to study the complete mitochondrial genome, the Y-chromosome (inherited from father to son) and a selection of a hundred or so nuclear markers in each ancient genome. The idea was to enrich the data set by capturing information about the same genetic markers across all the samples. This enrichment technique would retrieve genetic information for direct comparison of samples, even in cases where very little DNA was available, due to degradation. For all our individuals (over 200 in total), mitochondrial analysis was complemented with data from the Y-chromosome and a panel of 120 genetic markers inherited from both parents. Whole genome sequencing was achieved for fifty-eight individuals, albeit with a low coverage, allowing the team to consider specificity (informative markers from all individuals) with quantity (as much material as could be retrieved from a few well-preserved individuals). When the team increased the number of markers and maximized the genetic information retrieved through whole genome sequencing, a much greater amount of information was available for analysis.

The language of numbers can cause breakdowns in communication across teams because—perhaps counterintuitively—multiple markers from a single person can reveal information beyond the genetic profile of that specific person. This is particularly important when we consider how few ancient human remains we have access to. To understand how multiple genetic markers can be used to maximize information, we must take a step back and consider that each genetic mutation has its own history, its own distribution, lineage, and ancestry profile. As an example, we can look to the oft-quoted observation that everyone with blue eyes shares a common ancestor. There is a mutation in the genetic code affecting melanin production in the iris, one which "dilutes" brown eyes to blue. The scientists identifying this trait commented on the lack of variation across melanin expression in modern blue-eyed people—despite their high number and wide distribution—concluding that they share a single, common ancestor.[20] However, if we were to imagine all the blue-eyed people in the world today and to draw a family tree tracing back through time and leading to one common ancestor, such an image would be misleading. All of us have many different genetic mutations and all of us also have many, many common ancestors. We can draw many different family trees depending on how many genetic markers we look at. We are more than our eye color.

Each individual—regardless of where or when they lived—is part of the human family. From this perspective, we can assume that any two people, regardless of how distanced they are through time and space, are related in some way by virtue of their humanity. Our individuals from the Neolithic were related to their own ancestors, to each other, to other individuals from the Neolithic described in different studies, and—obliquely—to their modern-day descendants, for whom we have far more genetic resources. The question is, to what degree are all these different people, past and present, related? Direct relatives or very distant cousins? While we can learn about relative relatedness of different people using multiple genetic markers from across the genome, it is important to be aware that a genetic sequence—even thousands of genetic sequences—does not act as a perfect proxy for an individual's ancestry. In this respect, as geneticists we are looking at an individual's genetics, modeling multiple possible scenarios of "relatedness," and making our "best guess" as to which one fits.

Our best guess relies on an additional discipline—biostatistics and, in particular, modeling—that allows archaeologists and geneticists to leverage *known* data (genetic information from existing samples) to navigate the uncertainty of *missing* data (sequences of DNA that we cannot decode due to degradation). Even more important than missing sequence data is the gap of who is missing—all those people contemporary with those excavated from burial sites; people whose genetic profiles we know nothing about. Knowledge of statistics, and what can and cannot be justified through their use, is a mainstay of genetic culture, but one that is often lost in translation. There is a common temptation to view statistical modeling as a "black box" into which questions are put and from which answers appear. The language of numbers—literal formulae in methodology sections of papers—can be less accessible than words. Our partners working in archaeology or the humanities were often disenfranchised from statistical knowledge-making processes by their unfamiliarity with the field and, it could be argued, by our inability to offer adequate translations. This has limited the opportunities for those without biostatistical knowledge to have meaningful input to modeling strategies, with the effect that methodologies have sometimes been designed with limited acknowledgement of key archaeological data. Also, outputs are potentially misinterpreted when reviewed by researchers who may lack the knowledge base to critically determine what makes a good model.

Of all the disjuncts we noted, this was one of the most critical, since the choice of genetic markers, samples, or calculation models can change the "answer" to a research question—sometimes dramatically so. As demonstrated by Marianne Sommer and Ruth Amstutz elsewhere in this volume (chapter 2), even the same finding can be given a radically different interpretation depending on the tools used to visualize the data. Equity of knowledge with regard to statistics, modeling, and computations is an important prerequisite for collaboration in a context where so much of the research depends on understanding the numbers. For geneticists, statisticians, and those modeling population dynamics, a challenge will be to bridge this knowledge gap. While it may not be feasible to impart a career's worth of training, those with numerical proficiency could take responsibility for communicating the key issues, choices, and elements of statistical analysis such that colleagues across the team are able to have an active voice and input. This effort may enrich future methodologies and support a culture in which all team members are able to contribute their expertise.

Conversely, those with a scientific or statistical background have much to learn from their humanities colleagues. One example may be a humility in terms of what can be modeled statistically given the profound ambiguity of the past. Archaeogenetics as a discipline may need to accept that certain questions may never be answered in exhaustive ways, because the remains of ancient societies are always fragmentary. There is a danger that uncertainty can be amplified by gaps in both molecular and material data, creating a problem if statistics are used to “smooth over” the unknowns. The need for interdisciplinary teams to ensure a strong understanding of biostatistics and models across the team is crucial if researchers are to signpost caveats and limits to their interpretation of the data.

Stories

Our genetics both reflect our unique individuality and anchor us to a shared humanity, and so do our stories. How we perceive these stories forms a key aspect of how we collaborate. At the Bergheim site, the Ancestra project team assessed a structure—silo 157—where ten portions of left upper limbs and, directly above, eight bodies were stacked in various positions without any particular organization. There were two men, two women, and four children. In addition to the traces of cutting blows related to amputations, the upper limbs also bore traces of cut-marks. The remains of an individual with an amputated arm had several traces of blows, especially on the head, thought to correspond to a violent death.

Scientific neutrality is difficult to maintain in the face of human suffering and the stories that may explain it. The dispassionate evaluation of genetic material, which conjures images of colorless liquids, laboratory machinery, and databases, stands in stark contrast with the excavation environment archaeologists are familiar with. Here, physical remains are anchored to landscape and material culture, with all the emotional charge these may bring.

It is, therefore, unsurprising if research based within the purview of genetics becomes enmeshed with preexisting, emotive stories. For example, the characterization of an individual genome from well-preserved human remains dated to the Mesolithic—Cheddar Man—maps on to contemporary discussions around race.[21] In particular, the highly evocative reconstruction of Cheddar Man, for whom sequencing analysis suggested a dark skin color and blue eyes, captured imaginations across a substantial press movement and stimulated much highly-politicized debate.[22] The original paper by Brace and colleagues, which notably did not contain the iconic image, balanced the excitement of the findings with context (in the form of other sequenced genomes), raw data, and thoughtful scholarship.[23] Much of this was lost when the story became caught up in far less restrained dialogues around national identity that emerged in the aftermath of the UK's Brexit.

Elsewhere in this volume (chapter 6), media historian Andreas Nyblom explores how another "celebrity" of ancient DNA—the Birka warrior—was determined to have two X-chromosomes (indicative of "female," where sex is determined through chromosomal status). The Birka warrior became an iconic figure who stimulated much public discussion of gender roles, gender-identity, and feminism.[24] Archaeogeneticists run the risk of genetic science being reinterpreted and leveraged to offer a seal of closure on issues that go beyond biology or the remit of genetics and that deserve a balanced consideration of many different types of evidence.

During the writing of this chapter, a film—*The Lost King*—was released depicting the story of the much-celebrated finding of Richard III's burial site. This provides an interesting example of how stories interplay with evidence. The final resting place of this English king had been lost since the friary he was buried in—Grey Friars in Leicester, England—was destroyed in the sixteenth century. When human remains were excavated near the place where the friary was thought to have stood, the juxtaposition of the site (a prosaic parking lot) with the cult status of the lost king made for a compelling story. Substantial evidence to support the claim that the body was that of Richard came from different archaeological sciences: the osteological analysis was consistent with historical records regarding the king's age at death and physical deformities (scoliosis rendering one shoulder higher than the other).[25] As the last king of England to die in battle, perimortem wounds were assessed and found indicative of a violent demise, and radiocarbon dating suggested a death during 1485.[26]

To provide the genetic perspective, Turi King and colleagues were able to successfully compare mitochondrial DNA from two purported living descendants from Richard III's female line with the ancient sample.[27] They found a match for both. To get such a complete correlation between the ancient DNA and modern is rare enough to be considered highly indicative of ancestry. However, Y-chromosome data from five putative male relatives told the opposite story: the genetic data suggested the men were not descendants of the possible king. The genetic findings were, in other words, in conflict with each other. Given the broader framework of information, the authors concluded that the Y-chromosome data should be discounted on the grounds of likely nonpaternity. Given the number of generations between Richard III and his modern-day descendants and the potential inaccuracy of genealogy over this time scale, this seems a plausible explanation, particularly when compared against the robusticity of the other archaeological, historical, and genetic data. However, it gives pause for thought: if only male relatives had been available, would the genetic data have been used to undermine the other types of evidence, or perhaps left unpublished? The authors of this study show a balanced and extensive review of multiple information sources, but how many instances are there where authors are perhaps less assiduous in evaluating different data or do not consider the whole picture? Are genetic data underreported if they do not support the story?

The paper itself cross-references and contextualizes the genetic data tightly to the archaeological information available but it also uses the discussion to go beyond key conclusions of Richard III's identity. The authors explore the idea of nonpaternity and, in doing so, introduce a rather left-field story that exemplifies the type of claim that can set interdisciplinary teams into conflict:

> One can speculate that a false-paternity event (or events) at some point(s) in this genealogy could be of key historical significance, particularly if it occurred in the five generations between John of Gaunt (1340–1399) and Richard III. . . . A false-paternity between Edward III (1312–1377) and John would mean that John's son, Henry IV (1367–1413), and Henry's direct descendants (Henry V and Henry VI) would have had no legitimate claim to the crown. This would also hold true, indirectly, for the entire Tudor dynasty.[28]

Theoretically, this observation, if true, could undermine the historic lineage of the British monarchy. It is this type of statement that tends to polarize readers, and certainly those working in archaeogenetics. Within our own respective teams, opinions on speculative stories differed. To some, this kind of speculation—if clearly framed as such—provided interest and allowed for a stimulating discussion point. More critical voices felt that researchers, regardless of their specialty within a team, had a responsibility to resist the temptation to create or give credence to inflammable stories.

As in general life, politics invariably engenders strong views and conflict within archaeogenetics teams, and not solely between but also within disciplinary boundaries. Depending on your definition of politics, stories involving demographics can easily become political. This creates a dilemma for any archaeogenetics collaboration: How do our findings map onto preexisting stories embedded in a politicized environment?

There are some contexts where we, as researchers, may be acutely sensitive to the impact of our findings in the political world and other contexts—such as the distant past—where it may feel relatively “safe” to propose more speculative ideas. If we believe the past is a safe space in which to follow blue-skies thinking, we can propose various scenarios without fear of censure. However, this brings us to a dilemma that affects many collaborations: To what extent can we argue that it is appropriate to apply certain assumptions and techniques (for example, the use of genetic relatedness to enable categorization of ethnic groups) in some contexts but not others? If we accept that there are some stories that would incur severe ramifications on modern populations, how do we then perceive those stories that appear less hazardous but that rely on the same principles? How do we maintain our research and the valuable contribution that genetics can make while navigating the broader implications of our stories? Our teams may not have resolved these questions in the course of our research projects, but we see a value in proposing them for deeper consideration.

Answers

Ancient DNA contains information that can be reintegrated into a broader framework for understanding the past, yet, as alluded to throughout this chapter, this is no easy task. Radiocarbon dating is often cited as a comparator technology, one that offers some prospects for how DNA analysis might, in the future, become seamlessly integrated into archaeological science.[29] As C14 dating gives an age to remains, the hope is that archaeogenetics can provide us with a genetic library of ancient individuals. Contemplating how best to integrate genetic techniques through consideration of C14 dating seems an interesting thought experiment, yet to our archaeological colleagues it provoked significant concern and so serves as a useful exemplar for unpacking conceptual differences.

In terms of knowledge production, radiocarbon analysis is used for chronological dating to define temporal context. Genetic science is often (though not exclusively) used to define ancestral relations, migration events, and gender status. In doing so, it becomes inexorably linked to narratives that are far more complex and changeable than chronological dating. Yet, if we were to suppose that genetic analyses were to take more of a back-seat position and become a single part of a much bigger puzzle—that is, a piece of contributory evidence rather than a defining component—we are still left with a problem of inherent ambiguity. Radiocarbon dating requires a precise frame of reference to be calibrated correctly. The "reference point" for C14 calibration is a year, a commonly accepted calendrical term. No easy equivalent exists for aDNA; the options are to reference comprehensive modern genetic libraries or other ancient DNA samples, the latter often being distanced geographically and temporarily. The issue of how data are then interpreted in the wake of the temporal gap between these libraries and the populations they seek to reconstruct remains a topic for scrutiny. It is not an agreed, precise science, but more of an art form. Genetic data cannot, therefore, be as easily translated into current systems of archaeological knowledge production as C14 dating, since the information contained within the genome can be calibrated only against reference points that are themselves subjectively chosen and open to debate.

A further difference with C14 data is the route of communication. C14 "answers" are incorporated into archaeological publications, yet while these may cite archaeogenetic data, primary findings are often presented in scientific journals that impose a highly structured format and a tight word count. An unintended consequence of this may be that "answers" are not subject to a more lateral scrutiny that assesses the choices of research question, samples, or a priori assumptions. Extensive interpretation is, in scientific journals, provided in the discussion, where findings can be placed in context and uncertainty can be reintroduced. However, word counts limit the coverage. Archaeological journals offer a greater opportunity to expand on detail, favoring a more open, narrative discourse, but the methodologies and statistical frameworks needed to interpret genetic data are not usually a good match for these vehicles. An additional consideration is the relative ranking in terms of impact factor and other journal metrics that favor scientific journals—*Nature* will usually be a preferable target to *Antiquity*. The lack of a publication "home" able to straddle the breadth of information yielded in these studies means that the strengths of interdisciplinarity do not fully come into play.

This poses a serious question around interdisciplinary research for archaeologists and geneticists: if the context is a critical aspect of the story, extrapolating an "answer" from one piece of evidence without consideration of the broader framework could, in many cases, be misleading. The decoupling of the backstory may run the risk of authors (and readers) drawing meanings from their results that extend beyond what can be supported by the data. The conclusions may well be valid from the point of view of scientific procedure, and the genetic information may well support broader interpretations, but without contextual information—such as the consideration of grave goods, placement, and historic sources—the story lacks anchorage and foundation.

Gained in Translation

Noam Chomsky's idea that the act of interpreting language is inherently creative gains purchase in the practice of interdisciplinary research.[30] Here, divergences in language extend into working culture, where we may find conflict. If we are prepared to sit with the potentially uncomfortable task of reinterpreting ways of thinking which we have previously taken as unequivocal, we may, in these spaces of challenge and negotiation, find the creative insights that Chomsky alludes to. However, this requires us to do something inherently alien to many of us, to be at ease with discord long enough to understand it fully through reflection.

At first glance, archaeogenetics appears to be a discipline well versed in grievance airing and reflection.[31] In the past few years, several papers have critiqued the field of human aDNA, in some instances proposing a series of solutions designed to mitigate some of the friction inherent when researchers from diverse backgrounds come to work collaboratively. The urge to avoid friction is a very human one and it is to the credit of aDNA researchers that efforts to address the issues of the discipline are ongoing. However, while well intentioned, the desire to generate a universal common ground may lose us the opportunity for the fresh understandings and syntheses unique to each research project.

Archaeogenetics involves the meeting of two traditions—each with its distinct practices, ideals, and conceptualizations of research—and its investigations take place across vastly different vistas of temporal and geographic space. These considerations necessitate the involvement of different stakeholders. From museum curators to Indigenous communities, regional administrative bodies to local history groups, it is hard to predict the exact blend of perspectives and voices that any given research project may involve. The idea of a "research team" goes, therefore, beyond the purview of individual investigators and encompasses a richer diversity, a broader meeting of minds. This encounter—in some cases, a volatile one—poses the challenge of reconciling stark differences in perspective, differences that cannot truly be anticipated by procedural guidelines. We see a value in research teams—using the widest definition of the "team"—navigating their way through these differences together.

In our experience, what makes these differences both stimulating and exasperating is that they are often sharply personal. Academics have devoted much time and intellectual resources to the pursuit of knowledge. They may struggle to confront a somewhat humbling reality of interdisciplinary research; while they hold expertise in their discipline, they are not necessarily an expert in their own project. Key truths, sometimes painfully obtuse ones, are held by other team members—not always from the same academic background—and these truths may be critical to the nuance and accuracy of the project's findings. In an age of financial cuts and intense competition, academia itself borders on a vocational enterprise. We are often arguing the case not merely for our research tradition—be it rooted in genetics or archaeology—but for our own life choices. It is hardly surprising therefore that our position as researchers is often entangled with our identity and deeply rooted beliefs. Our emotional investment in our project work animates our discussions, even as we recognize that it is only through collaboration that we can operate in this world of contrasts.

To conclude: archaeogenetic research is an open-ended exploration in which we can expect the world to be complicated. Our role in such a situation of exploration is to embrace and express that complexity in order to bring it to light for a wider audience. By seeking to contain critical conversation, we risk creating a silo in which problems are defined by their preformulated solutions. The resulting research culture becomes inherently reductive. Instead, there is a desperate need for profound conversations on difficult issues. Natural science, with its current command of the attention economy, has a crucial role to play in such a discussion.

Notes

1. Sam Hamill quoted in Anne-Marie Cusac, “Sam Hamill Interview,” *Progressive Magazine*, April 1, 2003, https://progressive.org/latest/sam-hamill-interview.

2. See, for example, Ewen Callaway, “Divided by DNA: The Uneasy Relationship between Archaeology and Ancient Genomics,” *Nature* 555, no. 7698 (2018): 573–576; Gideon Lewis-Kraus, “Is Ancient DNA Research Revealing New Truths—or Falling into Old Traps?” *New York Times Magazine*, January 17, 2019; Krystal S. Tsosie et al., “Ancient-DNA Researchers Write Their Own Rules,” *Nature* 600, no. 7887 (December 2021).

3. See, for example, Mary E. Prendergast and Elizabeth Sawchuk, “Boots on the Ground in Africa’s Ancient DNA ‘Revolution’: Archaeological Perspectives on Ethics and Best Practices,” *Antiquity* 92, no. 363 (2018): 803–815; Kendra A. Sirak and Jakob W. Sedig, “Balancing Analytical Goals and Anthropological Stewardship in the Midst of the Paleogenomics Revolution,” *World Archaeology* 51, no. 4 (2019): 560–573; Songül Alpaslan-Roodenberg et al., “Ethics of DNA Research on Human Remains: Five Globally Applicable Guidelines,” *Nature* 599, no. 7883 (2021): 41–46.

4. Anna Källén et al., “Petrous Fever: The Gap Between Ideal and Actual Practice in Ancient DNA Research,” *Current Anthropology* (forthcoming).

5. Tsosie et al., “Ancient-DNA Researchers Write Their Own Rules.”

6. Cristina Gamba et al., “Genome Flux and Stasis in a Five Millennium Transect of European Prehistory,” *Nature Communications* 5, no. 5257 (2014): 1–9.

7. See Katri Huutoniemi, “Interdisciplinarity as Academic Accountability: Prospects for Quality Control across Disciplinary Boundaries,” *Social Epistemology* 30, no. 2 (2016): 163–185.

8. Källén et al., “Petrous Fever.”

9. Anna Källén et al., “Archaeogenetics in Popular Media: Contemporary Implications of Ancient DNA,” *Current Swedish Archaeology* 27, no. 1 (2019): 69–91; Susanne E. Hakenbeck, “Genetics, Archaeology and the Far Right: An Unholy Trinity,” *World Archaeology* 51, no. 4 (2019): 517–527.

10. Päivi Haapasaari, Soile Kulmaka, and Sakari Kuikka, “Growing into Interdisciplinarity: How to Converge Biology, Economics, and Social Science in Fisheries Research?” *Ecology and Society* 17, no. 1 (2012): 295–320; Vincent Larivière, Stefanie Haustein, and Katy Börner, “Long-Distance Interdisciplinarity Leads to Higher Scientific Impact,” *PLoS One* 10, no. 3 (2015): 1–15.

11. The search terms were “archaeogenetics,” “paleogenetics,” “ancient DNA,” “archaeogenomics,” “paleogenenomics,” “aDNA” in all languages. The survey was limited to human studies and manually reviewed (titles and abstracts) for content and relevance. Alternative spellings of key search terms were used.

12. Källén et al., "Archaeogenetics in Popular Media," 69–91.

13. Haapasaari, Kulmaka and Sakari, "Growing into Interdisciplinarity," 1–12.

14. Martin Furholt, "Biodeterminism and Pseudo-Objectivity as Obstacles for the Emerging Field of Archaeogenetics," *Archaeological Dialogues* 27, no. 1 (2020): 23–25.

15. Janet Stephenson et al., "The Practice of Interdisciplinarity," *International Journal of Interdisciplinary Social Science* 5, no. 7 (2010): 271–282.

16. See the chapters in this volume by Magnus Fiskesjö (chapter 7), as well as by Marianne Sommer and Ruth Amstutz (chapter 2).

17. Anna Källén, *The Trouble with Ancient DNA* (Chicago: University of Chicago Press, 2024).

18. Alpaslan-Roodenberg et al., "Ethics of DNA Research"; Prendergast and Sawchuk, "Boots on the Ground"; Sirak and Sedig, "Balancing Analytical Goals."

19. A haplotype can be defined as a series of genetic variants that are inherited together on the same chromosome. In this example, where women share the same mitochondrial haplotype, it is indicative of matrilineal relatedness.

20. Hans Eiberg et al., "Blue Eye Color in Humans May be Caused by a Perfectly Associated Founder Mutation in a Regulatory Element Located within the HERC2 Gene Inhibiting OCA2 Expression," *Human Genetics* 123, no. 2 (2008): 177–187.

21. Selina Brace et al., "Ancient Genomes Indicate Population Replacement in Early Neolithic Britain," *Nature Ecology & Evolution* 3, no. 5 (2019): 765–771.

22. Källén, *Trouble with Ancient DNA*.

23. Brace et al., "Ancient Genomes Indicate Population Replacement," 765–771.

24. Charlotte Hedenstierna-Jonson et al., "A Female Viking Warrior Confirmed by Genomics," *American Journal of Physical Anthropology* 164, no. 4 (2017): 853–860; Källén et al., "Archaeogenetics in Popular Media."

25. Richard Buckley et al., "'The King in the Car Park': New Light on the Death and Burial of Richard III in the Grey Friars Church, Leicester, in 1485," *Antiquity* 336, no. 87 (2013): 519–538; Jo Appleby et al., "The Scoliosis of Richard III, last Plantagenet King of England: Diagnosis and Clinical Significance," *Lancet* 383, no. 9932 (2014): 1944; Jo Appleby et al., "Perimortem Trauma in King Richard III: A Skeletal Analysis," *Lancet* 385, no. 9964 (2015): 253–259.

26. Angela L. Lamb et al., "Multi-Isotope Analysis Demonstrates Significant Lifestyle Changes in King Richard III," *Journal of Archaeological Science* 50 (2014): 559–565.

27. Turi Emma King et al., "Identification of the Remains of King Richard III," *Nature Communications* 5, no. 5631 (2014): 1–8.

28. King et al., “Identification of the Remains,” 4.

29. Sirak and Sedig, “Balancing Analytical Goals,” 560–573; David Reich, “The Future of Ancient DNA,” in *Who We Are and How We Got Here: Ancient DNA and the New Science of the Human Past* (Oxford: Oxford University Press, 2018), 274–286.

30. Noam Chomsky, *For Reasons of State* (New York: Pantheon, 1973), 402.

31. See, for example, Callaway, “Divided by DNA”; Lewis-Kraus, “Is Ancient DNA Research Revealing New Truths?”; Källén et al., “Petrous Fever.”

2 Diagrams of Human Genetic Kinship and Diversity: From the Tree to the Mosaic and the Network?

Marianne Sommer and Ruth Amstutz

Genealogy is traditionally expressed in the shape of a family tree, and this also holds true for human evolution. Just like the tree of life, the human family tree visualizes the descent of hominin species.[1] With the turn toward an evolutionary understanding of human origins and the discovery of fossil remains, such trees have been based on the comparative anatomy of living and fossil species. The tree shape has also been used to speculate about inner-human differentiation: the evolution and kinship of what used to be called "human races."

In the second half of the nineteenth century, the influential evolutionary biologist Ernst Haeckel considered both physical characteristics and comparative linguistics to analogize the evolution and kinship of languages to trees of "racial descent." Thus, a structure that lent itself to depicting both the genealogy of individuals and the descent of species came to be applied to groups of humans. In these "racial trees," long, independent branches led to the different "modern human races," suggesting that such "races" had evolved in isolation and stayed "pure" over long periods of time. Indeed, Haeckel and others thought that the differences between the "human races" were at least equivalent to the differences between species. The tree was a picture adequate to capturing their understanding of intrahuman as well as hominin evolution.[2]

By the 1960s, the time was ripe for a new way of drawing phylogenetic trees. Computer technologies and genetic data allowed the Italian population geneticist Luigi Luca Cavalli-Sforza and the British statistician and geneticist A. W. F. Edwards to publish what they called the first tree of human populations. This was before it was possible to sequence DNA. Cavalli-Sforza and Edwards analyzed twenty alleles[3] from the five main blood group systems of fifteen human populations. The analysis resulted in a phylogenetic tree that separated a wild mix of population labels—from “English” to “Eskimo (Victoria 1)”—into different branches.[4] While some of the labels had a legacy in the history of racial and colonial anthropology, the emergent study of human population genetics was very different from traditional racial typology. It was genetic variation that was of central interest, and the notion of pure races and race in general was often emphatically rejected.

Figure 2.1 represents a population tree, also produced by Cavalli-Sforza and colleagues, but based on an analysis that, compared to the study mentioned above, used far more alleles sampled across many so-called aboriginal populations. For the original tree, archaeological dates for steps in human expansion were used to calibrate genetic differentiation as well as to check for constant rates of genetic evolution.[5] Like Haeckel, Cavalli-Sforza saw in the evolution of languages a powerful tool to support genetic trees. In its original form, figure 2.1 was seen as indicating parallel linguistic and genetic evolution.

Although such tree figures suggest that the human populations have a common origin, the human groups appear to have separated at one point (more or less) back in time and to never have mixed again. Such trees would thus make it seem as if human populations were discreet, homogeneous entities that had independent evolutionary histories after the last population split. Indeed, Cavalli-Sforza and colleagues used only data referring to populations that were supposedly “aboriginal, with little or no admixture.”[6] Despite the rejection of many of the notions of racial anthropology—most importantly its typological understanding of race—the tree image that supported this understanding was thus carried over into human population genetics. The early human population geneticists were, however, not unaware of the issues with population trees. As early as the 1970s, Cavalli-Sforza suggested that trees might work only for populations that are geographically far apart, because otherwise, “instead of a ‘tree’ one may have to estimate a ‘network’; such methods do not yet exist.”[7]

At the end of Cavalli-Sforza’s career at the beginning of the twenty-first century, new theoretical, statistical, and computational approaches could be brought to bear on the organization and interpretation of an unprecedented amount of human genomic data. It was now possible to analyze and visualize the degree to which present-day individuals and populations are the result of admixture between human groups. With the introduction of such

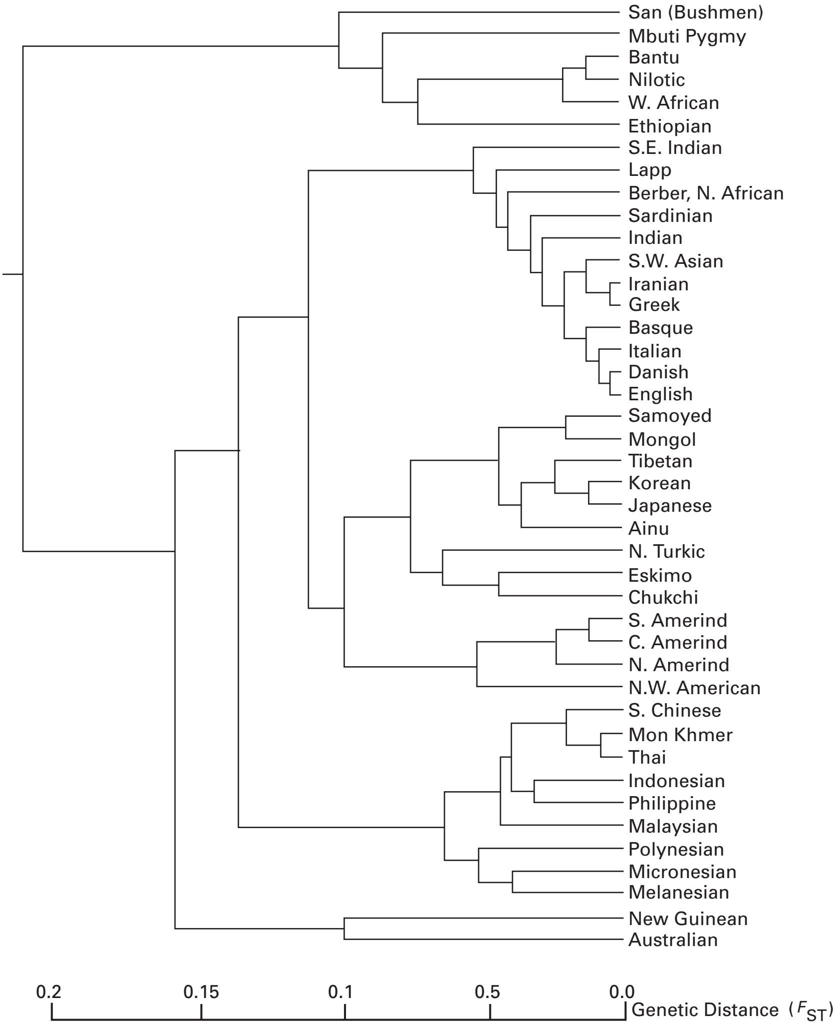

Figure 2.1

"Average linkage tree for 42 populations." Used with permission of Princeton University Press, from Luigi L. Cavalli-Sforza, Paolo Menozzi, and Alberto Piazza, *The History and Geography of Human Genes* (Princeton, NJ: Princeton University Press, 1994), 78. Permission conveyed through Copyright Clearance Center Inc.

statistical computer software, the visual black box of these seemingly discreet and homogeneous entities—human populations—was opened. Individuals and populations now often came to be represented as colored bar plots indicating their admixed histories. Accordingly, extant human genomes at the individual and population level were now conceived of as a mosaic: that is to say, they comprised genetic elements from ancestral populations of different geographical origins.[8]

The era of population genomics also witnessed the possibility of extracting DNA from the fossils of hominins and ancient humans, and integrating these ancient DNA data into the analysis of evolutionary history and kinship. The advancing field of aDNA research relied on population genomics, from which it adopted terminologies, methodologies, and visualization techniques. At the same time, by bringing in a new deep-historical structure, the inclusion of aDNA into population-genomic models and visualizations shifted the focus more strongly toward processes of ancestral admixture, even between archaic humans, such as the Neanderthals, and modern humans.

With the advent of aDNA, the understanding of human history and diversity thus seems to have changed considerably. To find out how this shift is reflected—or not—in the images used in the field, we follow the representation of human history and diversity through the admixture paradigm in human population genomics and the shift toward the inclusion of aDNA data. Our focus thereby rests on prominent models and tools, on the meaning that representations seem to carry regarding human diversity, and on how this meaning fits the assumptions of practitioners. We build on the observation that underneath the representation of individual and populational genetic kinship and diversity in terms of admixture and as mosaics continues to lurk the hierarchically organized tree that suggests independent (nonadmixing) histories of discreet populations.[9] We argue that although there was a paradigm shift toward the idea of a mosaic structure for human populations, the tree image was not dissolved by the new—and aDNA-driven—models that emphasize admixture, introgression (the transfer of genetic material from one population to another), and gene flow.

From the Tree to the Mosaic

At the beginning of the twenty-first century, a new standard for the analysis and representation of population genetic variation emerged through novel model-based clustering software that was typically developed by mathematicians together with statistically and computationally trained geneticists. The first of these clustering programs, STRUCTURE, was released in 2000. In the following years, it became one of the major tools to estimate ancestry from genome-wide human data, and the same holds true for the diagrammatic representation of the results of such analyses.[10] The diagram commonly used to represent the results from STRUCTURE was first used for the visualization of a genome-wide analysis of the Human Genome Diversity Panel in 2002 (see figure 2.3).[11] A software package that generated bar plots from STRUCTURE analyses, called DISTRUCT, was published two years later. Today, other programs are mainly in use, and these include follow-up programs of DISTRUCT as well as clustering software, such as ADMIXTURE, first published in 2009. The functions and the standard graphical representation of STRUCTURE and ADMIXTURE analyses are only marginally different. The main advantage of ADMIXTURE over STRUCTURE is that the program is considerably faster, allowing the processing of a much larger set of markers.[12]

With STRUCTURE, it was for the first time possible to compute genetic admixture by analyzing genome-wide data. At a very general level, the term “admixture” in this context means two things. First, it denotes a historical process: the mixing of at least two distinct populations through migration and reproduction. Second, it refers to a state of relatedness: the genetic makeup of individuals and populations in terms of so-called ancestry coefficients[13] and population structure.[14] These two levels of meaning are commonly understood to be causally related: admixture as a process is thought to result in admixture as a state. However, as we show below, the relationship between these two meanings of admixture is far more complex, and the significance of the term varies depending on the context of use. Whereas the inventors of STRUCTURE particularly emphasized the utility of their program for population genetics, in which the historical processes of admixture are of crucial interest, the developers of ADMIXTURE advertised their program as a tool for medical genetics, where the interest in admixture is typically limited to present genetic structures.[15] However, ADMIXTURE is used beyond this context of application.

STRUCTURE and ADMIXTURE are based on the assumption that human genetic diversity is substantially shaped by admixture. At the same time, geneticists usually understand certain populations to be “more admixed” than others. As data scientist Daniel Lawson and geneticists Lucy van Dorp and

Daniel Falush—the latter being one of the coauthors of the second version of STRUCTURE—have pointed out, the admixture model on which STRUCTURE and ADMIXTURE are based was derived from a very specific case of such “recent admixture”: that of African Americans.[16] It relied on the assumption that every African American individual has ancestry from two genetically distinct “sources”—West Africa and Europe—and that before their abduction to, or settlement of, America, both groups had minimal contact. Therefore, the history of African Americans is divided into two phases: a phase of thousands of years of independent evolution and a phase of admixture in the past few hundred years. In other words, most of the ancestors of contemporary African American individuals who lived 500 or more years ago are taken to have been either Africans or Europeans.

By comparing multiple different sequences of individual whole-genome samples, STRUCTURE and ADMIXTURE identify subgroups in which certain gene variants (alleles) occur at different frequencies. In this process, samples are grouped into several clusters (K), the number of which is chosen in advance but can be varied across independent runs of the algorithm. Figure 2.2 shows a bar plot as it is typically generated in the course of STRUCTURE and ADMIXTURE analyses. Here, ADMIXTURE is set to K=4, which means that the membership coefficients of the individual samples are calculated in relation to four different clusters. The clusters are represented by different colors. From left to right, we see a line-up of brightly colored lines that represent the individual samples. The arrangement of these lines is based on the populations from which the samples were taken. Below the graph, the standardized abbreviations of these sample populations are given. In the present example, these are populations that were defined in the framework of the International

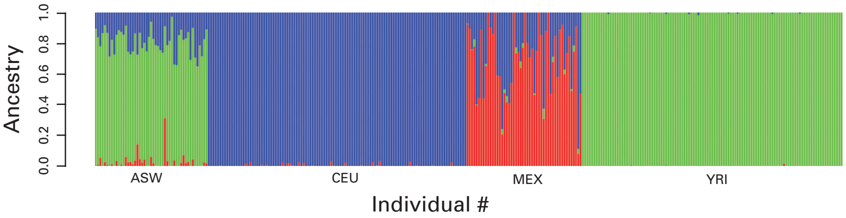

Figure 2.2

ADMIXTURE bar plot. David H. Alexander et al., *Admixture 1.3. Software Manual* (2020), https://dalexander.github.io/admixture/admixture-manual.pdf.

Haplotype Map Project. ASW stands for “African Ancestry in South West USA,” CEU for “Utah residents with northern and western European ancestry,” MEX presumably for “Mexican Ancestry in Los Angeles” (the standard abbreviation for this population is MXL), and YRI for “Yoruba in Ibadan, Nigeria.” From top to bottom, the estimated membership coefficients of the individuals in the four clusters are represented by the corresponding lengths of sections in the respective colors of the clusters. What these “membership coefficients” refer to is specified to the left of the graph. A scale from 0 to 1 titled “Ancestry” clarifies that the analysis is intended to provide information about the ancestry composition of the sampled individuals and populations. The authors of STRUCTURE and ADMIXTURE thus assume that the clusters inferred by means of those programs correspond to what they call “source populations”[17] or “ancestral populations,”[18] and that individual genomes can be understood as composites of these “sources.”

Two years after STRUCTURE was released, a group of researchers around population geneticist Noah Rosenberg—among them Jonathan Pritchard, one of the coauthors of STRUCTURE—used the program to analyze global genome-wide data from the Human Genome Diversity Panel.[19] The resulting paper provides an example of how STRUCTURE derives population structure from individual ancestry coefficients. In the paper, the authors aimed to show that individuals from different present-day cultural and geographic groups—from ethnoreligious and ethnic groups (such as “Druze,” “Han,” or “Uyghur”) and nationalities (such as “Russian” or “Italian”) to regional subgroups of these nations (such as “Sardinian” or “Tuscan”)—show different patterns of allele frequencies. Thereby, they wanted to prove that these “predefined populations” correspond to human populations in a genetic sense.[20]

The analysis with STRUCTURE generally supported this assumption. However, what Rosenberg and his coauthors particularly emphasized was that the diagram produced through STRUCTURE identified these populations as composites of “six genetic main clusters, five of which correspond to major geographic regions.”[21]

The legend for the diagram explains that “each individual is represented by a thin vertical line, which is partitioned into K colored segments,” with K representing the number of clusters. It further explains that these colored segments “represent the individual’s estimated membership fractions in K clusters.” The black lines separate individuals of different populations,

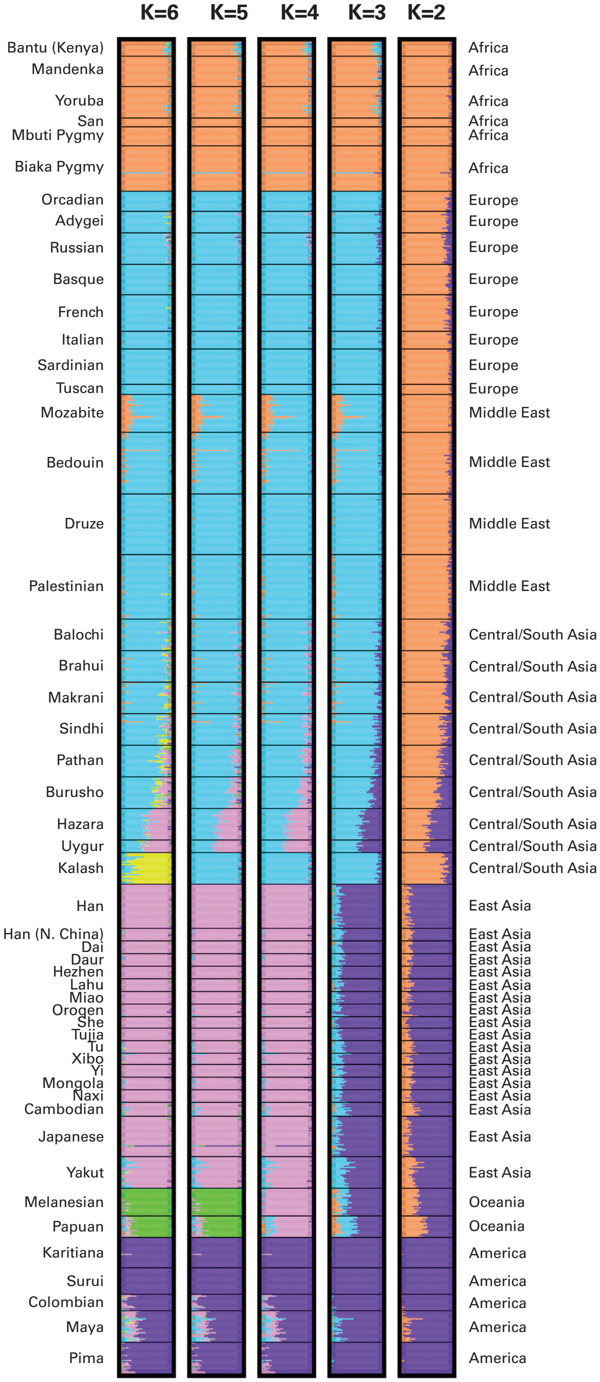

Figure 2.3

Representation of the first genome-wide analysis of global human genetic diversity with STRUCTURE. From Noah A. Rosenberg et al., “Genetic Structure of Human Population,” *Science* 298, no. 5602 (2002): 2382. Reprinted with permission from AAAS.

and these populations are labeled below the figure, with their regional affiliations above it.

This last point is significant, since the developers of STRUCTURE stressed that their program allows the clustering of samples without any "population information," that is, without relying on any information about the sampled individuals' affiliations to cultural and geographic groups.[22] Nevertheless, after clustering the individual samples independent of population information, STRUCTURE is set to reintroduce this information in order to visually arrange and label the individual data according to their prior assignment to cultural and geographic groups. In the diagram, the vertical lines representing the ancestry of the individual samples become hardly distinguishable. Instead, those predefined cultural groups become the salient entity of analysis and emerge as horizontal bars with a characteristic pattern of colors divided by black lines. Since this kind of representation is used as the de facto standard for visualizing STRUCTURE results for *any* kind of inquiry into the structure of human genetic variation, this rearrangement and labeling seems to subvert one of the crucial innovations of STRUCTURE: the purely inductive method of analyzing human genetic diversity without the use of population information. Rather, this kind of visualization reinforces the idea that human genetic variation is essentially structured by genetically distinct populations that largely match notions of ethnicity, nation and religion.

Looking at a single STRUCTURE bar plot, there appears to be no hierarchical or temporal order. Rather, the rainbow-colored diagram represents an ahistorical snapshot of human population genetic diversity, in which a patchwork of genetically reified cultural groups of varying scale come to stand together on the same plane. But this is not how STRUCTURE analyses are usually conducted. Typically, such analyses proceed according to the principle of trial and error. First, one assumes that there are two clusters and lets the program compute how much of the ancestry of every individual "comes" from each cluster. Then one proceeds with three, four, five clusters and so on—until the optimal number of clusters is identified. Determining this "optimal number" of clusters consists in assessing how well the results of the different analyses fit the data. The inventors of ADMIXTURE, for instance, suggested that the choice of K—the number of clusters—should be guided by knowledge about the history of the predefined groups that are being analyzed.[23] This strategy might be adequate in cases where ADMIXTURE is used for its originally stated purpose in medical genetics, that is, to mine for genetic variants associated with disease. Historical interpretations of ADMIXTURE analyses, however, are ultimately turned into circular arguments by the strategy of determining K based on historical knowledge.

The way Rosenberg and colleagues interpreted their bar charts exemplifies the role that the choice of the number of clusters may have in terms of conceiving of those clusters as "ancestral populations" that actually existed at some point in the past. One interpretation in the paper was derived from a single bar plot of five clusters.[24] The authors suggested that this was basically congruent with a continental pattern, since the colors of the clusters align with the geographical designations at the top of the diagram: Africa is mainly orange, Europe mainly blue, East Asia pink, Oceania green, and America purple, whereas the Middle East, Central and South Asia emerge as mixes of their geographical neighbors. This interpretation blurs statistical clusters with the idea of distinct and relatively homogenous groups of a clear continental origin. It basically suggests that clusters can be understood in the sense of continental groups that align with common notions of "race."

The second interpretation arose from all bar plots in combination. The authors observed that "at K = 2 the clusters were anchored by Africa and America, regions separated by a relatively large genetic distance." They went on to state that "each increase in K split one of the clusters obtained with the previous value. At K = 5, clusters corresponded largely to major geographic regions."[25] Thus, by looking at several bar plots in succession, they arrived at a narrative of subsequent splitting along the lines of a human evolutionary history that is essentially shaped by the divergence of continental groups. These are the "ancestral populations" that—in line with the dominant model of admixture exemplified by the demographic history of African Americans—are supposed to have undergone a long period of divergence, followed by a relatively short period of convergence that created the current genetic mosaics.

Such simple interpretations of STRUCTURE bar plots seem to be common enough to have induced a group of data scientists and geneticists to publish a paper entitled "A Tutorial on How Not to Over-Interpret STRUCTURE and ADMIXTURE Bar Plots" in 2018.[26] The authors simulated populations with specific patterns of allele frequencies, as they would theoretically form based on three historical scenarios, and then subjected these simulated populations to analysis with ADMIXTURE.[27]

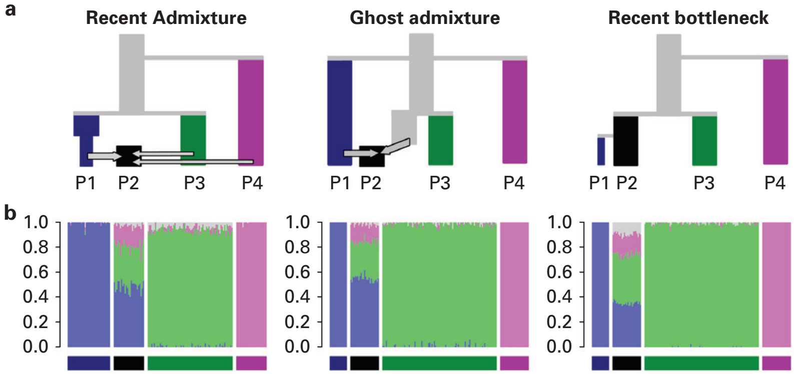

Figure 2.4

"Three scenarios that give indistinguishable ADMIXTURE results." Daniel J. Lawson, Lucy van Dorp, and Daniel Falush, "A Tutorial on How Not to Over-Interpret STRUCTURE and ADMIXTURE Bar Plots," *Nature Communications* 9, no. 3258 (2018): 3.

The top line shows three different demographic scenarios involving four simulated populations represented by different colors (dark blue, black, dark green, and dark magenta). The lower part of figure 2.4 consists of the admixture analyses for each of the respective simulated populations. The clusters to which the individuals of the simulated populations were thereby assigned to are represented by lighter shades of the colors that are used to distinguish the populations in the upper part of the illustration (blue, light green, magenta).

This color scheme visually anticipates and emphasizes the controversial assumption that the simulated populations are mixtures of different pure ancestral populations.[28] However, the illustration is actually intended to demonstrate that admixture constructs nearly indistinguishable bar plots from the different scenarios. The first scenario represents a history qualitatively similar to the one that is assumed for African Americans, but with three instead of two "ancestral populations." In the second scenario, we see admixture between a known population (P1) and an unknown population giving rise to a mixed population (P2) as well as two populations (P3 and P4) not involved in any kind of mixing. The third scenario does not involve processes of admixture at all.

For the first scenario, an interpretation that assumes the African American admixture model, and therefore interprets the patterns as representing the proportions to which each genome was inherited from different "ancestral populations," seems adequate. However, this interpretation is misleading for the second and third scenario. The simulations show that the patterns of an admixture analysis might reflect the length of time that each population has evolved independently from the others, rather than the proportion of ancestry resulting from admixture. As the authors of the paper point out, these distortions occur because the algorithm attempts to find the combination of clusters and admixture proportions in the data that best supports a simple admixture model—regardless of whether that model is historically accurate.[29]

As we will see, such difficulties are exacerbated with the use of aDNA in ADMIXTURE analyses. Suffice it to say here that groups that contain fewer samples are likely to be represented as mixes of populations with a greater sample size, rather than being assigned to their own "ancestral population." Even if the aDNA sample is older than the separation date of the modern populations with which it is compared, the ancient sample is typically represented as an admixture of the modern populations.[30]

Enter Ancient DNA: Mosaic and Trees

While, as we have seen, there is a certain tendency to correlate genetic clusters with "the five continents," which gives the impression that human genetic variation neatly corresponds to these regional divisions, ADMIXTURE analyses also have a subversive potential. When one experiments with ADMIXTURE, it seems that the more fine-grained the analyses become, the obscurer the population structures get. In other words: the bigger the number of clusters, the more "previously pure populations appear as admixed." This tendency of "bursting populations" is reversed in the tree structure. An example of this can be found on an online blog which features an ADMIXTURE analysis that moves from K = 1 up to K = 15.[31]

In figure 2.5, the clusters—in this case fifteen—are not visualized in the way typical for such colored bar plots produced by STRUCTURE or ADMIXTURE (as shown in our figure 2.3), but we can see the 139 smaller populations that were studied and to which the 2,230 individuals whose DNA was analyzed belong. It is indeed a beautiful mosaic that evokes a cheerful picture of humankind in all colors of the rainbow. Nevertheless, the "ancestral populations" from which the current populations and individuals form mixtures are still inferred (and indicated by the fifteen different colors in the numbered key on the right side of the figure). This becomes apparent when the same data are used to generate a phylogenetic tree for the fifteen "original" or "ancestral" components or populations identified by ADMIXTURE. In this

Figure 2.5

Cluster diagram with K = 15. Dienekes Pontikos, "Human Genetic Variation: The First ? Components," *Diekenes' Anthropology Blog*, December 15, 2010, http://dienekes.blogspot.com/2010/12/human-genetic-variation-first.html.

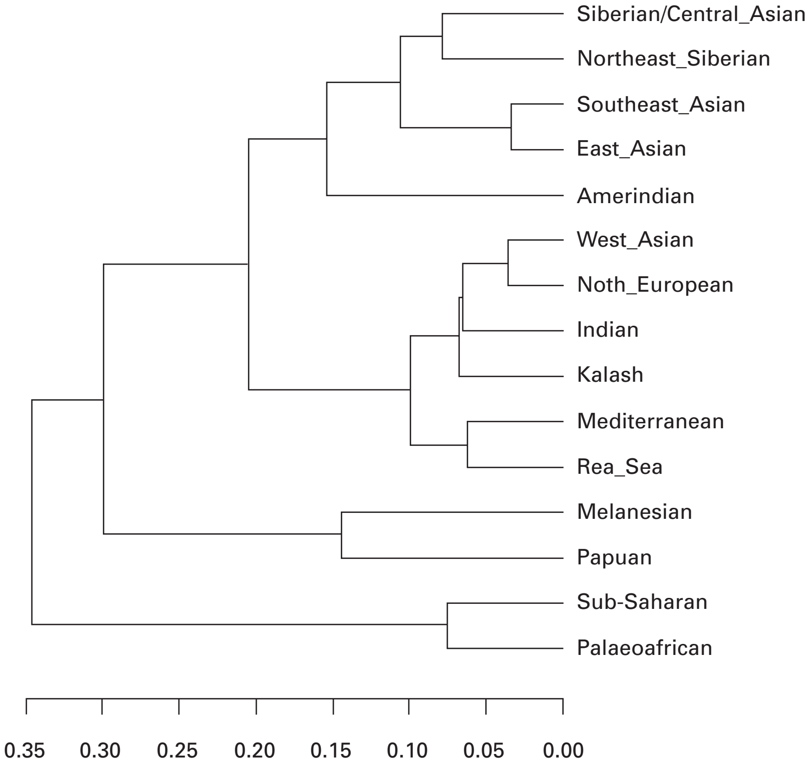

Figure 2.6

Dendrogram of hierarchical clustering of the fifteen components. Dienekes Pontikos, "Human Genetic Variation: The First ? Components," *Diekenes' Anthropology Blog*, December 15, 2010, http://dienekes.blogspot.com/2010/12/human-genetic-variation-first.html.

process, the admixture disappears, and we return to a diagram that creates a hierarchical order from the "Sub-Saharan Africans" to the "Siberians." Instead of a human mosaic, in figure 2.6 we again see the diaspora in which the fifteen populations seem to have differentiated without converging. This is represented in the typical form with a first branch that separates "Africa" from "the rest," and therefore not only ascribes originality to the continent and its people, but also marks them as the first "other."[32]

It seems, therefore, that while admixture has become the center of attention, underneath it still lurks the conception of originally pure populations (each marked by a single color in figure 2.5) hierarchically ordered in a tree. The ancestral component called "Palaeoafrican" in the tree actually refers to the “Pygmies and San” (*sic*), which raises the question of how the entry of actual ancient DNA into these models affected diagrams of human diversity.[33]

With technical developments, such as next-generation sequencing and the increasing accessibility of ancient DNA in both quantity and time depth, the potential for aDNA research is said to have exploded from limited individual ancient genomes to the scale of population genomics.[34] In this process, aDNA data are integrated into the models discussed in the previous section. However, as different numbers of individual DNA samples available across populations can misrepresent the relative frequencies of the ancestry components, clustering methods are susceptible to sampling biases, This is even more problematic when recent and ancient DNA samples are compared, because the former are generally overrepresented in related to the latter. In fact, aDNA samples from different times and places may be pooled to increase the number of samples.[35] Of greater concern to us is the issue that such clustering analyses do not rely on explicit population models and assume a defined number of ancestral populations. They therefore might not fit complex admixture histories, which become increasingly probable with the integration of aDNA data.

Figure 2.7, taken from a paper on “the genetics of the African continent,” shows such clustering analyses of modern DNA, on the one hand, and aDNA, on the other. The cluster diagrams of modern and ancient “African

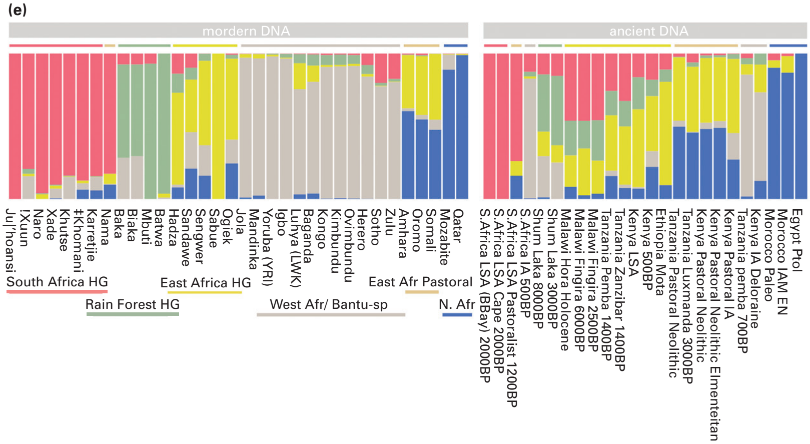

Figure 2.7

Clustering analyses of modern DNA (left) and aDNA (right).[36] Mário Vicente and Carina M. Schlebusch, “African Population History: An Ancient DNA Perspective,” *Current Opinion in Genetics & Development* 62 (2020): 10.

genomes"—among other visualizations—stand for complicated population histories within the continent and genetic exchange with Eurasia. At the same time, data so far seem to suggest an isolation-by-distance pattern for deep population history (hunter-gatherers [HG] before farming) and present-day hunter-gatherer groups.[37] In a way then, today's hunter-gatherers are seen as conserving the deep-past genetic order in the form of a tree spread across a continent, creating a simultaneity of the nonsimultaneous in their coexistence with more strongly admixed populations. To conceptualize this, we might think of an image such as an ancient tree covered by entangled mistletoe. However, the authors of the paper remind us:

> From European modern-day and subsequent aDNA studies, we have learnt that isolation-by-distance patterns can mask several large-scale movements and replacements in the distant past, especially if no un-admixed present day groups are remaining. Thus the deep history of Africa remains to be clarified, but aDNA studies already started to contribute inferences.[38]

This suggests that while the existence of unadmixed populations tends to be pushed further back in time, they remain the vanishing point: there once *was* a tree of unadmixed populations. On the basis of genomic data, the paper posits that the Khoe-San population can be considered the first to branch off from "the rest of us." But the authors, Mário Vicente and Carina Schlebusch, again caution: "While hierarchical bifurcating tree models provide a good estimation of general relatedness between groups, it is certainly a simplified representation of human history, and more complex models incorporating gene-flow, migration and deep population structure need to be considered in future research."[39]

Indeed, aDNA studies seem to be undermining the tree more and more, and at ever deeper segments. It has been suggested that some of the most groundbreaking and surprising findings of the last seven years have to do with ancient genetic introgression events, from extinct lineages to those lines that lead to modern human populations, as well as with evidence of ancient admixture between different archaic lineages.[40] Neanderthals are estimated to have contributed 1.5–2.1 percent to present-day non-African genomes, and Denisovans seem to have contributed to the genomes of modern Papuans, Melanesians, Aboriginal Australians, and other Southeast Asian islanders, as well as, to a lesser degree, those found in mainland East and South Asia.[41] Further research has suggested possible deep-rooting admixture by an ancient "ghost population"—genetic traces of unknown ancestors—indicating "ghost-modern admixture" in West Africa as well as large-scale Neanderthal admixture in African populations.[42] So it turns out that even humans as a species cannot be thought of as a "pure entity."

With new technologies, increasing data, and the so-called aDNA revolution, the once predominant model of human evolution as a tree on a map—a distant common origin with subsequent population splits and evolution of populations in relative isolation—seems to have tumbled. Intricate reticulate models now appear more likely, with complex migration and admixture histories not only for modern humans, but also for archaic humans—a history that involves interaction between as well as among populations of modern and archaic humans.

However, it should be noted that the idea that archaic and modern humans interbred whenever they met, which is driven by increasing reports of admixture, is contested.[43] Furthermore, and more central to our concern, the diagrams that express this new knowledge of interaction between modern and archaic populations still tend to closely resemble trees. They suggest that admixture and gene flow are mostly imagined as having taken place in one event of short duration—an event that now creates a link between two branches and that is often referred to with terms such as "introgression event," "admixture pulse," and "episodic migrations." Interbreeding thus appears as the great exception to the normal course of evolution-in-isolation. This is clearly evoked by a diagram from a 2014 paper that visualizes these short events, pulses, or episodes as darts between the branches of an overall tree structure:

However, we again find a discrepancy between text and image when the authors of the paper conclude:

> We present evidence for three to five cases of interbreeding among four distinct hominin populations. . . . Clearly the real population history is likely to have been even more complex. For example, most cases of gene flow are likely to have occurred intermittently, often in both directions and across a geographic range. Thus, combinations of gene flow among different groups and substructured populations may have yielded the patterns detected rather than the discrete events considered here.[44]

Furthermore, while in figure 2.8 recent human groups are at least embedded in a blue bubble—which we might interpret as genetic exchange among them—in the tree in figure 2.9, which suggests an additional introgression from the modern human into the Neandertal lineage, the modern human populations again appear as unmixed among themselves.

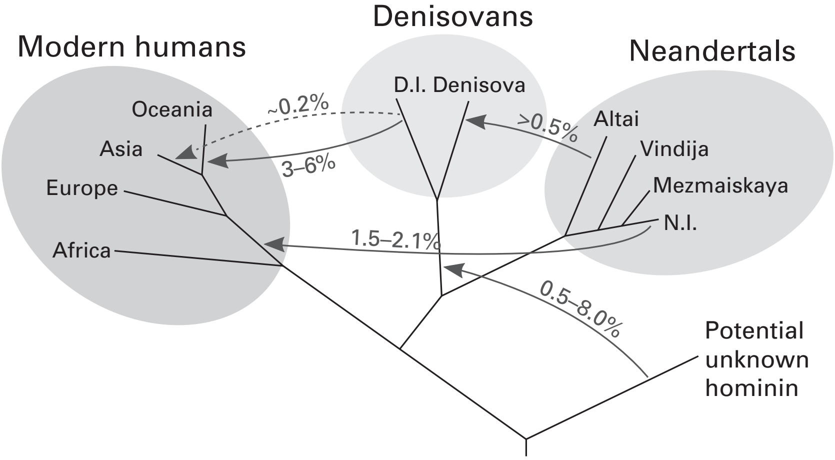

Figure 2.8
"A possible model for gene flow events in the late Pleistocene." Kay Prüfer et al., "The Complete Genome Sequence of a Neanderthal from the Altai Mountains," *Nature* 505, no. 7481 (2014): 48. Reproduced with permission from SNCSC.

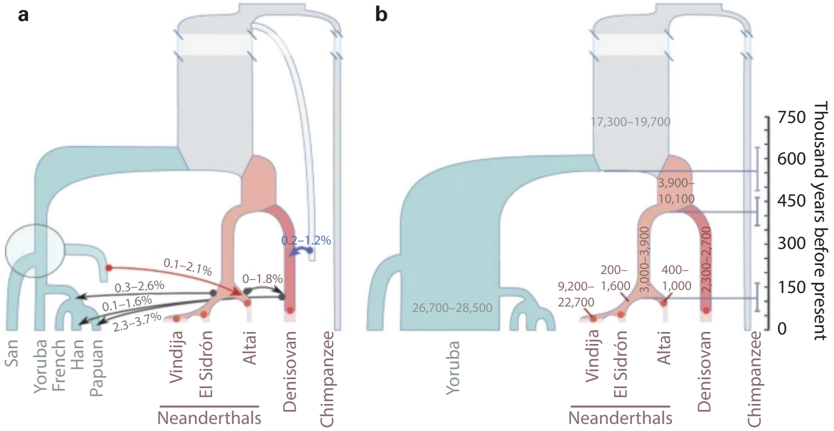

Figure 2.9
"Refined demography of archaic and modern humans." Martin Kuhlwilm et al., "Ancient Gene Flow from Early Modern Humans into Eastern Neanderthals," *Nature* 530, no. 7591 (2016): 432. Reproduced with permission from SNCSC.

Finally, some archaeologists, geneticists, and paleoanthropologists—including physical anthropologist Chris Stringer, who was a key figure in the synthesis of approaches around the out-of-Africa model—have issued criticism. They have proposed a complete replacement of archaic humans by incoming modern humans in Eurasia and reject many of the proposed admixture events. They defend the out-of-Africa scenario for modern human populations, even though it is not possible to pinpoint one geographical or temporal origin of modern human genomic ancestry in Africa, and even though this origin is not limited to Africa. As Stringer and colleagues explain in a paper from 2021:

> Although a mitochondrial "Eve," a hypothetical female ancestor of everyone alive today, will have existed and probably lived about 200 [thousand years ago], the location where she, or her Y-chromosomal "Adam" counterpart, lived is not necessarily expected to be the birthplace of all human ancestry. Furthermore, the small mitochondrial history traces just one out of a multitude of paths through the greater human genealogy. In many other parts of the genome, the most divergent branch will be found elsewhere in Africa, or sometimes outside of Africa.[45]

This leaves us with the conundrum that even though "trees are poor representations of genetic history,"[46] as the authors put it, this history continues to be represented with a rather treelike figure (figure 2.10):

The observations so far are obviously connected to the development of technologies used to study human and hominin demographic history and diversity on the bases of modern and ancient DNA. Programs such as STRUCTURE and ADMIXTURE, which underlie the study of African population history discussed above, assess the genetic similarity between individuals and the extent to which populations form distinct clusters. However, the integration of aDNA presents problems, not least due to sample sizes, sample quality and chronological and geographic representativity. Significantly, these programs do not have underlying population-genetic models or hypothesis testing components. As we have seen above, the recovered genetic substructures could have been brought about by several different population histories. Evolutionary geneticist Liisa Loog therefore observes that "conclusions can be easily steered by the subjective biases of a particular researcher."[47] Even though, as we have pointed out above, researchers may assume that living people and populations are a product of admixture between a certain set of distinct ancestral groups that once existed in the past, the observed genetic patterns could be the result of other demographical histories. One

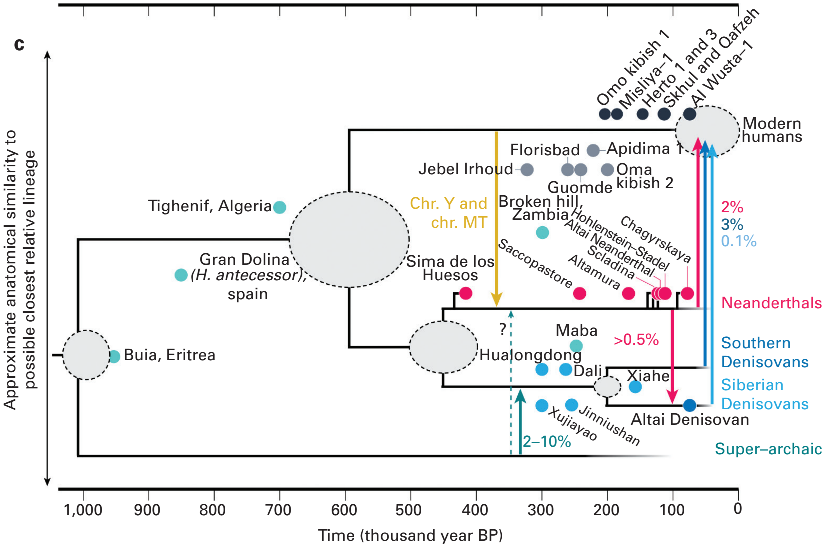

Figure 2.10

"Separation of modern human and archaic ancestries in the past one million years." Anders Bergström et al., "Origins of Modern Human Ancestry," *Nature* 590, no. 7845 (2021): 234. Reproduced with permission from SNCSC.

cannot, for example, differentiate between one or several admixture events using these programs.

These may be some of the reasons why programs such as STRUCTURE, ADMIXTURE and FINESTRUCTURE, despite their popularity, are not sufficient for many scientists, especially those working with aDNA. Researchers often refer to the early history of human population genetics, and specifically to Cavalli-Sforza's work, as discussed at the outset of this chapter, when accounting for the fact that they work with methods that can both model population relations and formally test admixture histories.[48] In other words, it was partly due to that early history of the field that methods were developed to describe population-tree topologies that could include admixture events. These methods analyze individual genomes, or the allele frequency patterns among populations, and compare the amount of genetic drift to establish population histories.[49]

In the context of our chapter, the graph-building techniques that visualize data outputs are of particular interest. As geneticist Ajaj Pathak puts it, these techniques "analyse the genetic diversities of many populations and suggest an elaborate treelike topology, illustrating their mutual relationships."[50] Tools like TreeMix, MixMapper, and qpGraph build trees of populations that explain their evolutionary histories, including episodic migrations (or gene flow) and admixtures.

The program TreeMix, designed to estimate the most likely population trees taking admixture into account, was applied by Kay Prüfer and colleagues to produce figure 2.8. It uses a graph representation to allow for admixture events as well as population splits. There are diverse techniques that are suitable for different purposes and different datasets, and all have their inherent assumptions, possibilities, and limitations, as well as pitfalls that may be exacerbated in the case of aDNA.[51] Most significantly for our context, graph-based models such as TreeMix infer a tree structure (only in subsequent steps "correcting" for admixture or gene flow events), which becomes evident in figure 2.11.

The researchers from whose paper figure 2.11 is taken assume that human population history is treelike in order to simplify the search for the "best graph" for the data. While this technique may be computationally efficient—a standard desktop computer could provide the tree structure in five minutes and

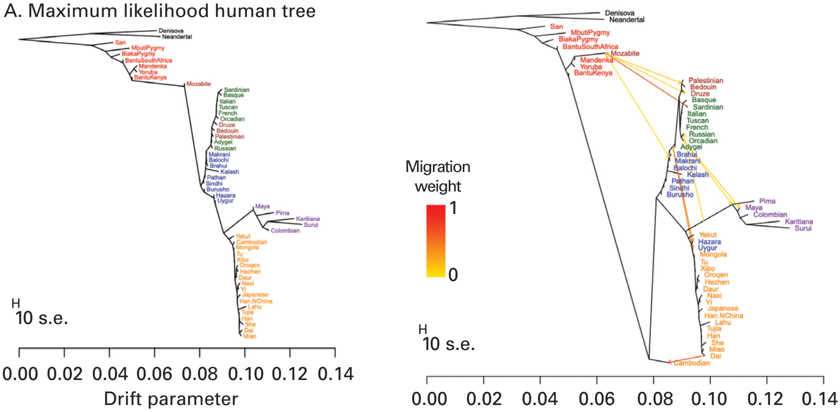

Figure 2.11

(Left): The inferred maximum likelihood tree of human phylogeny relating modern and archaic humans without considering gene flow between them. (Right): The same tree allowing for ten admixture events between continental groups of modern humans on the basis of TreeMix. Joseph K. Pickrell and Jonathan K. Pritchard, "Inference of Population Splits and Mixtures from Genome-Wide Allele Frequency Data," *PLoS Genetics* 8, no. 11 (2012): 8, 10.

test for admixtures in a few hours—it models "migration between populations as occurring at single, instantaneous time points," which the authors of the paper admit is "a dramatic simplification of the migration process." The researchers express their expectation that the assumption of treeness could eventually be relaxed with an improved search algorithm.[52] The appearance of a treelike structure of human history and relatedness respectively diversity may also be enhanced because admixture graphs such as qpGraph focus on admixture between populations of interest, hiding the admixed status of populations that are beyond the scope of a study.[53]

In the case of qpGraph, researchers are required to define the number of admixture events as well as the populations that are considered to be admixed. In the case of TreeMix, the determination of the phylogeny is automated, but the users still decide the list of populations and the number of admixture events. This, combined with the fact that TreeMix starts from an unadmixed tree (which is a problem especially if many populations are admixed), is regarded as the main drawback of such approaches.[54] It has also been observed that tools that require a model for the histories of the populations not in question might lead to erroneous admixture results if these histories are modeled wrongly—again, this is especially a risk in aDNA studies.

Knowledge about population histories is not necessary for the statistical tool qpAdm, which can identify plausible admixture histories and estimate admixture proportions. It has become a widely used tool, especially in aDNA studies, to test whether the genetics of a certain population can be explained by admixture between two or more source populations. qpAdm is seen to yield accurate results even where data coverage is low, data are missing to a significant degree, or aDNA is damaged. However, scientists in the field have cautioned that ancient and present-day DNA should not be analyzed together, and that qpAdm should not be used for population histories that might include extended periods of gene flow between groups.[55] As with TreeMix, the tool assumes a single pulse in a short time, even though, as evolutionary biologist Éadaoin Harney and colleagues note, "real population histories often involve continuous gene flow that occurs over a prolonged period of time."[56] Even in a case of continuous gene flow, qpAdm might suggest plausible admixture proportion estimates as a single pulse.

Some tools are not only able to approximate rates of gene flow between different branches of a putative tree from sequence data, but also estimate past population sizes and the dates of population splits. One such tool is the software package G-PHOCS, which was used in the construction of figure 2.8. In most cases, tools for dating admixture events, such as ROLLOFF, ALDER, and MALDER, once again assume one single admixture pulse and cannot, therefore, capture continuous mixing of populations. As we have seen, and as also suggested by the trees in figure 2.11—where the right-hand tree allows for ten admixture events but not for continuous exchange—this is a general problem with these visualizations. As geneticists Joseph Pickrell and David Reich have observed, "One question is whether changes in populations over time are typically gradual—owing to consistent, low-level gene flow between neighboring populations—or punctate, with migration events rapidly altering the genetic composition of a region. One line of work on modeling human history explicitly assumes the latter."[57]

While the assumption of such "punctate" events and their implementation in analytical tools are among the factors that seem to favor the persistence of treelike images of human population histories, geneticists have observed that most population genetic models more generally "rely on the assumption that the relationship between populations can be represented as . . . a phylogenetic tree, i.e. as abrupt splits between different branches of the tree, followed by independent evolution with potential for subsequent episodes of gene flow between them."[58]

Conclusion

We began this chapter with a cursory look at the visualization of human history, diversity and kinship in early human population genetic research, when the tree was fundamental. From this foundation, we have identified something akin to a visual paradigm shift with the advent of programs such as STRUCTURE and ADMIXTURE that were associated with an interest in processes of mixing, and in individuals and populations as mixed. The mosaic structure of the colored bar plots produced by ADMIXTURE contradicts an essentialist understanding of the categories of "individual" and "population"—indeed, these categories seem to be in the process of dissolution.

At the same time, there is also a pull in the opposite direction, since the ADMIXTURE bar plots imply pure "ancestral populations" that current populations are thought to be mixtures of. This gains clear visual expression when the findings are converted into a tree that suggests independent evolution, and thus "pure populations." Similarly, even though the advent of aDNA in population genomics has increased the focus on admixture and introgression, and these processes have been given a deeper history through aDNA, the amount of contact and genetic exchange between groups that researchers envisage tends to be minimized in modeling and visualizing, leaving us with trees that include relatively few connections between branches.

This is probably due to several factors, one of them being that ways of thinking and doing are handed down from one generation of researchers to the next. These ways may be disproportionately shaped by particularly influential scientists and labs.[59] There is also the history of methodological and technological developments in a stricter sense—as in the necessity to build on what is already there—and the fact that statistical analyses aim to reduce the complexity of data or fit it to parametric models.

While we might think of computer statistics as automatized, neutral tools, they are in fact shaped by assumptions. We have seen how models that have been developed for aDNA analyses rely on previous patterns of knowing and thinking about kinship and human evolution, most notably the tree form. Although more complex models are appearing on the horizon, human population genomics—also in its so-called revolutionized state after the advent of aDNA studies—instantiates tree-thinking and tree-building that tends to render archaic and modern human groups as more or less discrete, homogeneous entities. Such tree-thinking and tree-building runs in danger of inadvertently conveying older notions about human diversity in terms of race which, as we have pointed out in the beginning of this chapter, also used to be visualized as trees.

Notes

1. In this context, the tree of life is a metaphor to describe the relationships between all organisms, both extant and extinct.

2. Marianne Sommer, "The Meaning of Absence: The Primate Tree that Did Not Make It into Darwin's *The Descent of Man*," *BJHS Themes* 6 (2021): 45–61.

3. An allele is one of two or more versions of a gene. The word is used to describe genetic variation among genes, but it can also be used to describe genetic variation in noncoding regions.

4. Luigi Luca Cavalli-Sforza and Anthony W. F. Edwards, "Analysis of Human Evolution," in *Genetics Today: Proceedings of the XI. International Congress of Genetics, The Hague, The Netherlands, September 1963*, vol. 3, ed. S. J. Geerts (Oxford: Pergamon, 1965), 929.

5. Luigi Luca Cavalli-Sforza et al., "Reconstruction of Human Evolution: Bringing Together Genetic, Archaeological, and Linguistic Data," *Proceedings of the National Academy of Sciences* 85, no. 16 (1988): 6003.

6. Cavalli-Sforza et al., "Reconstruction of Human Evolution," 6003; Marianne Sommer, "Population-Genetic Trees, Maps, and Narratives of the Great Human Diasporas," *History of the Human Sciences* 28, no. 5 (2015): 108–145.

7. Luigi Luca Cavalli-Sforza, "Analytic Review: Some Current Problems of Human Population Genetics," *American Journal of Human Genetics* 25, no. 1 (1973): 96; Sommer, "Population-Genetic Trees," 120–121.

8. Sommer, "Population-Genetic Trees," 123–135; Marianne Sommer, *History Within: The Science, Culture, and Politics of Bones, Organisms, and Molecules* (Chicago: University of Chicago Press, 2016), part III. For histories and critical studies of human population genetics without a special emphasis on visualizations, see Jenny Reardon, *Race to the Finish: Identity and Governance in an Age of Genomics* (Princeton, NJ: Princeton University Press, 2005); Catherine Nash, *Genetic Geographies: The Trouble with Ancestry* (Minneapolis: University of Minnesota Press, 2015).

9. Sommer, "Population-Genetic Trees," 134–139; Sommer, *History Within*, 379–384.

10. John Novembre, "Pritchard, Stephens, and Donnelly on Population Structure," *Genetics* 204, no. 2 (2016): 391–392; Kai Yuan et al., "Models, Methods and Tools for Ancestry Inference and Admixture Analysis," *Quantitative Biology* 5, no. 3 (2017): 237–238; Mark Stoneking, *An Introduction to Molecular Anthropology* (Hoboken, NJ: Wiley-Blackwell, 2017): 169–170; Daniel J. Lawson, Lucy van Dorp, and Daniel Falush, "A Tutorial on How Not to Over-Interpret STRUCTURE and ADMIXTURE Bar Plots," *Nature Communications* 9, no. 3258 (2018): 2.

11. Noah A. Rosenberg et al., "Genetic Structure of Human Populations," *Science* 298, no. 5602 (2002): 2381–2385.

12. David H. Alexander, John Novembre, and Kenneth Lange, "Fast Model-Based Estimation of Ancestry in Unrelated Individuals," *Genome Research* 19, no. 9 (2009): 1655–1656.

13. In this context, ancestry coefficient refers to a statistical measure used to describe the relative degree of shared ancestry.

14. Alexander, Novembre, and Lange, "Fast Model-Based Estimation," 1655; Jonathan K. Pritchard, Matthew Stephens, and Peter Donnelly, "Inference of Population Structure Using Multilocus Genotype Data," *Genetics* 155, no. 2 (2000): 945.

15. Pritchard, Stephens, and Donnelly, "Inference of Population Structure," 945; Alexander, Novembre, and Lange, "Fast Model-Based Estimation," 1655.

16. Lawson, van Dorp, and Falush, "Tutorial," 2.

17. Pritchard, Stephens, and Donnelly, "Inference of Population Structure," 945.

18. Alexander, Novembre, and Lange, "Fast Model-Based Estimation," 1656.

19. Rosenberg et al., "Genetic Structure," 2381–2385.

20. Rosenberg et al., "Genetic Structure," 2381.

21. Rosenberg et al., "Genetic Structure," 2381.

22. Pritchard, Stephens, and Donnelly, "Inference of Population Structure," 945–946.

23. Alexander, Novembre, and Lange, "Fast Model-Based Estimation," 1663.

24. At the left-hand side of the diagram, there are the number of clusters (abbreviated with the letter K), to which the individual samples are assigned in the corresponding bar plots.

25. Rosenberg et al., "Genetic Structure," 2382.

26. Lawson, van Dorp, and Falush, "Tutorial," 2.

27. Lawson, van Dorp, and Falush, "Tutorial," 10. In a STRUCTURE or ADMIXTURE analysis with "real" data, these simulated populations would be what is commonly called "predefined populations."

28. Sommer, "Population-Genetic Trees," 133–135; Sommer, *History Within*, 380–381.

29. Lawson, van Dorp, and Falush, "Tutorial," 4.

30. Lawson, van Dorp, and Falush, "Tutorial," 10; Morten Rasmussen et al., "Ancient Human Genome Sequence of an Extinct Palaeo-Eskimo," *Nature* 463, no. 7282 (2010): 760–761; Pontus Skoglund et al., "Origins and Genetic Legacy of Neolithic Farmers and Hunter-Gatherers in Europe," *Science* 336, no. 6080 (2012): 467.

31. Dienekes Pontikos, "Human Genetic Variation: The First ? Components," *Dienekes' Anthropology Blog*, December 15, 2010, http://dienekes.blogspot.com/2010/12/human-genetic-variation-first.html.

32. See also Sommer, "Population-Genetic Trees," 26–28; Sommer, *History Within*, 380–384.

33. Pontikos, "Human Genetic Variation."

34. Charlotte Lindqvist and Om P. Rajora, eds., *Paleogenomics: Genome-Scale Analysis of Ancient DNA* (Cham: Springer International, 2019).

35. Michela Leonardi et al., "Evolutionary Patterns and Processes: Lessons from Ancient DNA," *Systematic Biology* 66, no. 1 (2017): 1–29.

36. "HG" in the figure stands for "hunter-gatherers."

37. Mário Vicente and Carina M. Schlebusch, "African Population History: An Ancient DNA Perspective," *Current Opinion in Genetics & Development, Genetics of Human Origin* 62 (2020): 12. See also Mário Vicente et al., "Genetic Affinities among Southern Africa Hunter-Gatherers and the Impact of Admixing Farmer and Herder Populations," *Molecular Biology and Evolution* 36, no. 9 (2019)): 1849–1861; Pontus Skoglund et al., "Reconstructing Prehistoric African Population Structure," *Cell* 171, no. 1 (2017): 59–71.

38. Vicente and Schlebusch, "African Population History," 12.

39. Vicente and Schlebusch, "African Population History," 12–13. See also Carina M. Schlebusch et al., "Southern African Ancient Genomes Estimate Modern Human Divergence to 350,000 to 260,000 Years Ago," *Science* 358, no. 6363 (2017): 652–655.

40. Skyler D. Resendez et al., "Structural Variants in Ancient Genomes," in *Paleogenomics: Genome-Scale Analysis of Ancient DNA*, ed. Charlotte Lindqvist and Om P. Rajora (Cham: Springer International, 2019), 375–391.

41. Leonardi et al., "Evolutionary Patterns and Processes," 1–29.

42. Vicente and Schlebusch, "African Population History," 8–15.

43. See below, and also Shyamalika Gopalan et al., "Inferring Archaic Introgression from Hominin Genetic Data," *Evolutionary Anthropology* 30, no. 3 (2021): 214–216.

44. Kay Prüfer et al., "The Complete Genome Sequence of a Neanderthal from the Altai Mountains," *Nature* 505, no. 7481 (2014): 48.

45. Anders Bergström et al., "Origins of Modern Human Ancestry," *Nature* 590, no. 7845 (2021): 233.

46. Bergström et al., "Origins," 233.

47. Liisa Loog, "Sometimes Hidden but Always There: Assumptions Behind Demographic Inference from Ancient DNA Data," *Philosophical Transactions of the Royal Society B: Biological Sciences* 376, no. 1816 (2021): 2.

48. Joseph K. Pickrell and Jonathan K. Pritchard, "Inference of Population Splits and Mixtures from Genome-Wide Allele Frequency Data," *PLoS Genetics* 8, no. 11 (2012): 1–2; Ajai K. Pathak, "Identifying Admixture and Genetic Ancestry in Human Populations via Genetic Drift Pattern," *Polymorphism* 4 (2020): 6.

49. On admixture methods in general, see Pathak, "Identifying Admixture"; Nathan K. Schaefer, Beth Shapiro, and Richard E. Green, "Detecting Hybridization Using Ancient DNA," *Molecular Ecology* 25, no. 11 (2016): 2398–2412.

50. Pathak, "Identifying Admixture," 13.

51. Pathak, "Identifying Admixture," 5–20.

52. Pickrell and Prichard, “Inference of Population Splits,” 9, 13.

53. Mark Lipson, “Applying f_4-Statistics and Admixture Graphs: Theory and Examples,” *Molecular Ecology Resources* 20, no. 6 (2020): 1664.

54. See Lipson, “Applying f_4-Statistics,” 1666.

55. Éadaoin Harney et al., “Assessing the Performance of QpAdm: A Statistical Tool for Studying Population Admixture,” *Genetics* 217, no. 4 (2021): 1–17.

56. Harney et al., “Assessing the Performance of QpAdm,” 13.

57. Joseph K. Pickrell and David Reich, “Toward a New History and Geography of Human Genes Informed by Ancient DNA,” *Trends in Genetics* 30, no. 9 (2014): 382–383.

58. Loog, “Sometimes Hidden,” 4.

59. See Elsbeth Bösl, *Doing Ancient DNA: Zur Wissenschaftsgeschichte der aDNA-Forschung* (Bielefeld: transcript Verlag, 2017).

3 Past Pathogens and Precarious Futures

Venla Oikkonen

Over the past decades, ancient DNA (aDNA) has emerged as a culturally appealing means of reimagining the connection between the past and the present. In public discussions, aDNA research is often portrayed as providing a material, indisputable link to a prehistoric time. Such a portrayal is based on the idea that aDNA constitutes a fixed, immutable entity that can be unveiled through scientific observation to tell stories about how we became "us."[1] For example, genetic ancestry tests that promise to trace customers' "Neanderthal" or "Denisovan" ancestry,[2] or excited media portrayals of aDNA sequences retrieved from hominin remains,[3] seek to root us in a particular version of the past that may be at odds with knowledge produced within archaeological research, communal tradition, or traditional family genealogy.[4] Importantly, the presumed genetic connection between the past and the present is also understood to be shaping the very contours of the future through, for example, communities and identities that have emerged around geneticized belonging.[5] While the apparent naturalness of aDNA as a means of belonging has been challenged by scholars noting that paleogenomic knowledge relies on choices of datasets, methods, and statistical models, aDNA remains a highly appealing, affectively invested object in cultural discourse.[6]

However, hominin and animal aDNA is not the only type of genetic material that has fueled discussion about how the distant past shapes the present. This chapter turns to another type of ancient genetic material—that of past pathogens—to understand the role of aDNA as a means of imagining trajectories between the past, present, and future. Pathogens are biological entities able to cause disease. They include, for example, bacteria and viruses. Most pathogens contain some type of genetic material, yet there are also crucial differences in their organization and functioning. For example, bacteria can multiply on their own, whereas viruses require a host cell to replicate.

When frozen past pathogens are thawed, some of them can, at least hypothetically, be reactivated and cause disease. Pathogen aDNA thus carries a capacity that human or animal aDNA lacks, as the latter cannot spontaneously come "alive" and become a new living organism. Yet, notably, traces of ancient pathogens are often discovered while analyzing hominin and animal aDNA from old remains.[7] Archaeological and paleontological sites are therefore increasingly seen as a potential source of not only hominin and animal aDNA, but also pathogen aDNA.

Like aDNA from early hominin remains, discovered pathogen aDNA has received considerable public attention. However, whereas the former has mostly garnered fascination, past pathogen discoveries have invoked concerns. Cultural anxieties around past pathogens focus on the perceived liveliness of pathogens as material entities. Such anxieties center on the idea that the genetic material in past pathogens is essentially different from contemporary pathogens and, in the right circumstances, might give rise to reemerging illness. In other words, past pathogens are represented as being potentially able to spontaneously shape our destinies and to hold the future a prisoner of the past. Understanding how past pathogens are conceptualized in culture and science thus complicates the current popular understanding of aDNA as simply telling the story of our genetically rooted belonging. The temporal trajectories between the past, present, and future imagined through aDNA from pathogens are structured by affective tensions and societal concerns that are not typically present in cultural portrayals of hominin aDNA as a genetic document from the past.

Cultural representations of past pathogens center on a particular context: permafrost, ground that is frozen throughout the year for several consecutive years. In cultural discourse and popular science, permafrost is often portrayed as nature's "freezer" because it has emerged as a source of very old biological material that would not have survived in warmer temperatures. Crucially, this freezer is thawing with climate change, thereby exposing old biological material. With cases such as "Ötzi the Iceman," whose 5,000-year-old remains were discovered in melting ice in the Alps in 1991,[8] or the 2010 reconstruction of the first ancient human genome from 4,000-year-old hair found in permafrost in Greenland,[9] permafrost has increasingly been seen as a gateway to previously unknown evolutionary history and early population movement. At the same time, researchers have retrieved traces of deadly pathogens, such as those causing bubonic plague or smallpox, as well as previously unknown viruses and microbes, in the melting permafrost.[10] These examples suggest that past pathogens emerging from permafrost not only are sources of knowledge, but may also in some cases constitute potentially viable entities. This is reflected in how past pathogens buried in permafrost are often portrayed as sharing a likeness with refrigerated viral and bacterial samples stored in a microbiology lab.

The idea of an unknown viral or microbial threat lurking in melting permafrost is present in both scientific and public discourse. For example, the review article "Future Threat from the Past" by medical researchers Amr El-Sayed and Mohamed Kamel posits remains buried in permafrost as objects of particular concern for the future of human life.[11] The authors reflect on the revival of "*Bacillus sphaericus* and *Staphylococcus succinus* . . . from 25 to 40 million-year-old Dominican amber." Other articles highlight the urgency of the issue while noting that little is known about whether old microbial and viral material released from permafrost ground constitutes a direct risk to human health and in what circumstances such risk might materialize.[12] Concerns about the vitality of emerging pathogens are echoed in media stories, such as the 2017 article "There Are Diseases Hidden in Ice, and They Are Waking Up," originally published on the BBC's website. It describes how "permafrost soil is the perfect place for bacteria to remain alive for very long periods of time, perhaps as long as a million years," which means that "melting ice could potentially open a Pandora's box of diseases."[13] In a similar vein, a *Scientific American* article called "Deep Frozen Arctic Microbes Are Waking Up" highlights the unpredictability of dormant pathogens, warning that "organisms that co-evolved within now-extinct ecosystems . . . may also emerge and interact with our modern environment in entirely novel ways."[14]

In this chapter, I locate a key tension at the heart of cultural and technoscientific visions of how past pathogens in permafrost may shape the future. The chapter engages with two cases: an unexpected anthrax outbreak in Siberia in 2016 and the reconstruction of the 1918 pandemic influenza virus. The cases demonstrate two different potentialities. In the first one (anthrax), the past unexpectedly takes over the present; in the second one (pandemic influenza), the past is drawn on to prepare for future pandemics. These differences make visible the ambiguous role of past biological material in the societal search for future health. I will draw from materials ranging from bioscientific articles to media texts and popular science articles on discoveries of past pathogens in permafrost. These materials shed light on how past pathogens and pathogen aDNA discoveries are shaping the ways in which the connection between the past, present and future is imagined in contemporary society.

The Cryopolitics of Pathogens and Permafrost

Old pathogens and aDNA emerging from permafrost are part of the larger politics of freezing and thawing life. Such politics have been called "cryopolitics," a term coined by historian Michael Bravo and physicist Gareth Rees.[15] Science and technology studies scholars Joanna Radin and Emma Kowal have developed the concept further to address technologies and practices of freezing and thawing in biomedicine and science.[16] They approach frozen life as "latent life," a liminal state in which biological matter is neither alive nor dead, yet may—in suitable conditions—come alive.[17] This conceptualization of cold temperature, time, and liminality helps to shed light on how past pathogens and their genetic material, when emerging from the frozen ground, are perceived to carry a potentiality to shape the future. Radin and Kowal highlight that cryopolitics centers on the indeterminacy of that future.[18] In the case of pathogens and permafrost, the link between what has been and what will be is largely unknown, heightening the affective stakes of permafrost discoveries. Old pathogens may, or may not, engender illness or death.

Different practices and technologies of freezing and thawing life have been discussed widely in science and technology studies as well as other social sciences in recent years.[19] The emergence of past pathogens from permafrost resonates with practices of freezing and thawing life-giving entities such as blood, eggs, sperm, embryos, and plant seeds. Like these entities, bacteria and viruses carry the potentiality of generating or shaping life. Yet, there is a crucial difference: the awakening of latent life emerging from permafrost is in itself not a technoscientific, controlled event—although it may result from human action responsible for warming climates. Rather, the melting of permafrost triggers the need for technoscientific intervention, such as public health management and genetic sequencing, including potential manipulation of the retrieved genetic material to create means of managing future diseases.

The cryopolitics of frozen pathogens is embedded in the cryopolitics of permafrost. Permafrost is not just any ice or cold. It is entangled with complex histories and the politics of place and difference. Writing in the context of the North American Arctic, anthropologist Jennifer Hamilton notes that arctic cold has been seen in a popular evolutionary framework as a symbol of a lack of civilization as well as a resource to be exploited by capitalist systems outside the Arctic, for example as a source of frozen meat.[20] In such histories, Hamilton notes, cold is associated with often stereotypical perceptions about Indigenous people living in the Arctic, with the result that cold temperatures have long been seen as a rationale for imperialism and settler colonialism. This colonialist logic is repeated in the long history of portraying the Arctic region and its Indigenous populations—both present and past communities—as a particularly important source of contemporary and ancient DNA through which scientists could presumably access human evolutionary history.[21] Paying attention to this popular association between indigeneity and cold is crucial in order to understand how ideas of pasts and futures are invoked and reinforced in cultural discourses around the two cases analyzed in this chapter. In both cases, the popular association between indigeneity and cold structures, for example, what kind of technoscientific interventions are perceived as necessary to prepare for and prevent future epidemics. Rooted in the colonialist logic, the association of cold and indigeneity also reinforces a sense of "otherness" and danger around Arctic communities and environments, as old pathogens are portrayed in popular discourse as lying in wait.

Finally, permafrost is also materially distinct from other forms of ice and cold. Landscape architecture scholar Leena Cho traces the emergence of permafrost "as an idea" through the development of US permafrost science and engineering.[22] Cho notes that permafrost as a material entity is "active, generative and vibrant," as it is continuously reshaped through changes in temperature.[23] Permafrost's vibrancy also arises from its mixture of organic and inorganic materials: as a place "where various things across earth's time—including ancient microbes, hydrocarbons, roots, toxins, scientific probes and building foundations—have been accumulated, separated and reconstituted," permafrost is unpredictable in its local melting patterns.[24] Permafrost, then, is plural, situated and entangled with other ecologies and infrastructures.

Revisiting the concept of cryopolitics, Michael Bravo highlights this vibrancy, noting how ice that has built up slowly over years can thin remarkably quickly within a few months.[25] Yet, the futures that may emerge from melting permafrost are not without limits. For example, Bravo explains, there may be no point of return: "The thin layer at the top of permafrost can slowly melt and refreeze annually, but when a critical threshold of permafrost melt takes place it collapses and does not regain its structure when refrozen."[26] Crucially, such thresholds shape whether and when forms of potential life—microbes, viruses, and genetic material—may emerge from organic matter such as remains buried in permafrost. This sense of unpredictability adds to the feeling of danger associated with past pathogens in cultural discourse.

The 2016 Anthrax Outbreak in Siberia

In July 2016, a local anthrax outbreak took place in the Yamalo-Nenets autonomous district in Siberia. A twelve-year-old boy died, dozens of people from the nomadic herding community were affected, and over 2,000 reindeer died of illness. The cause of the outbreak has been linked to the summer heatwave, which had reached 35 degrees Celsius, and the subsequent thawing of permafrost, as well as to longer-term patterns of climate change.[27] It was widely suggested at the time that the unusual heat had exposed a reindeer carcass preserved from the previous anthrax outbreak in the region in 1941. It thus appears that anthrax spores had survived seventy-five years in permafrost without losing their capacity to infect organisms.[28]

The 2016 anthrax outbreak raised considerable international interest. Part of this attention likely arose from the affectively charged cultural association between anthrax and bioterrorism—an association cemented in cultural discourse through the anthrax attacks that took place in the United States in 2001, shortly after 9/11. However, considerable attention focused on permafrost and climate change. Commentators asked: If there were large numbers of cattle burial sites in Siberia and other Arctic areas and the climate kept getting warmer, would there be regular anthrax outbreaks in such regions in the future? What other pathogens lay dormant in permafrost that could awaken like anthrax? These themes were repeated across the media. For example, an article on the website of National Public Radio (NPR) in the United States concluded: "The question for researchers is: Could these pathogens—like anthrax—ever be reactivated?"[29] A piece in *Scientific American* on the anthrax outbreak referred to how "the zombie microbes lurking in the permafrost" are "unknowable and unpredictable in their timing and ferocity,"[30] and a news article in the *Barents Observer* was titled "Scientist: Yamal Anthrax Outbreak Could Just Be the Beginning."[31] Likewise, the *Disease Daily* website noted that the case "raises questions about the potential impact of climate change on other pathogens suspended in the ice," as, for example, "smallpox and bubonic plague are also likely embedded in the Siberian ice."[32] Media and other cultural responses, then, extended beyond the case itself to look at the larger issue of melting permafrost. As a result, the anthrax spores released from the ice emerged as symbolic of all old pathogens presumably preserved in the frozen ground.

Much of the coverage of the 2016 anthrax outbreak portrayed the permafrost as a freezer. In the NPR piece mentioned above, for instance, environmental virologist Jean-Michel Claverie described the permafrost soil in the Yamal region as "a giant freezer" that provided "very, very good conditions for bacteria to remain alive for a very long time."[33] This framing connects the reindeer carcass exposed from the melting Siberian permafrost to larger cryopolitics, in which cold temperatures are manipulated to extend life, for example, by freezing embryos for future use.

However, the 2016 anthrax case differs from this technoscientific framework in a crucial way: the freezing and thawing of decades-old animal carcasses is beyond the immediate control of human actors. The media coverage of the 2016 anthrax outbreak clearly demonstrates the affective intensities that accompany this unpredictability. For example, an article in the *Washington Post* based on an account by a University of Missouri scientist describes how anthrax spores "play the long game, waiting in the soil for the temperatures to rise. Once it hits a certain threshold, they morph back into a more mobile, infectious state."[34] In a classic anthropomorphic rhetorical twist, the dormant bacteria emerge as uncanny actors with the power to shake the foundations of human life and society. They are not objects frozen by humans for technoscientific manipulation of life; instead, they are represented as invisible, potentially treacherous strangers within our seemingly familiar world.

At the same time, permafrost itself emerges as active and vibrant. While this is reflected in media stories of how ice that should stay frozen is melting at an alarming pace, it is particularly central to scientific accounts of pathogens, permafrost, and climate change. In an article published in 2011 and referenced in several of the 2016 news stories, medical researchers Boris Revich and Marina Podolnaya warn about the prospect of anthrax emerging at cattle burial sites in the Russian North.[35] In a now ominous tone, the authors predict that resulting from "permafrost melting, the vectors of deadly infections of the 18th and 19th centuries may come back, especially near the cemeteries where the victims of these infections were buried."[36] Crucially, Revich and Podolnaya arrive at this view from an understanding of the melting patterns of permafrost as situated and heterogeneous:

> As the permafrost temperatures in Yakutia increase, permafrost degradation becomes evident. For example, the depth of permafrost varies between 250 and 350 m in the center of this region (Yakutsk city). Under natural conditions, the depth of seasonal melting is 1.5–1.7 m for clay loams, 1.6–2.0 m for sand clays, and 2.0–2.5 m for sands. The temperature of surface layer of permafrost is predicted to increase by 1.5–2°C in West Siberia and Yakutia, and by 1.0–2.0°C in Chukotka and north regions of Far East.[37]

Here, permafrost is constantly shaped through local dynamics involving temperatures and the material qualities of the ground. Likewise, in an article published in 2020, environmental scientist Elisa Stella and colleagues examine permafrost's cyclical nature of wakefulness and how it may affect dormant anthrax spores. Developing a mathematical model that accounts for seasonal fluctuations rather than simply annual changes, they argue that "the seasonal and inter-annual dynamics of the active layer, and of the top surface of permafrost, can critically control the viability of spores and, in turn, the risk of triggering anthrax outbreaks."[38]

In these two examples from scientific literature, futures become pinned to the unpredictable, situated capacities of permafrost in specific material locations. The accounts thereby reflect Bravo's and Cho's theorization of permafrost as never stable and thus never quite manageable. The two examples also shift the focus of attention from the anthrax spores to the material entanglements of ice and soil as capable of shaping futures of health and illness. Affects such as anxiety and concern become attached to this unpredictability of melting ice and its potential ability to mold the future. At the same time, the ability of anthrax spores to come alive and cause outbreaks appear as dependent on these local peculiarities of vibrant permafrost. The perceived animacy of both anthrax spores and melting layers of permafrost are reinforced through their mutual entanglements.

Furthermore, the capacities of the anthrax spores and permafrost are made sense of through ideas of indigeneity in cultural discourses around the 2016 outbreak. As Hamilton notes, indigeneity and permafrost are historically entangled in cultural perceptions and are often interpreted through a popularized evolutionary framework of past-oriented (Indigenous) versus future-oriented (technoscientific) societies.[39] In the anthrax case, the nomadic herders were perceived to have unintentionally played a role in the spread of the outbreak since their herding practices moved a large number of reindeer through small, anthrax-contaminated space.[40] Furthermore, the culture of the herders was sometimes constructed as part of the problem. An article in *Deutsche Welle*, for instance, quotes a governor's spokesperson saying that one of the families who were ill "ate reindeer meat raw and drank the blood," adding that "the nomads do have this custom."[41] For the most part, though, indigeneity remained a relatively unprecise reference point whose affective power lay in the historically cemented popular association between indigeneity and permafrost rather than in any specific material detail.

In the media coverage of the anthrax outbreak, the association between anthrax, cold, and indigeneity operates through ideas of temporality. Anthrax was not only currently in the wrong place (outside the ice) but also originally in the wrong place (in the surface layers of permafrost). The burial practices of the past and unmarked graves were understood to have put anthrax in the wrong place. Anthrax was also in the wrong time: it belonged to the past, not the present nor the future.

At the same time, indigeneity has been commonly associated in popular discourse with the absence of modernity and as presumably unable to reach to the future.[42] Such organization of temporality into (presumably) neatly separable temporal zones—past, present, and future—is the cornerstone of technoscientific ideas of progress. It assumes that the three temporal zones should be kept separate and that the past should not claim a hold over the future. Building on such spatiotemporal politics of cold, indigeneity, and pathogenicity, the nomadic herders became seen as symbolic of the anthrax-ridden past threatening the future. The reindeer carcass as a source of past anthrax spores played a key role in this representation, as the connection between reindeer and indigeneity has a firm place in the imperialist imagination.[43] Familiar colonial images of racialized difference—reindeer herding, burial sites, endless ice—thus emerged in popular representations of the anthrax outbreak as the uncanny that challenges the inevitability of a future. This evocation of indigeneity, permafrost, and the past contributed to the affective intensity around the idea that past pathogens could threaten the future.

Past Pathogens and Evolutionary History

Popular discourses around the 2016 anthrax outbreak focused on the liveliness of the old anthrax spores and their capacity to threaten human health. However, the anthrax outbreak also engendered another type of knowledge: genetic sequencing of anthrax samples. Samples collected from the outbreak provided an entry point to placing the specific pathogen responsible for the outbreak in the context of the evolution of anthrax strains across time and space. This kind of genetic knowledge of pathogens has engendered considerable fascination in culture for its perceived high-tech approach and ability to reach back in time. In this, the sequencing of the anthrax samples from Siberia sits firmly within the larger project of aDNA research, which seeks to understand evolutionary processes through old DNA samples. The sequencing of the 2016 anthrax samples warrants attention, as it shows how aDNA research has expanded across bioscientific research, seeking to turn epidemics into sources of evolutionary knowledge. This case also provides a crucial contrast to the sequencing of the 1918 influenza virus, which—as we will see in the following sections—focused on the prevention of future epidemics. This shows that genetic knowledge of past pathogens occupies an ambivalent position as a means of knowing the past as well as managing the future.

The sequencing of anthrax samples from the 2016 outbreak took place in the context of ancient pathogen genomics. In the past decade in particular, geneticists have sought to identify and sequence pathogens discovered in archaeological and paleontological sites and in environmental samples, producing ancient sequences of pathogens behind, for example, salmonella, cholera, and louse-borne relapsing fever.[44] Central to ancient pathogen genomics is the geneticization and digitization of material differences between pathogens retrieved at different sites and representing different points in time. The resulting reconstructed evolutionary histories of pathogen strains are then employed to investigate how diseases have spread across regions over centuries.

A paper published in the science journal *PLoS ONE* in 2019 demonstrates how aDNA operated as a mode of knowledge production in the case of old anthrax strains.[45] In the paper, microbiologist Vitalii Timofeev and colleagues compared anthrax samples from the Yamal Peninsula linked to the 2016 outbreak and three samples retrieved from permafrost in Yakutia, about 2,000 kilometers east of the Yamal region. In the Yakutia case, a mining-related excavation had led to an unexpected discovery of frozen cave lion remains, and soil samples collected from the discovery site were in a 2016 analysis shown to contain anthrax. However, the anthrax was not connected to the animal remains but was of younger, unknown origin. Three different anthrax strains were identified at the depth of 2, 3, and 4 meters in Yakutia. The genetic sequencing placed the oldest of the Yakutia samples (at the depth of 4 meters) in the same anthrax lineage—the B clade—as the Yamal samples, while indicating that the other two Yakutia samples (discovered closer to the surface) represented two different branches of another lineage—the A clade. Drawing on genetic differences between the samples, the authors suggest that “the third and most recent introduction [of anthrax in Yakutia], detected at minus two meters, occurred as a side effect of Russian conquests and development of agriculture after the 17th–18th century,” while “the second introduction detected at minus 2 and minus 3 meters, would be the byproduct of Yakut’s population migration from Lake Baikal area after the 14th–15th century.”[46] Regarding the oldest of the Yakutia strains, discovered at the depth of 4 meters, the authors propose that “the location in the permafrost and its genetic proximity with the strain independently found in the Yamal peninsula may indicate that it is not more than a few centuries older than the second introduction.”[47] Such a comparison of sequenced anthrax samples paints a picture of anthrax as multiple and mutable rather than single and fixed.

This kind of genetically derived knowledge is oriented toward the past in the sense that the sequenced strains were used to understand the coevolution of humans and pathogens. In this, it stands in contrast to the idea of past pathogens as lively entities threatening the future that characterized media responses to the 2016 outbreak. Yet, the boundary between a spontaneous outbreak caused by a past pathogen and the analysis of soil samples from an excavation site for genetic information is not clear-cut. The article by Timofeev and colleagues notes that the anthrax strains from the Yakutia excavation turned out to be virulent when tested on mice.[48] At the same time, the sequencing of the old anthrax strains makes visible that the material and digital are fundamentally entangled. The digitization of anthrax’s evolutionary trajectories is enabled through the material differences between strains and samples. Approaching past pathogens within a genetic framework relies, in other words, on vibrant materiality that engendered the differences in the first place. At the same time, the sequencing provides evidence of the material mutability of anthrax as a pathogen, which, instead of being an end point to a history, presumably constitutes a midpoint from where further microbial mutations may arise.

Finally, the comparison of sequences from the outbreak and an excavation site makes visible that the question of cryopreserved and potentially vibrant past pathogens not only is a matter of unexpected processes of thawing but also underlies archaeological and paleontological projects in regions characterized by permafrost. Archaeological or paleontological study of the past in melting ground, the case suggests, could potentially turn into an event that shapes health in the present and the future. Yet, as the rest of this chapter will show, the sequencing of the old anthrax strains differs from the sequencing of the 1918 pandemic virus. In the latter case, the sequence becomes part of a technoscientific project of recreating the past pathogen as a lively, material entity with the hope of proactively preventing death and disease in the future.

Reconstructing the 1918 Pandemic Influenza Virus

The reconstruction of the 1918 pandemic influenza virus illustrates what happens when the past pathogen is not alive but embodies a theoretical potentiality—that is, it cannot spontaneously cause disease but can still be manipulated to produce a live pathogen. Unlike the remarkably durable anthrax spores preserved in permafrost, influenza viruses require a host organism. The case also sheds light on the complex technoscientific apparatuses that are needed to translate a genetic sequence to vibrant biological matter.

The story of the discovery and reconstruction of the "Spanish Flu" pandemic influenza virus that killed some fifty million people in several waves in 1918–1919 is often portrayed as epitomizing how science may use knowledge about past epidemics to prevent future disease.[49] In 1951, Johan Hultin, then a PhD student at the University of Iowa, had an idea for his doctoral work: to search for a sample of the 1918 virus in a permafrost grave. He chose Brevig Mission, an Inuit community in Alaska, where seventy-two of the village's eighty adult inhabitants had died within only five days in November 1918. After gaining permission from the village community, excavation started, but the gathered samples did not contain retrievable and analyzable viral material. Over forty years later, in 1997, virologist Jeffery Taubenberger's team at the Armed Forces Institute of Pathology in Washington, DC, published an analysis of the 1918 virus collected from old lung samples from a US army hospital. As the genetic analysis still had significant gaps, Hultin again traveled to Brevig Mission for another attempt. He and the local team managed to retrieve viral material from the lungs of the frozen body of an Inuit woman. Permafrost had preserved the virus sufficiently to enable genetic sequencing by Jeffery Taubenberger, Ann Reid and their colleagues.[50]

Permafrost as nature's "freezer" operated quite differently in the 1918 pandemic case than in the 2016 anthrax incident. The viral genetic material did not threaten health directly (although researchers, of course, protected themselves to minimize that possibility). Instead, the "resurrection of the 1918 pandemic virus," as it was framed in journalistic discourse, required extensive technoscientific work.[51] First, Taubenberger and colleagues used RNA—ribonucleic acid, the genetic material present in viruses—from stored samples along with the naturally cryopreserved lung samples that Hultin had brought back from Alaska. This combination of different biological materials made it possible to sequence the full viral genome.[52] Second, microbiologist Peter Palese's lab in the Mount Sinai School in New York produced plasmids that contained the genetic components of the virus necessary for the reconstruction of the virus as a material, virulent entity. The plasmids were inserted into human kidney cells to generate the production of the virus by microbiologist Terrence Tumpey at the Centers for Disease Control and Prevention headquarters in Atlanta.[53]

The connection between genetic sequence, the materiality of the virus, and the ability of the virus to cause disease is, however, complicated. In a discussion of the reconstructed 1918 pandemic influenza virus, anthropologist Frédérick Keck notes that genetic knowledge does not translate directly to "life" in the sequencing of naturally cryopreserved past viruses.[54] That is, although DNA is commonly portrayed as the code of life, it cannot generate biological processes—new life, an infection—alone. Furthermore, while the recreated pandemic influenza virus turned out to be highly infectious in animal and tissue tests, it could not be assumed that infectiousness would translate directly to deadliness among humans. Tests designed to identify possible mechanisms behind the mortality of the 1918 pandemic suggested that multiple material features of the recreated virus shaped its virulence.[55] In an ethnographic study of pandemic preparedness, anthropologist Carlo Caduff documents Peter Palese's skepticism about the direct line drawn by politicians and the public between reconstructed sequences and lively pathogens.[56] Caduff observes that *information* about a sequence of a past pathogen has become seen as dangerous—a question of biothreat, even bioterrorism—although highly skilled craft work is needed to reassemble viruses as material, lively entities, and liveliness does not necessarily mean lethality. In fact, pandemic threat often emerges through mutations on a previously harmless virus. Caduff also notes that there is no such thing as *the* 1918 pandemic virus, as viruses are always present in multiple forms.[57] This question of representativeness of the sample is also at the heart of public debates about aDNA research more generally, as samples and datasets from past decades and centuries are always limited in scope.

The reconstruction of the 1918 pandemic virus as a material entity relied on reverse genetics. In reverse genetics, a genetic sequence is used to produce a lively entity through a range of advanced techniques. The sequence may be manipulated to test the effects of mutations on cells or organisms. In the case of the 1918 pandemic virus, reverse genetics generated an entity that had, at least in theory, the potential to threaten human life, had the engineered virus escaped the high-security lab. At the same time, this entity had the capacity, through its recreated vibrancy and ability to cause disease, to show *materially* how the pandemic virus operated, for example, in live lung tissue, a main concern in deadly cases of the 1918 pandemic influenza.

Crucially, the use of reverse genetics to recreate the influenza virus was commonly justified through a link to the prevention of future pandemics: gaining knowledge that would presumably help in responding to new viral strains in the future. For instance, Jeffery Taubenberger and colleagues noted in 2007 that “revealing the biology of a pandemic that occurred nearly 90 years ago is not just a historical exercise,” but something that “may well help us prepare for, and even prevent, the emergence of new pandemics in the 21st century and beyond.”[58] A popular article published in the *American History* magazine and included on the *HistoryNet* website echoes this culturally appealing rationale: “Deciphering how a particular virus operates opens up insights into other viral strains and reveals how they grow, mutate, jump from animal to animal, and attack their hosts. . . . Ideally, someday scientists will build on Hultin and Taubenberger’s work to uncover a genetic Achilles heel in one strain that makes it possible to wipe out all of them.”[59] These quotations point to the affectively charged nature of reconstructed pathogens as cultural objects poised between the past and the future. Their technologically recreated vibrant materiality is portrayed as a threat to futurity as well as a key to securing future health.

Indigenous Samples at the Crossroads of Pasts and Futures

As in the anthrax case, cultural discourses around the reconstruction of the pandemic virus drew on associations between permafrost, cold, and indigeneity. Many scientific and popular accounts carefully mention that Hultin received permission from the Inuit community in Brevig Mission for the excavations and the removal of biological samples.[60] Yet, the use of Inuit human remains places the case within the larger cultural politics and technoscientific histories in which Indigenous biological samples—blood, tissue, genetic sequences—become the sources of knowledge for what is viewed by many research institutions and policy makers as the "common good," the future health of humanity, a framing reflected, for example, in a media portrayal of the reconstruction of the 1918 virus as "a vital service to global public health."[61] What the benefits of the use of Indigenous samples might be for the local community is often unclear, as many scholars have shown.[62]

In their retrospective account of the excavations, Taubenberger, Hultin, and David Morens provide a striking description of the specific materialities that the case relied on. According to them, the fact that the Inuit woman buried in permafrost was obese provided the preconditions for the survival of viral material, as this likely "had preserved the internal organs from decomposition during occasional short periods of thawing within the permafrost. Her lungs displayed the gross appearance of those seen in acute viral pneumonitis, expanded and dark red in colour."[63] Several news stories highlighted Hultin's reconstructed moment of realization that the body in question was not only preserved by the cold but had also become a freezer for the virus.[64] The remains thus emerged as carrying unique physical characteristics as well as being embedded in communal practices such as preservation of land from construction projects. The annual melting patterns of permafrost, the interactions between a unique body and temperature, and the burial practices of the Inuit community enabled the retrieval and sequencing of the virus. This shows that the potential liveliness of past pathogens preserved in permafrost is neither an outcome of some general pattern of thawing nor the result of technoscientific study of generic biological matter.

At the same time, Brevig Mission, and the Inuit woman's unexpectedly preserved body, were embedded in broader cultural ideas of indigeneity, time, and temperature. Whereas the nomadic herders in Yamal were portrayed by some as threatening the proper separation of the past and the future through their herding practices, the perceived embeddedness of the Brevig Mission Inuit community in the past as well as in the cold emerged in popular discourse as a source of both potential future health and as a risk to the future. Such a cultural framing adds intensity to hopes, concerns, and wonder around the potentialities of past pathogens.

While indigeneity is part of the complex relations that led to the retrieval of viral samples in Brevig Mission, these material conditions largely disappear from view when the retrieved lung samples are taken to the genetics lab, sequenced, compared with genetic material from other sources, and used as part of a reconstructed virus. In this chain of technoscientific events, the distance between indigeneity and the virus that once killed so many in Brevig Mission grows step by step. When the origins of the sequence are mentioned, it is often present only in the technical name of the strain from the Brevig sample: the influenza A/Brevig Mission/1/18 (H1N1) virus.[65] Yet, despite this relative invisibility, indigeneity and the temporalities and cold temperature associated with indigeneity in cultural discourse manifest around the case as a sense that the recovered and reconstructed viral material embodies temporal, spatial, and cultural difference. The virus, like the Indigenous human remains in the grave, is portrayed as being "frozen in time."[66] As in the anthrax case, what that difference is remains vague, but it carries associations with the perceived insularity of communal practices and the popular assumption that indigeneity is past-oriented.

Conclusion

This chapter has traced the role of past pathogens and permafrost in contemporary society through two pathogens known to have caused life-threating illness in the past: anthrax and the 1918 pandemic influenza virus. There are crucial differences between them as material entities: while anthrax is a microbe preserved in spores, the pandemic influenza virus is known for its fast mutation rate and dependence on a host organism. These differences demonstrate how different types of pathogens, when emerging or retrieved from permafrost, may open up different trajectories between the past and the future. The perceived durability of anthrax spores through centuries posits it as an uncanny stranger that lies in wait in the frozen ground on which society, facing climate change, relies. The reconstructed pandemic influenza virus, in turn, raises cultural concerns about futures through images of biothreat as well as hopes of preventing future outbreaks through technoscientific manipulation. This ambivalence ties past pathogens affectively with both hopes and concerns about the future of society and the continuity of life as we know it. How past pathogens are framed as potentially viable and unpredictable entities and as sources of genetic information and engineering shapes what kinds of expectations become attached to the search for aDNA in melting ice. At the same time, the ways in which the two cases draw on slightly different constellations of permafrost, indigeneity, and space emphasizes that the potentially lively materiality of past pathogens is always historically and politically situated. These constellations also contribute to affective intensities in how past pathogens are perceived as unknown or knowable.

I opened the chapter by asking how old pathogens emerging or retrieved from permafrost complicate the popular understanding of aDNA as a straightforward link between the past and the present. The chapter has highlighted that at stake in aDNA discoveries is not just our relationship to the past but also the very parameters—narratives, discourses, concepts—through which futures can be imagined. Past pathogens such as anthrax and the 1918 influenza virus unsettle the culturally cherished separation of the past, present, and future, and make visible that this separation is an illusion. The cases also demonstrate that the connections between the past and the future invoked through aDNA are ultimately ambivalent, as the potential liveliness of old pathogens, cryopreserved in permafrost, can materialize as both a threat to and a promise of futurity. In the case of the pandemic influenza virus, these potentialities coexist, intensifying the affective stakes of aDNA as a cultural object. In both cases, affective intensities focus on the unpredictability of the future that may arise from the potential vitality of pathogens, whether that of a spontaneously thawing pathogen (anthrax) or a technoscientifically created entity (pandemic influenza). Critical explorations of this foundational ambivalence as to how the past and future are entangled will help broaden and complicate the ongoing discussion about the cultural role of aDNA.

Notes

1. Prominent examples of this framing of aDNA as a gateway to the past include geneticist David Reich's book *Who We Are and How We Got Here* (Oxford: Oxford University Press, 2018), and geneticist Adam Rutherford's book *A Brief History of Everyone Who Ever Lived: The Human Story Retold through Our Genes* (New York: The Experiment, 2017).

2. Some genetic ancestry testing companies advertise an option for tracing the customer's relationship to early hominins such as Neanderthals and Denisovans (e.g., 23andMe and ADNTRO). For an analysis of how ideas of historical populations are invoked and incorporated into contemporary identity discourse, see, for example, Marc Scully, Steven D. Brown, and Turi King, "Becoming a Viking: DNA Testing, Genetic Ancestry and Placeholder Identity," *Ethnic and Racial Studies* 39, no. 2 (2016): 162–180.

3. For the relationship between aDNA research and the media and society, see, for example, Elizabeth D. Jones and Elsbeth Bösl, "Ancient Human DNA: A History of Hype (Then and Now)," *Journal of Social Archaeology* 21, no. 2 (2021): 236–255.

4. Alondra Nelson, *The Social Life of DNA: Race, Reparations, and Reconciliation after the Genome* (Boston, MA: Beacon, 2016); Venla Oikkonen, *Population Genetics and Belonging: A Cultural Analysis of Genetic Ancestry* (London: Palgrave Macmillan, 2018); Kim TallBear, *Native American DNA: Tribal Belonging and the False Promise of Genetic Science* (Minneapolis: University of Minnesota Press, 2013); Anna Källén et al., "Introduction: Transcending the aDNA Revolution," *Journal of Social Archaeology* 21, no. 2 (2021): 149–156.

5. See, for example, Daniel Strand and Anna Källén, "I Am a Viking! DNA, Popular Culture and the Construction of Geneticized Identity," *New Genetics and Society* 40, no. 4 (2021): 520–540.

6. Amade M'charek, *The Human Genome Diversity Project: An Ethnography of Scientific Practice* (Cambridge: Cambridge University Press, 2005); Venla Oikkonen, "Entanglements of Time, Temperature, Technology, and Place in Ancient DNA Research: The Case of the Denisovan Hominin," *Science, Technology, & Human Values* 45, no. 6 (2020): 1119–1141. See also in this volume Marianne Sommer and Ruth Amstutz, chapter 2.

7. See Venla Oikkonen, "Conceptualizing Histories of Multispecies Entanglements: Ancient Pathogen Genomics and the Case of Borrelia Recurrentis," *Journal of Social Archaeology* 21, no. 2 (2021).

8. Venla Oikkonen, "Belonging: Population Genetics, National Imaginaries, and the Making of European Genes," in *Bringing the Nation Back In: Cosmopolitanism, Nationalism, and the Struggle to Define a New Politics*, ed. Mark Luccarelli, Rosario Forlenza, and Steven Colatrella (Albany: SUNY Press, 2020), 89–106; David Turnbull, "Out of the Glacier into the Freezer: Ötzi the Iceman's Disruptive Timings, Spacings, and Mobilities," in *Cryopolitics: Frozen Life in a Melting World*, ed. Joanna Radin and Emma Kowal (Cambridge, MA: MIT Press, 2017), 157–178.

9. Morten Rasmussen et al., "Ancient Human Genome Sequence of an Extinct Palaeo-Eskimo," *Nature* 463 no. 7282 (2010): 757–762.

10. Amr El-Sayed and Mohamed Kamel, "Future Threat from the Past," *Environmental Science and Pollution Research International* 28, no. 2 (2021): 1287–1291; Matthieu Legendre et al., "In-Depth Study of *Mollivirus sibericum*, a New 30,000-y-old Giant Virus Infecting *Acanthamoeba*," *PNAS* 112, no. 38 (2015): 5327–5335.

11. El-Sayed and Kamel, "Future Threat from the Past."

12. See, for example, Kimberley R. Miner et al., "Emergent Biogeochemical Risks from Arctic Permafrost Degradation," *Nature Climate Change* 11 (2021): 809–819.

13. Jasmin Fox-Skelly, "There Are Diseases Hidden in Ice, and They Are Waking Up," *BBC*, May 4, 2017, https://sustyvibes.org/uncategorized/diseases-hidden-ice-waking.

14. Kimberley R. Miner, Arwyn Edwards, and Charles Miller, "Deep Frozen Arctic Microbes Are Waking Up," *Scientific American*, November 20, 2020, https://www.scientificamerican.com/article/deep-frozen-arctic-microbes-are-waking-up/.

15. Michael Bravo and Gareth Rees, "Cryo-Politics: Environmental Security and the Future of Arctic Navigation," *Brown Journal of World Affairs* 13, no. 1 (2006): 205–215.

16. Emma Kowal and Joanna Radin, "Indigenous Biospecimen Collections and the Cryopolitics of Frozen Life," *Journal of Sociology* 51, no. 1 (2015): 63–80; Joanna Radin and Emma Kowal, "Introduction: The Politics of Low Temperature," in *Cryopolitics: Frozen Life in a Melting World*, ed. Radin and Kowal (Cambridge, MA: MIT Press, 2017), 3–26.

17. Radin and Kowal, "Introduction," 8.

18. Radin and Kowal, "Introduction," 8–9.

19. Hannah Landecker, *Culturing Life: How Cells Became Technologies* (Cambridge, MA: Harvard University Press, 2007); Bronwyn Parry, "Technologies of Immortality: The Brain on Ice," *Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences* 35, no. 2 (2004): 391–413; Joanna Radin, *Life on Ice: A History of New Uses for Cold Blood* (Chicago: University of Chicago Press, 2017); Lucy Van de Wiel, *Freezing Fertility: Oocyte Cryopreservation and the Gender Politics of Ageing* (New York: New York University Press, 2020); Risa Cromer, "Saving Embryos in Stem Cell Science and Embryo Adoption," *New Genetics and Society* 37, no. 4 (2018): 362–386; Rodney Harrison, "Freezing Seeds and Making Futures: Endangerment, Hope, Security, and Time in Agrobiodiversity Conservation Practices," *Culture, Agriculture, Food and the Environment* 39, no. 2 (2017): 80–89; Sara Peres, "Seed Banking as Cryopower: A Cryopolitical Account of the Work of the International Board of Plant Genetic Resources, 1973–1984," *Culture, Agriculture, Food and the Environment* 41, no. 2 (2019): 76–86.

20. Jennifer A. Hamilton, “Reindeer and Woolly Mammoths: The Imperial Transit of Frozen Meat from the North American Arctic,” in *Meat! A Transnational Analysis*, ed. Sushmita Chatterjee and Banu Subramaniam (Durham, NC: Duke University Press, 2021), 61–95.

21. Radin, *Life on Ice*; TallBear, *Native American DNA*.

22. Leena Cho, “Permafrost Politics: Toward a Relational Materiality and Design of Arctic Ground,” *Landscape Research* 46, no. 1 (2021): 26.

23. Cho, “Permafrost Politics,” 30.

24. Cho, “Permafrost Politics,” 30.

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4 Twisting Strings: Hopi Ancestors and Ancient DNA

Stewart B. Koyiyumptewa and Chip Colwell

Loloma, a Hopi leader of the Bear Clan (Honwungwa) from the Third Mesa village of Orayvi in Arizona who lived a century ago, used to compare the collision of Hopi and European cultures to that of a weaving made from different strands of cotton or wool. Loloma would take one string and say that this represents all the good things of Hopi peoples: a rich and beautiful homeland, a reciprocity system, industriousness, respectfulness, stewardship. Above all, humility. Then, he would take another string and say that this represents all the things of European people: education, technology, science.

Loloma would then twist the two strings together and ask why we can't see and adopt the good in both. When two strands are brought together as one, they become stronger. If the Hopi people can learn to do this—to bring the wisdom they have gained over millennia to Western ways of doing things—then they would be stronger people, twice as strong.

In this chapter, we consider two strands of knowledge about ancestry and ancestors. We explore Hopi concepts of ancestry and compare these traditions with the ways that paleogenetics constructs and makes definitive claims about Native American ancestry in ancient DNA studies.[1] Notably, the paleogenetics framing of ancestry captures only a fraction of Hopi conceptions of ancestry. Given that many Indigenous peoples hold similarly complex and expansive understandings of ancestry, we must seriously consider Loloma's question of whether these differences can be reconciled. We argue that if the field of paleogenetics is to speak meaningfully about the relations of Indigenous peoples, it needs to be woven much more tightly with Indigenous knowledge. Twisting Western scientific and Indigenous ways of knowing together will require geneticists to make a much stronger commitment to collaboration with descendant communities, to adopt more nuanced understandings of what it means to be related, and to leave behind their "molecular chauvinism"—the tendency to privilege genetic data as more trustworthy and accurate than other forms of knowledge.[2] While this may be challenging to achieve, what is at stake here is whether paleogenetics can truly offer the insights it claims, and whether Native peoples come to see paleogenetics as a tool of self-empowerment or a new weapon of colonial science.

The Ancestry Concept in Paleogenetics

Over the last fifteen years, the development of new laboratory techniques and DNA sequencing technologies has stimulated rapid advancements in the field of paleogenetics. Numerous studies have sought to reconstruct and describe the ancestry and population histories of peoples around the world, and aDNA studies have helped elucidate the genetic ancestries of present-day Indigenous groups and their ancestors in the Americas. While some scientists have celebrated paleogenetics as having the power to resolve questions about Indigenous ancestries and relations, it is critical to consider what kinds of ancestries and relations paleogenomic studies actually speak to, and what they do not.[3]

As a science based on the study of genetic material, paleogenetics provides insights only into genetic ancestries and biological relations. Researchers can trace a person's direct maternal ancestors and matrilineal relationships by sequencing and analyzing the maternally inherited mitochondrial DNA, and they can also assess the direct paternal ancestry and patrilineal relationships of anyone with a Y-chromosome (typically males). These methods of analysis can therefore shed light on the mother's mother's mother's . . . line and father's father's father's . . . line, respectively, but not on any other ancestral relationships. Nor do they tell us the exact degree of relatedness between two people: two individuals might share a specific mitochondrial DNA sequence and thus a matrilineal ancestor, but this analysis cannot say if that shared ancestor lived one or many generations ago.

Paleogeneticists can gain a broader picture of genetic ancestry and relatedness by analyzing variation in nuclear DNA, which is inherited from both parents, and assessing the extent of similarity or difference with other individuals. These analyses can detect the contributions from more ancestors, not just the direct maternal and direct paternal lines. They are capable of determining the degree of biological relatedness for very closely related individuals—they can, for example, identify a parent and child, or first cousins—based on the percentage of the nuclear genome that is shared between the two individuals and as long as a substantial amount of the genome can be sequenced. However, this degree of specificity breaks down with more distant relationships; in those cases, researchers can say only that an individual is more or less genetically similar to another individual or group of people.

Furthermore, it should be noted that even this single line of investigation in paleogenetics—tracing genetic relatedness—can be complicated and fraught with problems. Like genomics more generally, paleogenetics relies on comparisons with preexisting reference data (i.e., genomic data already collected from other populations) to infer and characterize the ancestry of newly studied individuals or communities. In other words, assessing the ancestry of these individuals or communities involves comparing their DNA to DNA from those who have been previously sampled, and evaluating which of the previously studied individuals or groups are most genetically similar. Researchers then infer that the newly studied individual or community belongs to, or shares ancestry with, the people(s) who are most genetically similar. Ancestry inferences therefore depend entirely on whose DNA happens to be in the comparative reference dataset. Descriptions and understandings of genetic ancestry can change when different reference groups are included in the comparison.[4] Because many communities are not represented in existing genetic databases, inferring genetic ancestry and relatedness must be understood as a relational science based on incomplete datasets.

It should also be noted, as cultural geographer Catherine Nash has pointed out, that genomic science is situated within broader social contexts.[5] Thus, even as genetic inferences are derived from biological evidence, they are made and interpreted within the powerful social frames of gender, nation, ethnicity, and race. These frames influence how individuals are grouped for comparative analysis and how those groups are named, which in turn influences our understanding of genetic ancestry and biological relatedness. For example, if individuals living in Paris and Berlin are to be included in a reference database for comparative genetic analyses, should they be grouped together and identified as "Europeans" or treated as separate populations? If the latter, should they be considered representative of the French and German peoples and named accordingly, or representative only of more local populations (e.g., north-central France and the North German Plain, or even just Paris and Berlin)? And if people who lived in these locations 5,000 years ago are also being included in the analysis, should they too be named according to present-day geopolitical boundaries or to the continental/racial categories that are deemed meaningful today? Should they be grouped together with the present-day inhabitants of these regions or considered separate populations by virtue of the temporal divide? These decisions will determine how genetic variation in Europe is categorized and represented in the analysis and thus how the genetic ancestry of any newly studied individual is identified and named if they share variants with any of these individuals or reference populations.

Furthermore, as Nash has argued, it is important to recognize that results from genetic tests and genetic studies don't merely *reflect* historical kinship ties, they also *generate* genetic kinships as people reimagine themselves as related through their DNA.[6] Kim TallBear, the scholar in Indigenous Peoples, Technoscience, and Society at the University of Alberta, has warned that this is a particular risk of genomic research for Native Americans, since technologies that claim to offer merely a biological map in fact have the power to rearrange and dictate social relationships in ways that may threaten tribal sovereignty. Claims of identity, belonging, and relatedness can all be altered and reconceptualized as a result of DNA testing.[7]

The science of genetic ancestry must therefore be understood not simply as an investigation of biological relatedness and how molecules are passed down from one generation to the next but as an endeavor that lies at the intersection of nature and culture, as it both shapes and is shaped by the social worlds in which we live.[8] Indeed, it would be misguided to suggest that paleogenetics merely purports to explain biological relationships, when nearly all aDNA research on the human past is driven by larger questions of human migration, kinship, interaction, health, and more—all of which are necessarily cultural and historical questions. This is why paleogeneticists often collaborate with archaeologists, historians, and other scholars in the social and human sciences (even though they rarely choose to include Indigenous peoples in their circle of collaborators).

In the context of aDNA studies, it seems clear that paleogenetics can reveal much about the genetic composition, biological histories, and genetic relations of past populations. However, we must be cognizant that there is often an overreliance on the "truths" that emerge from this biology-based research, without sufficient consideration being given to the many relevant sociocultural contexts that influence our inferences about genetic ancestry and how we apply and make use of those inferences. We must also keep in mind that paleogenetic inferences are limited to *genetic* ancestry—which, as we will see below, is significant when we consider Hopi ancestors. The Hopi trace their ancestry through both biological and social relations, as well as through experiences and interactions with nonhumans and places.

Hopi Ancestor Concepts

To understand Hopi culture and Hopi conceptions of ancestry, it is important to recognize that Hopi culture emerged gradually over thousands of years across the southwest of the United States, a vast region that the Hopi consider their historic homeland. About 1100 AD, different groups of ancient people began to converge on the Hopi Mesas in northeastern Arizona. For centuries, the Hopi people lived in adobe and stone village apartments, thriving as desert farmers. After US colonization, millions of acres were taken from the Hopi and given to the Navajo Nation and surrounding non-Native communities. Today, the Hopi Reservation lies in present-day northeastern Arizona and is home to nearly 15,000 tribal members. The Hopi Tribe is sovereign and federally recognized, composed of twelve villages on three distinct mesas (First Mesa, Second Mesa, and Third Mesa).

Hopi conceptions of ancestry include both social and biological components. Everything that came before an individual—all that was involved in the migration and survival of Hopi ancestors—factors into what it means to be Hopi. In other words, ancestry is not confined just to human relatives, but includes plants, animals, and landscapes. It can be traced through oral histories, places, and objects.

For paleogenetics to be better informed by Hopi knowledge and ancestry concepts, researchers must keep three key issues in mind: biology, material culture, and Hopi philosophy. Biology involves descent traced through matrilineal clan membership; here, paleogenetics can align. Material culture is understood through created items that people use to identify who they are; here, archaeology can align. Left out too often in the academic study of Hopi history, though, is the incorporation of Hopi philosophy about ancestors and ancestry.[9] Critically, for many Hopi people, their connections to the past go far beyond their genes or things, to incorporate the land itself, the world of spirits, and the practices that maintain ancestral connections.

Biology: Hopi Clans

Like geneticists, Hopis rely on biological connections in enacting ancestry and relations. Clan membership, which is necessary for knowing one's ancestry, is passed down matrilineally—meaning traced through the female line. While Hopi people recognize relations from both one's mother and father, matrilineal relations define clan membership. Blood relations can help trace ancestry, but those that come from the mother define Hopi social obligations, such as a person's roles in religious ceremonies. Thus, Hopi concepts in a way parallel how paleogeneticists trace biological descent through the mother's line (using maternally inherited mitochondrial DNA), father's line (using paternally inherited Y-chromosome DNA), and both parents (using biparentally inherited autosomal DNA). In particular, tracing biological descent through mitochondrial DNA parallels how the Hopi trace descent through matrilineal clans. While Hopi recognize the role of genetics, even if not always defined as such, not all biological relationships are equal.

Clans are groups of people who trace descent from a common original ancestor. Each Hopi clan has a *wuuya*, a totem or symbol derived from animals, plant, beings, or objects that played a significant role in the clan's founding. These totems emerged on each group's unique journey to Tuuwanasavi, the Earth Center of the Hopi Mesas, over thousands of years.[10] Clans are related and grouped in different ways, with some originating in the north (Motisinom) and some in the south (Nùutungkwisinom).[11] About nine hundred years ago, these clans began to coalesce on the Hopi Mesas. Each clan arrived at the Hopi Mesas bringing with it ritual knowledge or other benefits to contribute to the conglomeration of people that became the Hopisinom, the Hopi people.

It is important to distinguish this history from mere "myth," such as in Norse folklore, which may be seen as cosmological. While Hopi oral tradition definitively includes cosmological dimensions, it purports to track real events, including the movement of people across the landscape, ancestral villages and cultural landscapes, and kin relations.[12] Although some skeptics limited to Western Enlightenment philosophy and settler logics might insist that "real" history can be known only if it is written—a position that leads to the conclusion that Hopi history cannot have existed before the word "Hopi" was used by a Spanish colonial stenographer—such a viewpoint ignores the expansive research that demonstrates the truth value of traditional knowledge in general and Hopi traditional knowledge in particular.[13] Scientists gain little by assuming false dichotomies between myth/history and oral/written histories when seeking to illuminate the past and pathways of Indigenous peoples.[14]

Today, there are thirty-four clans among the Hopi people. A clan is a relatively fixed, matrilineal category. Although the Hopi people know both their biological parents' clans, it is the mother's clan that is the most significant. Hence, even if a child has a biological mother who is Hopi and a biological father who is not Hopi, the child is Hopi because they are part of a clan that is traced through their mother, grandmother, great-grandmother, and on. Conversely, a child whose biological father is Hopi and whose biological mother is non-Hopi is traditionally not recognized as Hopi, due to the strict matrilineal and clan responsibilities to the ceremonial calendar. A child with this lineage does not have or can never hold responsibilities of the clanship and the ceremonies that the clan holds to the overall village.

A Hopi person's clan membership defines many social roles and religious responsibilities in his or her life. Clans do not merely care for particular sacred objects, they also control particular areas for farming and traditional activities like gathering eagles.[15] One's clan is one's family. A mother's brother (a matrilineal uncle) can therefore be as important a figure in a child's life as their biological father. Clan membership brings with it a web of relations to people, places, and things, which serves as the rules and privileges of Hopi clans. While clan membership is highly important, Hopi identity and responsibilities are shaped by one's village, mesa, and broader membership to the Hopi Tribe.[16]

Because of the centrality of clans in the Hopi way of life, to say that an ancient person is a Hopi ancestor means that they were a member of a clan traced through the matriline. These are people who were on the millennia-long journey to the Hopi Mesas. All these ancestors contributed to the formation of Hopi culture. Wherever they fulfilled their life, it is because of them that the Hopi people have traditional lands across the southwest United States. Because of their sacrifices—in their search for the Hopi Mesas, clans faced many hardships, such as flooding, droughts, and war—when the Hopi people think of ancestors they first provide thanks. It is because of their ancestors that the Hopi people have a beautiful home, a rich language, powerful ceremonies, religious beliefs, and a profound philosophy. To be on the rural Hopi Mesas is to be a safe distance from the fast-paced life of cities. And to travel along clans' migration routes and to their traditional lands is to enter their spiritual realm, so that Hopi today can continue the work of protecting their heritage and continuing their way of life. While the description above may seem irrelevant to Hopi biological concepts of ancestry, it is important. It shows how the biological concept of clan membership feeds into the real, lived experiences of ancestral kin and their descendants and creates the emotional connection that the living have to those who passed, who made life today possible through their sacrifices.

While geneticists may be able to trace descent through the matriline (and patriline), as the Hopi people do, merely tracing one's descent in this way leaves out all of the most important dimensions of what clan membership means in lived experience. It is science without humanity. Knowing one's biological ancestors is only the beginning point for a sweeping, even all-consuming, sense of belonging and identity that defines everything from one's farming plot and one's potential marriage partners to one's religious duties.

Material Culture: Hopi Things

Like archaeologists, the Hopi people have had to create terms based on material culture to map onto specific regions and times—particularly as Hopi people have learned from archaeological science and have been forced to make claims for objects and lands required through federal laws such as the Native American Graves Protection and Repatriation Act.[17] The two main categories are the Motisinom and the Hisat.sinom. The Mostisinom is used to describe northern clans, but also refers to the "First People," and thus describes ancient people who lived in a way that predates the Pueblo lifestyle of corn agriculture and living in adobe and stone villages (i.e., groups that archaeologists would describe as hunter-gathering Paleoindians and Archaic people).[18] Once the southern clans migrated from Mexico or deeper into Mesoamerica, and the distinct Pueblo lifestyle emerged as they joined with the northern clans, all of these people became the Hisat.sinom, a person of the remote past or ancient times. In this framework, Hisat.sinom refers to nearly all people living in the southwest United States from about 2,000 years ago to the arrival of Spanish invaders in the mid-sixteenth century. Hopi cultural leaders use material evidence such as painted pottery, above-ground adobe or masonry architecture, and sites of particular ritual practices, such as the ceremonial chambers called kivas, to identify where and when their ancestors lived.

The development of terms like Motisinom and Hisat.sinom from material evidence of ancient peoples is perhaps possible for Hopis because their identities are often bound up with objects. According to Hopi cosmology, in the beginning, when the ancestors emerged onto this world—the Fourth World—they were met by a spirit-being named Màasaw, who told them they would go on a long journey to find the Earth Center. He gave these people the use of his land, seeds, a planting stick, and a water gourd—objects that would define the Hopi people as farmers and also serve as simple instruments that are symbols of the Hopi virtue of humility. When Hopi tribal representatives visit archaeological sites, they often pay attention to the artifacts found there as indicators of ancestral relationships. For instance, the intricate rain and cloud symbols found on pottery can be seen not only as resonating with the power of water as an ancestral lifeforce for the Hopi but also as indicators of the southern clans' migration after surviving a flooding event at a place/epoch (meaning that it is traditionally viewed as both a location and a period of time) called Palatkwapi.

Another example of how Hopis draw connections of identity through things is the famous black and white designs on mugs of the Ancestral Pueblo sites found in the Four Corners area (where Colorado, Utah, New Mexico, and Arizona meet). As an illustration, we might consider a recent consultation in which Hopi cultural advisors were examining artifacts from a museum collection. While surveying the collection, they found a mug similar to one that had been found at the ancestral region of Chaco Canyon. This particular collection came from the site of Cliff Shadow Springs, much closer to the Hopi Mesas and associated with the Badger Clan's migration to the mesas. This was thus interpreted as material evidence of the mug tradition arriving at the Hopi Mesas, and thus historically and spiritually interlinking the Hopi Mesas to Cliff Shadow Springs to Chaco Canyon to the Badger Clan. In other words, by seeing the same type of mug in three different places, the Hopi advisers understood the people in these places to be connected—though separated by hundreds of miles and perhaps by centuries—and having ancestral relations.

What is key to understand here is how Hopis traditionally use objects not merely as functional utensils but as emblems and expressions of identity. This holds true for everyday items like woven objects and pottery, which are made with stylistic choices that demarcate the mesa and even village where the maker comes from. It is also true for ritual objects, which are at the heart of clan identities. For example, when ancestral spirits known in English as

Katsina Friends come to visit the Hopis in ceremonies, they bring gifts for children. In the village of Hotvela, they bring bows and arrows for boys, whereas in the village of Soongopavi they bring "lightning sticks." On Third Mesa, girls receive wicker baskets, which they are given through the years until they are initiated, whereas on Second Mesa girls receive a coil basket at birth. Similarly, the size of ceremonial smoking pipes indicates which village these were made in.

What do these objects have to do with ancestry? Made through clan-based knowledge, they reflect the ancestral lineage and can be made only by the clans that own them—items are often even made with a clan symbol imprinted on them. Furthermore, in Hopi society, clans are organized around particular ritual objects and responsibility over specific ceremonies, which serve to substantiate their existence and claims. In this way, each clan's legitimacy is traced through the performance of rituals with its objects at the different places that the clan journeyed through on its way to the Hopi Mesas.[19] Without these clan objects, there would be no clans. And without clans, Hopi concepts of ancestry would collapse. Hopi clans structure ancestry, and Hopi clans are made through things.

Paleogenetics often relies on material culture markers when genetic and archaeological data are combined. Additionally, paleogenetics often uses "archaeological cultures" (in the American Southwest, cultures like Hohokam, Salado, and Ancestral Pueblo) as labels to define and analyze specific populations. This practice of creating contemporary labels for ancient people is shared by Hopis, as demonstrated by the terms Motisinom and Hisat.sinom. For Hopis, however, identity-based concepts of material culture go far beyond the material-based cultural labels that paleogeneticists borrow from archaeologists. For Hopis, direct ancestral lineages can be derived from material culture, such as mugs. Things are emblems of one's mesa and village, which are composed of ancestral groups. It is through things that clans are legitimized.

Philosophy: Hopi Life

It is also important to note that the Hopi people conceive of ancestry in far more radical ways, departing altogether from biological relatedness and material culture. For some Hopi, it is difficult to explain what the English word "ancestor" means, because for them it can mean everything. It can include the rock at your foot and as far as you can see on the horizon—the most distant trees. Hopis pray to everything. To clouds, animals, plants, insects. All of these are ancestors who have taken these physical forms to check on the Hopi people. When visiting ancestral places, Hopi traditionalists are keyed into the sudden gust of wind or the appearance of a rattlesnake.[20] These are not chance events but the immediate and purposeful presence of the ancestors.

How can an animal such an eagle be a relative? There is no term in English that reflects Hopi traditional belief about the transformation that takes place when a Hopi person completes their life on earth. In English, we often say someone "passes away," which implies that their being has ceased to exist or, in certain faiths, that their soul travels to another realm that can be experienced only in death. For Hopis, when someone passes, that is not the end. Their breath, spirit, and soul are still alive. And once a person enters that state, Hopis believe the breath can be transformed, to be connected both to the afterlife and to the life we live here on earth. For example, an ancestor's soul or breath can change into a snake or eagle, or even a plant. So when Hopis approach an ancestral site and see a snake or eagle, they might say, "Oh! That's our ancestor!" because of their ancestor's ability to change to an animal or a plant. That is why Hopis say ancestral sites are not abandoned—souls of ancestors still inhabit the place. To humans, such a place may look run down—often described as "ruins"—but the breath sees the place at its height. It sees people still there, living and cooking and doing everything people do. The eagle is the way the breath of ancestors can be known to us still in this domain. The living animal and the ancient place are the connection between our world and the spiritual world inhabited by ancestors. Hopis consider it a gift from the ancestors when they reveal themselves in these ways.

To think of ancestors for Hopi people is to think of the unseen hardships they endured to ensure their children's survival. They gave the Hopi people the tools to protect what little they have left in today's world. Traditional Hopi today are combating smartphones and job security and foreign religions with a gourd of water, seeds, and planting sticks. Given this struggle for cultural survival, it is amazing to many traditionalists that the Hopi people are still able to hold onto the ceremonies inherited from their ancestors. For Hopis, these social changes amid the persistence of culture are directly related to ancestry because Hopis see themselves today *in relation to* where they have been. Hopi traditionalists are often pivoting between questions of how to live today and how their ancestors choose to live in the past. They see themselves as inheritors of a beautiful legacy, which requires them to see their lives in the context of their ancestors' desires, the work their ancestors did to ensure that Hopi culture can survive.

Hopi people are always trying to appease their ancestors through good deeds. Ancestors are always present, always watching. They witness Hopi communal activities, such as ceremonies, watching to ensure that everything is done right. The Hopi people invite ancestors to come with their spiritual force, taking the form of rain and other blessings. The Hopi people are still committed to the covenant between the northern and southern clans, the agreement to cohabitate. Thus, when Hopis conduct religious ceremonies, so many of which pivot around this covenant, they are living the promises their ancestors made. These ceremonies are a key means for Hopis to link themselves to the people who created this path forward; they are reaffirming constantly their ancestry relationships, which although they are given through clan membership must constantly be affirmed through their actions (such as farming and ceremonies).

This philosophy and understanding of ancestry extend far beyond the data that can be derived from DNA. Yet, if Hopi perspectives are to be brought into conversation with paleogenetics, they are relevant. Currently, however, paleogenomic analysis is rarely able to contend with such an expansive concept of ancestry. Although Hopis may see an eagle or snake as a clan relative, this is not a genetic claim, but a spiritual and metaphysical one. "Ancestry" in Hopi culture is thereby not a simple matter of genealogy or identifying a group of distinct artifacts. It involves the profound sacrifices of generations of people who are still present.

The Hopi concept of ancestry thus differs radically from the concept as it is conceived in the English-language definition. In the sense of Euro-American Enlightenment philosophy, ancestors are those who came before—those who are past. But for Hopis, ancestors both gave birth to those who followed *and* continue to be a part of their lives today. For the Hopi people, ancestors are alive.

The Risks of Ancient DNA

As we have shown, ancestry concepts in paleogenetics and Hopi tradition are often distinct, but at times they overlap. Inspired by Loloma's description of two worlds coming together, we therefore want to ask whether Hopis may see paleogenetics as a tool of self-empowerment or a new weapon of colonial science. The point here is to explore whether, with these varying concepts of ancestry, settler paleogenetics and Hopi culture hold irreconcilable viewpoints or whether there is an opportunity still for connections to be made. This exploration is necessary, as the Hopi Tribe has made clear that it is not antiscience. Rather, it wants scientific work—including genetics—to be done, but in a way that is respectful and does not replicate past harms. Many geneticists are also interested in working with Indigenous peoples—including Hopis—but may be uncertain how to bring together different worldviews and values. Understanding these different conceptions of ancestors is critical if researchers and Indigenous people are to braid Indigenous culture and paleogenetics together in a way that is meaningful and useful.

In recent years, some researchers have come to the Hopi Cultural Preservation Office—the tribe's central office related to cultural matters—to propose collaborative aDNA projects. When the advisory committee of tribal elders—the Hopi cultural resources advisory task team, a representative group of Hopi elders and experts who advise the tribal government on cultural matters—evaluated these proposals, it tended to be split about 50/50, though in some cases it allowed projects to go forward. For example, the committee recently issued a permit to a PhD student to study coprolites. People are interested in knowing more about what their ancestors ate, what their health was like, and whether lifespans have changed through the years.

However, one project that proposed studying DNA drawn from women's menstrual aprons was intensely debated. Some were interested to know what could be learned, but other members of the task team thought such a study would go against tradition and worried that any diseases in the aprons might resurface if studied. Also, given the history of scientists using genetic data for their own purposes, there was a strong mistrust of what might happen with that information. Could it be used somehow to harm Hopi people or question Hopi land claims? Could any information that challenges Hopi traditional history trickle up to the US government and be used to fight Hopi histories about being the first tribes in their homeland?

As noted above, the Hopi people are not antiscience. Rather, they are realistic about how science can be used to violate the rights and dignity of Native Americans. Hence, they are often struggling to balance a genuine interest in preserving and understanding their heritage while protecting their small reservation, modest political capital, and precarious way of life.

Since at least the late nineteenth century, Hopi leaders have faced constant encroachment on their homeland and a loss of control over their heritage sites. This encroachment does not impact only the general sense of wellbeing and concrete practices, such as the ability to gather plants, minerals, and animals needed for ceremonies, but also access to shrines that are located outside the Hopi reservation. The Hopi Tribe is small with minimal resources, and the surrounding American society is constantly looking to extract resources from the land. While the encroachment has often been led by Euro-American colonizers and settlers, conflicts with other tribes also pose challenges for the Hopis' ancestral claims. When other tribes claim ancestry—and thus rights—to particular ancient people, such as those at Chaco Canyon,[21] it becomes an existential crisis for the Hopi people. As a result, Hopis are put in the position of having to not only carefully manage their ancestral claims to people and sites, but also to concern themselves with the possible encroachments of the ancestral claims of other Indigenous groups.

This situation is metaphorically embodied in a Third Mesa rattle. This instrument is made from a hollowed gourd, with its large head painted. In the center is a green migration symbol with white clouds around it. Red color engulfs these symbols. The migration symbol represents the ancestral migration and the settling of the Earth Center. The clouds are the ancestors protecting this place. The red is all the dangerous ideas, harmful projects, and chaos that the US government has caused. The homeland is surrounded by turmoil, with the "footprints" of Hopi history constantly under threat. With each development project, with each ancestral archaeological site that is destroyed, Hopis lose a part of the track that they use to trace and affirm their clan ancestry—the evidence that the Hopi ancestors were the first people to dwell in this place. With each erased footprint, Euro-American colonizers and settlers come closer to their goal of assimilating the Hopi people and supplanting Hopi ideas with European ones.

While geneticists in a lab in Cambridge (Massachusetts or England) may feel that these issues are unrelated and distant to their work, for the Hopi there is an intimate connection. The goal for Hopi traditionalists is to cohabit with the natural environment and their ancestors who have passed on and come back in the form of rain, animals, insects, and wind. If paleogenetics operates as an extractive industry, it threatens to create disorder and risks erasing ancestral footprints more than restoring them.

From a Hopi perspective, science is too often all data and numbers. It is not human. It does not address or capture how real people—the Hopi people and their ancestors—interact to build intricate relations across time and space. Without a more relations-oriented science, paleogeneticists are just extracting DNA. Indeed, most genetic and archaeological work on Hopi ancestors has been conducted without Hopi participation or input and published in academic journals and books that are not accessible to nonacademics, including most members of the Hopi Tribe. More collaboration and engagement are clearly needed. If paleogeneticists wish to avoid perpetuating harm to Indigenous communities and produce science that reflects the realities of those who have a stake in their work, they must first recognize the damage of failing to include descendant communities and their ancestry concepts in this work. Like Loloma, scientists interested in Hopi ancestry would do well to twist the two strands of Hopi culture and settler science together.

Many Hopi people ask: “Why destroy ancestors’ bones to extract DNA?” or: “What is the benefit to the Hopi people?” Currently, many aDNA studies are little more than a new form of describing cultural history—tracking migrations, mapping how populations interacted or not, constructing regional population profiles. For a tribe like the Hopi, who know their migration history—indeed whose migration history is at the center of their lived identities—there is perhaps little that genomics can add regarding those topics. If geneticists and archaeologists proceed with aDNA research simply because they want answers to *their* questions without regard for what Hopi already know, they engage in a form of biocolonialism in which Native biological heritage is extracted for the researchers’ own benefit (e.g., grants, tenure, high-profile publications in *Nature* and *Science*). Such work is not about seeking benefits for the Hopi people from their own history but an externally imposed science for the benefit of non-Hopi people.

Some Hopi are also skeptical of what paleogenetics may suggest regarding the relationships between ancient people and people today, especially since Hopis have long been shaped by marriages and other interactions with people from other tribes and, later, Europeans. Navajos, Utes, and Apaches were infamous among Hopis as raiders, stealing Pueblo women for many centuries. Spanish, Mexican, and American soldiers often took women, too. Because of this history, there is, sadly, a tension in Hopi villages about the degree to which these non-Hopi genetic influences are present. Some are concerned that genetic research that identifies individuals with non-Hopi ancestors could be stigmatizing. These Hopi suggest that if scientists want to trace Hopi ancestors, they would do better to focus on communal systems and material culture, which may have clearer continuities.

To date, Hopis have largely seen genetics cause only harm to Native communities. They can point to a number of controversies, such as the Havasupai battle over misused blood samples—an example of the exploitation of Native genomes for medical research.[22] US museums and federal agencies still hold the remains of more than 100,000 Native American ancestors, including massacre victims and many others taken without the consent of descendant communities.[23] There is also the twenty-year battle over the Ancient One, in which archaeologists fought tooth and nail over—and conducted an extensive research project on—the remains of a 9,300-year-old man.[24] "They're going to use our blood" is a thought and fear echoing in many Hopi heads. It is therefore often thought safest to refuse proposed scientific projects.

In the metaphor of the rattle, paleogenetics lies, for now, mostly within the red. DNA cannot illuminate Hopi ancestry and history as much as paleogeneticists hope it will.

Conclusion

Paleogenetics has positioned itself as a powerful apparatus for elucidating and characterizing the ancestry of Indigenous peoples like the Hopi. However, the disconnects between settler scientific and Indigenous concepts of ancestry are often substantial. For example, where paleogeneticists think solely about genetic relationships and characterize ancestry and descent in strictly biological terms, the Hopi trace ancestry through both social and biological relations—with matrilineal relationships mattering most—as well as through their experiences and interactions with plants, animals, and landscapes. As we have shown, the Hopi concept of ancestry encompasses much more than genealogy, and ancestors are not simply those who lived in the past.

Many Indigenous peoples hold similar expansive views of ancestry, and have quite extensive knowledge of their ancestors. Such knowledge does not rely on paleogenetics. In many cases, paleogenomic research has only "confirmed" what Indigenous peoples already knew. For example, in several cases across the United States and Canada, where aDNA research has served to support the repatriation of ancestors and to advance tribal recognition by establishing genetic links between descendant communities and the ancestors, the concerned tribes had already known these links before any genetic testing.[25] In such cases, aDNA research simply upholds already known relations. It is perhaps telling that while paleogenetics has proved critical to the successful repatriation of ancestors, it is because DNA has played an important role in convincing outsiders of an ancestor-descendant relationship. For the Indigenous communities themselves, however, aDNA has not provided any new information about their ancestry. In one recent case where geneticists revealed a matrilineal linage between individuals buried at Pueblo Bonito in Chaco Canyon, this knowledge was already held by the Hopi Tribe, who, as noted above, maintain an ancestral connection with Chaco Canyon.[26] The authors of the paper themselves cited ethnographic evidence of matrilineal descent, demonstrating that tribes held knowledge prior to the study. This provides yet further evidence that ancestry knowledge produced by paleogenetics is often redundant.

The current landscape of paleogenetics is one in which many researchers do not engage in any significant way with descendant communities and their ways of knowing ancestry. This lack of engagement has hindered paleogenomic studies to offer meaningful contributions in the eyes of Indigenous people. If scientists are to provide more valuable insights about Indigenous ancestry and ancestors, they must be better informed by the concepts of ancestry and knowledge of ancestors held by Indigenous peoples in the area being studied. More broadly, for aDNA studies to accurately describe and interpret the relations of Indigenous peoples, researchers in the field need to make a much more serious commitment to collaboration with Indigenous communities and to building a much more nuanced understanding of what it means to be related. Given that paleogenetics is a historical science and cares deeply about history and the lived past experiences of people, it should seriously seek ways to consider the full range of historical experience rather than reduce history merely to biology.

A call for collaboration between scientists and Indigenous communities is one possible way forward for paleogenetics, especially when descendant communities desire a collaborative project. But we must also confront the reality that many paleogeneticists are not trained in anthropology, know little to nothing of Indigenous cultures or political rights, and may in fact care little about the Indigenous peoples they study. As one reviewer of this chapter made plain: to some, Indigenous peoples are little more than fascinating pieces of a biological puzzle they are trying to put together. When scholars are so indifferent or even antagonistic to Native worldviews and traditions, these perspectives will be irreconcilable. Such scientists should not study Native American history or culture.

Additionally, there may be cases in which paleogenomic research is unnecessary and in fact detrimental to Indigenous sovereignties. When undertaking a study, paleogeneticists must ask themselves if their projects concerning Indigenous ancestors have any meaningful input and direction for descendant communities. If not, paleogenetics runs the risk of undermining Indigenous peoples' self-determination and ability to make definitive claims about their ancestors, especially when settler science continues to occupy the authoritative role in knowledge production. In such cases, collaboration is not enough; it would not even be genuinely possible.

When Loloma spoke of the metaphor of twisted strings, he was trying to convince his council to accept all the good things of Hopi ways as well as the new intrusions of technology and Euro-American ways of thinking. Importantly, he hoped that his people could put together these different ways into one, for the benefit of the Hopi people, so they could move forward. He was likely referencing introduced foods like peaches and possibly new farming techniques like the plow. Loloma was a visionary who thought that if Hopi children learned the ways of Euro-Americans, they could be the tribe's eyes and voice and not being duped by the invaders. Loloma and other Hopi leaders of the time knew the military might of the US government. They knew they were surrounded and outnumbered. They knew about the massacres and other violence wrecked upon Native peoples. Loloma was trying to lessen these threats by accepting the good that was brought to the Hopi, to embrace new ideas to see if they worked. If they did, the Hopi people would be twice as strong.

Loloma's wisdom speaks to two key conditions that guide decisions about the tribe's willingness to work in collaboration with scientists such as paleogeneticists. The first is that Hopis are willing to collaborate, but only if there are benefits to their community. When scientists are out for only their own interests, there is no basis for collaboration. Hopis feel that such work should not be done at all on their ancestors. Hopi cultural advisers repeatedly emphasize that they are not willing to allow their ancestors to serve as some geneticist's sample or as the playthings of scientists who know little or care little about Hopi people. There has already been enough damage done to Hopi ancestors in the name of science. Work can proceed on their ancestors only on the basis of genuine mutual respect and benefit sharing.

The second condition is related to the fact that Loloma understood the gulf of power that existed between his small tribe and the surrounding Euro-American culture. He perceived that he could not stop the invaders, just as Hopis today know they have no true legal or other means to stop the most powerful genetics labs and museums in the world. Their only option for survival is to find ways to partner with those who are willing to be sincere friends, and publicly object to the work of those who are not.

What Loloma knew was that the strings of knowledge can be twisted together, but they can also be pulled apart. It remains to be seen how well the strands of Indigenous knowledge and paleogenetics can be twisted together.

Notes

1. In this chapter, we use "paleogenetics" or "paleogenomics" to describe the disciplinary field of ancient DNA (aDNA) studies.

2. K. Ann Horsburgh, "Molecular Anthropology: The Judicial Use of Genetic Data in Archaeology," *Journal of Archaeological Science* 56 (2015): 141–145.

3. David Reich, *Who We Are and How We Got Here: Ancient DNA and the New Science of the Human Past* (Oxford: Oxford University Press, 2018).

4. Kim TallBear, "Genomic Articulations of Indigeneity," *Social Studies of Science* 43, no. 4 (2013): 509–533.

5. Catherine Nash, "Genetic Kinship," *Cultural Studies* 18, no. 1 (2004): 1–33.

6. Catherine Nash, *Genetic Geographies: The Trouble with Ancestry* (Minneapolis: University of Minnesota Press, 2015).

7. Kim TallBear, *Native American DNA: Tribal Belonging and the False Promise of Genetic Science* (Minneapolis: University of Minnesota Press, 2013).

8. Marianne Sommer, *History Within: The Science, Culture, and Politics of Bones, Organisms, and Molecules* (Chicago: University of Chicago Press, 2016).

9. Leigh J. Kuwanwisiwma, T. J. Ferguson, and Chip Colwell, eds., *Footprints of Hopi History: Hopihiniwtiput Kukveni'at* (Tucson: University of Arizona Press, 2018).

10. Tuuwanasavi is a cosmological concept that situates the Hopi Mesas as the center of the world and universe.

11. Wesley Bernardini, "North, South, Center: An Outline of Hopi Ethnogenesis," in *Religious Transformation in the Late Pre-Hispanic Pueblo World*, ed. Donna M. Glowacki

and Scott Van Keuren (Tucson: University of Arizona Press, 2011), 196–220; Thomas E. Sheridan et al., eds., *Moquis and Kastiilam: Hopis, Spaniards, and the Trauma of History*, vol. 2 (Tucson: University of Arizona Press, 2020).

12. Wesley Bernardini et al., *Becoming Hopi: A History* (Tucson: University of Arizona Press, 2021).

13. Wesley Bernardini, *Hopi Oral Tradition and the Archaeology of Identity* (Tucson: University of Arizona Press, 2005); Paulette F. C. Steeves, *The Indigenous Paleolithic of the Western Hemisphere* (Lincoln: University of Nebraska Press, 2021); Jan Vansina, *Oral Tradition as History* (Madison: University of Wisconsin Press, 1985).

14. David Hurst Thomas, "A Shoshonean Prayerstone Hypothesis: Ritual Cartographies of Great Basin Incised Stones," *American Antiquity* 84, no. 1 (2019): 1–25; Peter M. Whiteley, "Archaeology and Oral Tradition: The Scientific Importance of Dialogue," *American Antiquity* 67, no. 3 (2002): 405–415.

15. Jesse Walter Fewkes, "Property-Right in Eagles among the Hopi," *American Anthropologist* 2, no. 4 (1900): 690–707.

16. Mischa Titiev, "Old Oraibi: A Study of the Hopi Indians of Third Mesa," *Papers of the Peabody Museum of American Archaeology and Ethnology* 22, no. 1 (1944).

17. T. J. Ferguson, ed., *Yep Hisat Hoopoq'yaqam Yeesiwa (Hopi Ancestors Were Once Here): Hopi-Hohokam Cultural Affiliation Study* (Kykotsmovi: Hopi Cultural Preservation Office, 2003).

18. T. J. Ferguson and Chip Colwell-Chanthaphonh, *History Is in the Land: Multivocal Tribal Traditions in Arizona's San Pedro Valley* (Tucson: University of Arizona Press, 2006).

19. Wesley Bernardini, "Identity as History: Hopi Clans and the Curation of Oral Tradition," *Journal of Anthropological Research* 64, no. 4 (2008): 483–509.

20. Stewart B. Koyiyumptewa and Chip Colwell-Chanthaphonh, "The Past Is Now: Hopi Connections to Ancient Times and Places," in *Movement, Connectivity, and Landscape Change in the Ancient Southwest: Proceedings of the Southwest Symposium*, ed. Margaret C. Nelson and Colleen Strawhacker (Boulder: University Press of Colorado, 2011), 443–455.

21. The Hopi people and other Pueblo tribes see sites such as Chaco Canyon as ancestral to them, while the Navajo Nation—the largest tribe in the United States, with a reservation that entirely surrounds the Hopi Reservation—also claims affiliation to it.

22. Nanibaa' A. Garrison, "Genomic Justice for Native Americans: Impact of the Havasupai Case on Genetic Research," *Science, Technology and Human Values* 38, no. 2 (2013): 201–223.

23. Chip Colwell, *Plundered Skulls and Stolen Spirits: Inside the Fight to Reclaim Native America's Culture*. (Chicago: University of Chicago Press, 2017).

24. Armand Minthorn, "Bringing the Ancient One Home: Genetic Data and the Case for Repatriation Kennewick Man," in *DNA and Indigeneity: The Changing Role of Genetics in Indigenous Rights, Tribal Belonging, and Repatriation*, ed. Alexa Walker, Brian Egan, and George Nicholas (Burnaby, BC: Simon Fraser University, 2015), 10–12.

25. For some of these cases, see Joanne L. Wright et al., "Ancient Nuclear Genomes Enable Repatriation of Indigenous Human Remains," *Science Advances* 12, no. 4 (2018): 1–12; Alissa L. Severson et al., "Ancient and Modern Genomics of the Ohlone Indigenous Population of California," *Proceedings of the National Academy of Sciences* 119, no. 13 (2022): 1–10.

26. Douglas J. Kennett et al., "Archaeogenomic Evidence Reveals Prehistoric Matrilineal Dynasty," *Nature Communications* 8, no. 14115 (2017): 1–9; Amanda Daniela Cortez et al., "An Ethical Crisis in Ancient DNA Research: Insights from the Chaco Canyon Controversy as a Case Study," *Journal of Social Archaeology* 21, no. 2 (2021): 157–178.

5 Whitewashing the Neanderthal: Doing Time with Ancient DNA

Amade M’charek

In the summer of 2016, I was with my family in France, where we visited the National Museum of Prehistory in Les Eyzies.[1] At the entrance, I was struck by a reconstruction of an adult Neanderthal man and a child (figure 5.1). Both were sitting on the floor in scenery that gave the impression of a father and a son talking to each other about the things of life. As I was studying this scene, I started to realize how it evoked a sense of proximity rather than distance, and familiarity instead of strangeness. Perhaps this was due to the fact that the reconstructions cast the Neanderthal as scarcely haired and as almost transparently white.

Slowly, it dawned on me that ancient DNA research had started to do its job. With the discovery of our genetic relationship with this hominid group, the Neanderthal, traditionally depicted as brutal, dumb, darkish, heavily furred, and often ape-like, has become portrayed as a human, even European. At the Neanderthal Museum in the German town of Mettmann, we can even admire the Neanderthal in a suit in a display called “Meet Mr. 4%” (figure 5.2).[2] Seeing him in this CEO-like outfit, one is tempted to think his Tesla is parked just outside the museum.

It seems that as an effect of aDNA, the Neanderthal and its relation to humans has radically changed, from the apelike appearance described by French paleontologist Marcellin Boule and depicted by Czech artist Frank Kupta (figure 5.3) at the beginning of the twentieth century to a contemporary white man, a relative.[3] These depictions make visible to the naked eye how the Neanderthal has been drawn into a racial politics.

To be sure, I see value in the way such reconstructions manage to generate attention from a broad audience. Evoking curiosity and familiarity is an interesting way of engaging a public with the past and the results of scientific

Figure 5.1
Author studying the Neanderthal reconstructions in the Musée National de Préhistoire, Les Eyzies, France.

inquiry. But these reconstructions are not neutral. The niceness of the Neanderthal, and the way this hominin group is embraced and drawn into our family, are troubling. By highlighting similarities, the Neanderthal is made part of an *us-ness* which stands in contrast to conventional depictions of the Neanderthal as alien. Through this change of appearance—the whitening and acculturalization of the Neanderthal, as well as the assumed genetic relatedness—a *sameness* is produced. Moreover, in this way, the Neanderthal is made part of one single story in which everything is subsumed into a European linear temporality where “we” are located at the end, as the crown of evolution.

The Danger of a Single Story

In her famous TED Talk “The Danger of a Single Story,” Nigerian writer Chimamanda Ngozi Adichie unravels the politics of homogenizing narratives, in particular Eurocentric stories about certain people, and their lives and cultures, in places far off the Center. This is a politics that reduces Europe’s other to one single identity, a stereotype. “The single story creates stereotypes, and

Figure 5.2
Mr. 4% at the Neanderthal Museum in Mettmann, Germany.

the problem with stereotypes is not that they are untrue, but that they are incomplete," Adichie says. "They make one story become the only story."[4]

Here, I would like to add that single stories tend to rely on a particular rendering of time—a linear modernist time axis on which events and especially people and their various kinds can be ordered.[5] At the end of the line, "the now," in the words of Homi Bhabha, there is us, the West, Europe.[6] European man. The line means that complexities are subsumed in favor of progressive development, that is, all entities of humans and nonhumans develop and move according to one single tempo and can be located at different points on the line. So it naturalizes time as a given, rather than an effect.[7] But it also naturalizes relations and our narratives of those relations. When I arrived in

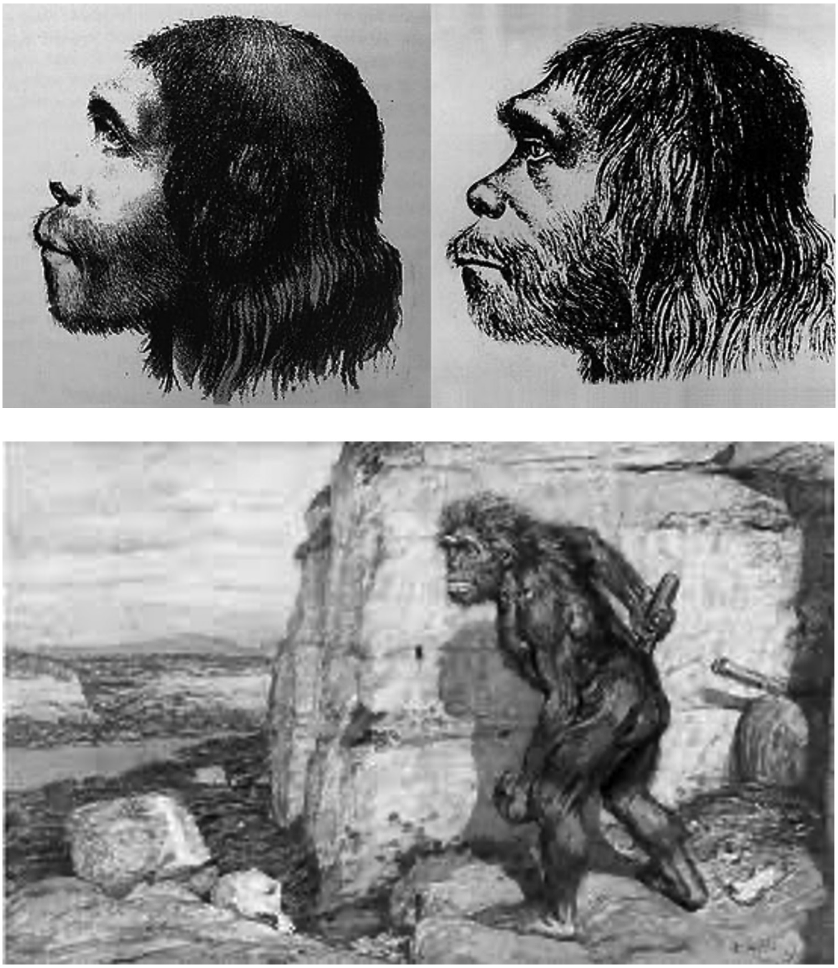

Figure 5.3
The Neanderthal as depicted (a) by German paleoanthropologist Hermann Schaaffhausen in 1876/1888, and (b) by Czech artist Frank Kupta in 1909.

the Netherlands as a young girl—an immigrant daughter eleven years old—I was asked in school where I was from. "Tunisia," I said. "Ah, Tunisia, you are fifty years behind, then," my schoolteacher responded. Although I was there with my classmates, I was actually fifty years behind them.

This is the trouble that I address in this chapter. It is concerned with time and temporalities in relation to race, through the case of the Neanderthal. I will proceed in three steps. First, I take you to the lab where we will attend to laboratory practice and how the genetic study of the Neanderthal started to take shape. Second, I elaborate theoretically on my analysis of race in relation to time as well as to sameness and resemblance. Finally, I analyze a postcard featuring a reconstruction of the "the human family," organized more or less around the Neanderthal. Here, I will use the postcard to elaborate on the cultural effect of genetic knowledge in relation to race.

Encountering the Neanderthal in the Lab

It is November 14, 1996, and we are at the laboratory for evolution and human genetics in Munich, the former lab of Swedish geneticist Svante Pääbo. That morning I entered the lab, where I had my bench.[8] I had already put my coat and bag in the locker down the hall, had a quick look at my lab journal to recall the experiments that I had planned for that day, and went to get myself a cup of coffee. As usual, I walked through the small writing room, situated between the lab and the so called "tea room." I noticed champagne glasses, empty bottles, packs of cigarettes, and full ashtrays all scattered about the long writing desk. The cigarettes especially drew my attention. For people may have dinner in the lab, or sleep in the lab, but smoking in the lab? That just never happened. A colleague came in and asked me whether I had heard about Matthias Krings, one of the population geneticists working in the lab. There had been a party last night, she told me, because Krings had sequenced the Neanderthal for the second time and found the same mitochondrial DNA sequence.

I became aware of Matthias's absence. Normally, he would be working day and night. My colleague went on telling me about the excitement of the event and described how Krings and Ralf Schmitz, the curator of the Landesmuseum in Bonn, who had made the Neanderthal bones available, were looking attentively at the computer screen while the gel was run on the so-called ALF (automated laser fluorescent) sequencer.[9] As the data became visible, the sequence turned out to be the same as the previous one that Matthias had found. This indicated that they were looking at the first ever mitochondrial DNA sequence of a Neanderthal. They called Svante, who rushed back to the lab. After this, they decided to have a small party.

This was for many reasons a moment worth celebrating. First, obtaining hominin DNA from 40,000-year-old fossilized bones is already a challenge. To then go on and map the DNA is a true technical feat. The problem with ancient DNA is that it is often degraded, for example because it is cut into small pieces by bacteria that seize organisms from the moment of death. So, in practice, researchers usually find the DNA of these bacteria or, through contamination, the DNA of modern humans, like the researchers', or anyone else who has been in contact with the material. The problem of contamination was a greater problem in 1996, since when techniques have emerged to identify contaminants and remove their sequence data.

For that reason, the success of Matthias and Svante was indeed a milestone in ancient DNA research. This achievement and what followed have contributed crucially to the emerging field of aDNA research.

The mitochondrial DNA sequence was eventually published in 1997 in the journal *Cell*.[10] Based on comparisons between Neanderthal DNA and various contemporary European, Asian, and African populations, it was found that the Neanderthal differed from all modern humans, indicating that the two groups had not interbred.

In those days, when I was in Svante's lab, I was interested in biases and normativities of the human mitochondrial DNA reference sequence that had been produced in Cambridge in 1981. I was asking questions such as: Whose DNA was used to produce the sequence? How and where was it done? And why it was seen as a European sequence?[11] During one of the population group meetings, we discussed these biases. Svante indicated that it would not be possible to avoid a kind of optical bias, because the reference sequence would always be closer (and thus more similar) to one population than another (depending on whose material was used for sequencing the reference sequence). And he added jokingly: "It might be a good idea though to start using the Neanderthal sequence as the new reference. It is equally far away from all humans."

Almost ten years earlier, in 1987, the field of genetics had produced another sensation. *Nature* published the startling paper "Mitochondrial DNA and Human Evolution," which provided genetic evidence for the hypothesis of a single origin of all humans and demonstrated that this origin was in Africa. It thus confirmed the out-of-Africa theory of human origin.[12] Based on the analysis of the mitochondrial DNA of 147 individuals—quite an achievement at the time—the paper showed that genetic diversity was higher among African populations than among populations living in other parts of the world.[13] The tantalizing conclusion was thus that the mitochondrial DNA of modern humans can be traced back to one common ancestor who lived about 200,000 years ago. Paradoxically, notwithstanding the conflict between biblical and evolutionary time scales, in an accompanying editorial of the journal this ancestor was referred to as Mitochondrial Eve: an interesting double anachronism, or simply an "irony" in the sense that contradictory things necessarily go together.[14] The researchers behind the study, Alan Wilson and his team at Berkeley, were taken by surprise when they found themselves in a media frenzy because their research immediately became part of a debate about the (non)existence of racial groups.[15] The Mitochondrial Eve paper provided the genetic arguments as to why the idea of biological races is untenable and therefore provoked controversy with paleontologists.

The then prevailing theory in paleontology was that the origins of early humans went back much further in time. According to the so-called candelabra theory, it was one million years, whereas other multiregionalist scientists estimated the migration out of Africa to have happened two million years ago.[16] According to these theories, the first humans migrated from Africa much earlier than, say, 100,000 to 50,000 years ago, and subsequently developed into different "races" in different places in the world. The Mitochondrial Eve paper, by contrast, contributed to the understanding that anatomically modern humans underwent the same development and genetically belonged to one human family.

One of the authors of the paper, geneticist Mark Stoneking, happened to be visiting Svante's lab when I was there. I interviewed him about the Mitochondrial Eve paper and the controversy it provoked. He pointedly stated the difference between genetics and paleontology: "We geneticists know that our genes must have had ancestors, but paleontologists can only hope that their fossils had descendants."[17] The implication of Stoneking's statement is that the relation between paleontological artifacts from the past and modern humans is not evident, whereas DNA self-evidently implies a connection between now and then: DNA comes from somewhere, and the task is to excavate that past.

The Neanderthal sequence extracted by Krings was one such fossil that was thought to have no descendants. In Krings's 1997 paper in *Cell*, it was concluded that "the Neanderthal mtDNA sequence . . . supports a scenario in which modern humans arose recently in Africa as a distinct species and replaced Neanderthals with little or no interbreeding."[18] The paper thus confirmed the dominant notion that the Neanderthal was a dead end. While the Neanderthal lived in the Middle East and Europe for a very long time, this hominid was (violently?) replaced by modern humans who joined the scene later.

Going Nuclear

However, in 2006, Pääbo's lab, now housed at the Max Planck Institute in Leipzig, took the challenging route of nuclear DNA and embarked on sequencing the forty-six chromosomes of the Neanderthal. By this time, it was hypothesized that anatomically modern humans and Neanderthal people might have shared more than just a time corridor in which they both walked around on Asian and European soil.

The challenge is due to the size of the genomes: whereas the mitochondrial genome consists of about 16,000 base pairs, the nuclear DNA genome consists of about 3 billion base pairs. After a journey of finding suitable bones that would yield enough DNA, securing the money and technology for the sequencing, collecting the brains that could help figure out how to analyze the data, and deciding which journal should be granted the scoop, the sequence was published in 2010 in *Science*.[19] And indeed, while the mitochondrial DNA analyzed in Matthias Krings's 1997 paper indicated genetic distance between humans and Neanderthals, nuclear DNA revealed astonishing proximity.[20] Moreover, the Neanderthal seemed to have contributed between 1 and 4 percent of their genes to modern humans.[21] The results cannot be understood as anything other than that they had sex with each other, and that a substantial number of children were born from it. The Neanderthal is not an evolutionary dead end, after all, but lives on in us. In addition, the results suggested that while Europeans and Asians were found to share DNA with the Neanderthals, African populations seemed not to do so. By now, we know that this was a problematic and not so accurate conclusion.[22] At the time that the paper was published, however, geneticist David Reich, who was one of the coauthors, stated that "we do not find any evidence of Neanderthal gene flow in Africans."[23]

This mesmerizing research and the surprising genetic relations it helped to uncover have also caused trouble in terms of race. As we will see below, the assumption that the Neanderthal had exchanged genetic material with European populations has contributed to a whitewashing of the Neanderthal, which has made it a figure in racial politics. Before going into that discussion, however, I will first provide some theoretical background for my analysis of race.

Race and Sameness

Given the troubled history of genetics in the slipstream of the Human Genome Project and the key role that genetics and genomics have since come to play in science and society, a flourishing scholarship has emerged on race and genomics.[24] For good reasons, this ever-growing scholarship has focused on questions of difference, how differences are produced in scientific practice, and how genetics might contribute to the production or essentialization of differences. Yet, although differences combined with biology should make us nervous and alert, this focus has also contributed to the assumption that while differences are produced, sameness is a given baseline. Indeed, the emphasis on difference suggests that in the context of race, differences are inherently political. As a consequence, this has led to the curious impression that similarities are apolitical. Due to our nervousness about difference (in relation to race and genomics), the production of sameness, resemblance and equivalence has received little attention in critical analyses. Inspired by the Neanderthal, I want to switch focus from difference to sameness and explore the versions of racialization this helps us to see.

The taken-for-granted nature of sameness in scholarship on race might in fact have deeper, more structural roots. In his seminal book *The Invention of Humanity* from 2017, historian and political scientist Siep Stuurman shows how modernity and the modern states of justice are based on the sameness of humans as the norm and their equality before the law as its consequence. Stuurman argues that there have historically been three crucial "modalities" that have helped to invent the thing called humanity. The first modality is the acknowledgement of a common humanness, that is, that humans belong to the same species. The second modality is related to the "anthropological turn," through which cultural differences came to be understood as variation on a common theme, assuming a shared human culture. The third modality is a temporal regime that helped render human civilization as an evolutionary development, in the way that even if some peoples are not there yet—not yet modern—they are assumed to undergo similar development and eventually arrive in modern times.[25]

Although the three modalities that have helped to establish the paradigm of humanity have been widely shared by different civilizations across the globe, so Stuurman argues, the coupling of equality and sameness became pivotal in the racial order of Europe during the Enlightenment. According to that dictum, to become equal is to become *like those* who are already equal, that is, the European whites. Enlightenment thus became the obligatory point of passage for becoming equal.

The crux of Stuurman's point is that sameness has become a normative baseline in the modern equality paradigm. His argument makes clear that becoming equal requires work and entails an ideological take on human relations. But as sameness has become the norm, the process through which this sameness is created has moved to the background and become largely obscured. By contrast, the ways in which difference and deviance are produced has typically attracted attention, alarm, or dismay.

Rather than taking sameness for granted, I focus on how sameness comes about, what it is made to be, and how it effects specific racializations. I demonstrate how different versions of sameness bring about different versions of race.

Time and Temporality

As indicated at the beginning of this chapter, race is entwined with notions of time and temporality. Time and temporality are sources of conflict and have been identified as modes of imperial governance.[26] Given the pivotal role granted to the dating of, let's say, stones, bones, and genes, the Neanderthal provides us with a good case for studying race in relation to time. But rather than taking time as a given natural phenomenon, I want to attend to how time is made and how this affects the ways similarities and differences are enacted.

In her 2015 book *The Mushroom at the End of the World*, anthropologist Anna Lowenhaupt Tsing uses the case of the matsutake mushroom to unravel the devastating relation between the capitalist trope of "development" and ecological degradation and the production of precarity.[27] She urges us to move beyond progressive narratives toward multiple temporalities. By way of the matsutake, the mushroom that thrives on forests disturbed by human chemicals, she invites us to attend to modes of unintentional life and to develop the art of living on a damaged planet. Rather than looking ahead and imagining a future of progress or looking back in time toward moments supposed to be less advanced, Lowenhaupt Tsing suggests that we "look around."[28] Moreover, she suggests that we develop an art of noticing and a taste for curiosity. In this way Lowenhaupt Tsing offers an interesting suggestion to reconfigure our relations with other species, a way, perhaps, of moving us beyond a single story—a phenomenon that is unfortunately so prevalent in science.

To illuminate the question of race, time, and the Neandertal, I further draw on the work of the French philosopher and mathematician Michel Serres. Serres contrasts his approach of time to what he calls classical, or linear, time. Linear time is typically connected with modernity and progress, something that is central to scientific practice. Serres calls this the time of the line: a time that can be cumulative, continuous, or interrupted, yet always remains linear. In Serres's universe, however, time is topological. It assumes different shapes, lines, folds, circularities, and is therefore heterogeneous. Serres states that time does not flow, but percolates, as through a sieve. As he puts it, "it passes and it doesn't pass."[29] It flows in turbulent and more chaotic ways. This is because time is not a natural given. It is an effect of relations between entities.

To make this more tangible, consider the German artist Gunter Demnig's art project *Stolpersteine*, "stumbling stones." Made of brass and bearing the name, date of birth, date of deportation, and death date of individual victims of Nazi Germany, these memorials are to be found in many European cities. They are typically placed on the sidewalk, in front of the last residence of the named victim.

Clearly, these stones are made to commemorate the victims. They do so, however, by producing time. Imagine you are going about your everyday business, going to buy your groceries, but stumble over such a stone. You might look down, read the information, and immediately, the street, the house adjacent to the stone changes. At such a moment, time gets made. From an event more than eighty years ago, it becomes a "now." From being a line, time gets crumpled and an event from the past gets "folded" in the here and now.[30] Here, in front of your eyes, things happened, and your imagination enfolds. This is an example of the art of noticing, in Lowenhaupt Tsing's words, and simultaneously an example of the multiplicity of time that Serres alerts us to. Time passes (linearity) and does not pass (crumpling and folding). Just like the history of the Holocaust is not left behind but materialized in postwar European cities, the history of race science in general has also sedimented in varieties of practice in science and society. For example, in laboratory practice, data and samples collected in colonial times (like biometric measurements and skulls) are still relevant, and not just in the field of physical anthropology.[31] Although it would be wrong to state that current laboratory practice is racist, these collections, data, and methods might in specific situations (e.g., in combination with specific questions) help mobilize former practices and reintroduce and produce "race."

Let us now return to the time of the Neanderthals in order to analyze time, race, and sameness.

Time and Race

In recent years, it seems that research on the Neanderthal has developed a certain art of noticing, to evoke Anna Lowenhaupt Tsing. Rather than reducing the Neanderthals in place and time, it seems that both the kind of questions that are being asked and the technologies available to examine the artifacts are producing a more complex picture than the popular one, in which the Neanderthal is cast as the simple and brutish other "us."[32] We are now learning that Neanderthals not only had large brains but were also capable of complex cognition, such as copying of technology; they had a language that allowed them to perform complex tasks; they produced art, music, jewelry, and personal ornamentation, indicating a symbolic life and taste for aesthetics; they produced interesting artistic configurations that raise questions about possibilities of rituals and in any case index the ability for complex social organization.[33] Increasingly, the perspective in research and social representations emphasizes not so much the differences between modern humans and Neanderthals as the similarities. They are like us. "They were very similar in many respects," as paleontologist Katerina Harvati explains in the documentary *First Peoples*.[34]

I am both intrigued and troubled by the emphasis on sameness. It makes me wonder about the normativity of sameness and how sameness comes about.[35] In what follows, I attend to one specific example—a postcard—and analyze how proximities and distances are made. As I will show, this postcard is instructive of the ways knowledge about the Neanderthals is homed in, comfortably placed within dominant imaginations, to become part of a racial politics.[36]

Werde Teil der Menschenfamilie

“Werde Teil der Menschenfamilie” (Become part of the human family) is a nicely inclusive invitation to this postcard on the website of the Neanderthal Museum in Mettmann, Germany (figure 5.4).

What we are looking at is a picture representing modern and not-so-modern humans at the Neanderthal Museum. The postcard is in my view a “folded object.”[37] It is a time machine, where a heterogeneity of time is ordered in counterintuitive ways, producing proximities and distances. But let us first appreciate the impression and have a closer look at the figures represented. The card displays a familiar scene, evocative of a bourgeois moment. People are gathered in what looks like a casual library. In comfortable Chesterfields one can ponder nature and enjoy its wonders, read a book, or sip from a glass. Importantly, we have a gathering of a diversity of people, a family—the human family, we are made to think. The atmosphere is relaxed. A child is playing chess with a young woman. An interestingly diverse man, not too dark and not too light-skinned, is put centerstage, staring at us in a

Figure 5.4
“Werde Teil der Menschenfamilie.” Image/postcard on the website of the Neanderthal Museum in Mettmann, Germany.

more or less self-contained way, as if he is in the know about what our common future is. Various other figures are nicely displayed. The scene seems to capture a spare moment in the day, a moment of casually being together before moving on to the dining room to enjoy a nice meal.

This postcard, which I received from friends who visited the museum, has been hanging in my office for three years. I have been stared at by these figures and I have been staring back at them. My eyes have been drawn between the center and the flanking regions, between the idealized diversity man-of-the-future in the center, Mr. 4% to the left, and the Turkana boy from Kenya and a stone-age man from Jebal Irhoud in Morocco on the right.[38] Moving my eyes from left to right and back again, I have not been able to overlook a racial-typological impression, as if we see evolution in action from the right to the left, arriving at the CEO-like Mr. 4%.

Let us consider the different figures. We see a collection of modern humans, consisting of four women, two men, and a young boy. We have three representatives of Neanderthals: there is Mr. 4%, a young Neanderthal girl called Kina, and a Neanderthal man in the center (who could easily pass for a traditional shepherd) called Mr. N. But we also have a version of Lucy (*Australopithecus*) down left, as well as the figures mentioned above to the upper right: the *Homo erectus* Turkana boy, and the oldest *Homo sapiens sapiens*, the Stone Age man from Jebal Irhoud. The image thus condenses a time span from 3.2 million years ago (Lucy) to our own time. Yet all figures seem to be present in the now. The folding of evolutionary time is here produced by the very realistic rendering of these ancient hominids. To be sure, if they would have been represented as skeletons, this radical folding of time would not have been as effective, and a distance would have been produced between us and them.

But the picture does more, if we would consider that "things could have been otherwise."[39] Let us first consider Lucy and the Turkana boy by comparing and contrasting the reconstruction of them here with the ones at the Musée National de Préhistoire in Les Eyzies.

There is visibly something going on here. Although the reconstructions of Lucy and the Turkana boy are based on the same bones/artifacts, they differ in an obvious way. To be sure, the forensic artists who produce such reconstructions have to work with the material that they have. And such reconstructions are artistic expressions of sorts. But they are still based on the same models of the bones/artifacts found and the same state of knowledge about

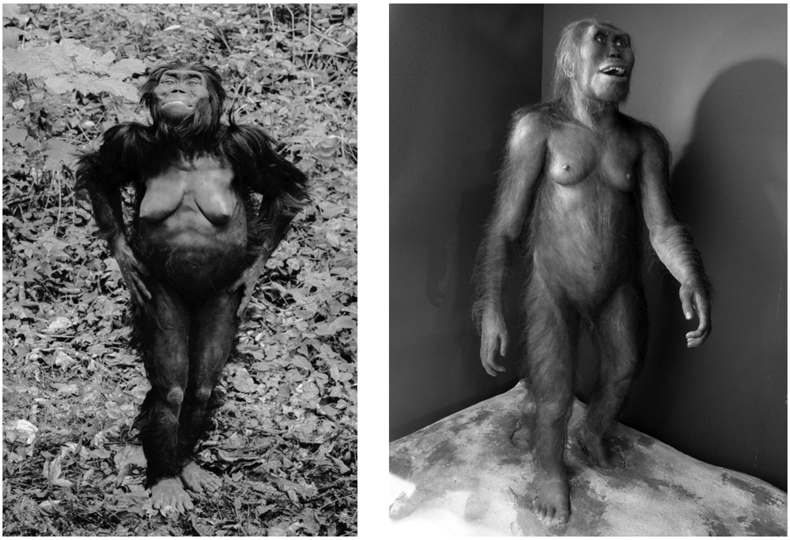

Figure 5.5
Lucy as depicted at the Neanderthal Museum in Mettmann (left) and at the Musée National de Préhistoire, Les Eyzies (right).

early hominids. The reconstructions at both the Neanderthal Museum and the Musée National de Préhistoire in Les Eyzies depict Lucy and the Turkana boy as more or less naked, yet the differences between the reconstructions are stark. Whereas the Neanderthal Museum seems to emphasize their wildness and difference, the Museum of Prehistory seems to invite the viewer to consider both the similarities and differences between modern humans and the depicted figures. At the Neanderthal Museum, Lucy is rendered an apelike figure and the otherness of the Turkana boy, a very dark-skinned bundle of muscles, cannot be overlooked. Moreover, both are placed outside in the “wilderness,” as if to underline their wildness. Juxtaposed with the coarse and vulgar depictions of the Neanderthal Museum, the matter-of-fact-ness of the representations in Les Eyzies is striking. In addition, both Lucy and Turkana Boy are depicted as if posing for a camera. A representation familiar, everyday, and modern in its gestures, yet it presents the “wrong” subjects. It thus mocks and dramatizes, just like a reversed minstrel figure, and so racializes the differences. Lucy and the Turkana Boy are not just wild, but also humanity’s other. Finally, and contributing to their racialization, is the sexualization of these depictions at the Neanderthal Museum. Lucy is displaying

Figure 5.6
Turkana boy as depicted at the Neanderthal Museum in Mettmann (left) and at the Musée National de Préhistoire, Les Eyzies (right).

her body to the viewer. Similarly, the Turkana Boy is sexualized by his very pose, as if presenting his nakedness. By contrast, the Lucy at the Museum of Prehistory seems totally indifferent to the viewer; she is self-contained and not in need of our appreciation, whereas the Turkana Boy, whose private parts are covered, is standing in a highly commonplace way.

Comparing and contrasting the reconstructions at the Neanderthal Museum and the Museum of Prehistory help articulate their normativity, not only in terms of racial representation, where skin color is a strong signifier, but also in terms of gender. The sexualization of Lucy and the Turkana Boy at the Neanderthal Museum contributes to their further racialization and othering. This familiar mode of racialization through othering helps us see the politics of such reconstructions. As Paul Gilroy reminds us, however, this mode of seeing and recognizing difference is historically situated. “Seeing race,” Gilroy argues, takes a specifically trained human “sensorium” attuned to the recognition of racial types and kinds.[40]

In what follows, I analyze racialization not as an effect of difference through "otherness" but of sameness through "us-ness." Returning to the family picture postcard at the Neanderthal Museum and considering time in relation to sameness, we can observe an interesting configuration that underscores the racial character of this depiction. In this scene, Lucy becomes almost a pet. Even as a pet, however she is drawn into the human family, domesticated and made part of the family. The same happens in the postcard to the Neanderthals, whose similarities with modern humans are underlined by their clothing and gestures, such as the human hand touching the Neanderthal man who has a stick.

However, this proximity stands in a stark contrast to the Turkana Boy and the Stone Age man of Mount Irhoun. They both seem to be set apart from the human family. Their nakedness does not fit the bourgeois ambiance. Their representations give way to typical visualizations of the black male body.[41] In addition, the juxtaposition between their splendid nakedness and the erotic pose of the Turkana Boy spills over and sexualizes the body of the Stone Age man and makes him more naked than he actually is. So even though this man is in fact our closest ancestor, he oscillates between *Homo erectus* and our stereotypes about blackness, thus ending up outside the "human family" of the postcard. While Lucy and the Neanderthals are homed in to successfully become part of this family, our closest ancestor is pushed outside it and made part of a different collective.[42]

Through these relations of proximity and distance, time is reconfigured in novel ways, here crumbled, there stretched out, contributing to what is considered *same* or *different*. Both collectives—the family of "us-ness" as well as of "other-ness"—become racialized in this depiction. However, the specificities of the collectives matter, since their *sameness* differs radically, and so does the associated configuration of race. First, the version of sameness that is related to the *other* is fairly unspecific. It is a category in which people are lumped together, and one in which the phenotype and the body play crucial roles. These markers turn them into "phenotypic others," a category that, based on bodily markers of difference, can assume anything that is not-us or can be radically reduced.[43] By contrast, sameness as a version of *us-ness* is an open and generous category which makes space for individuality—as was the case with Mr. 4%—but also for family, as well as for belonging to a specific cultural place. Each member belongs to the family and the place but cannot be reduced to any of these. Thus, although this version of sameness is racialized, the members of this collective retain their individuality and with it the possibility of being "in time" instead of "out of time."

Conclusion

Philosopher of science Joyce Havstad has coined the term "sensational science" to describe ancient DNA research. Sensational science is a "science which empirically speculates, to the public's delight and entertainment, about scintillating topics such as when humans evolved, where we came from, and who else we were having sex with during our early hominin history."[44] Ancient DNA research is consequently, and as I have shown in this chapter, an *affective* field, one that invites a wide audience to project different kinds of aspirations, feelings, and vested ideas.[45]

In this text, I have attended to ancient DNA in the lab, but also outside of it, to analyze how it affects representations of the Neanderthal. A lot can be said—and has been said—about what Anna Källén and colleagues have addressed as the "aDNA revolution." In their analysis, the story of this revolution comes with "a sense of direction and inevitability of the way forward."[46] It is this propensity that tends to contribute to the modernist single story in which diverse histories and experience are subsumed. On the pages above, I have examined how "the danger of a single story" of evolution, a story that comes with a specific rendering of time and temporality, feeds into knowledge produced in the field of aDNA. I have argued that the fact that Neanderthals have contributed parts of their DNA to modern humans through interbreeding has led to a novel racialization of the Neanderthal.

By now, we know that Neanderthal genes are shared not only in Europe and Asia, but also among African populations.[47] Yet, the powerful and single story about European-Neanderthal lineage has remained dominant. Its effect is a whitewashing of the Neanderthal. This is a politics in which the Neanderthal genes become the ultimate markers of European-ness.[48] In the analysis of the postcard (which is more than a postcard), "Become part of the human family," we have zoomed in on who is made part of this human family and how. I have shown that it is helpful in this case not to analyze race through the common register of difference, but rather to zoom in on sameness.

Attending to the material details of racial politics and focusing on the way time gets made and how it produces proximities and distances, and thereby different collectives, I have shown how a racialized collective of "us-ness" gets produced. Crucially, sameness in relation to "us-ness" leaves ample space for differences within, space for individuality, while sameness based on "other-ness" reduces the collective of the other to one or a limited set of markers. Whereas modernist narratives, including those of science and of science museums, are firmly committed to a linear rendering of time, the case analyzed here shows a comingling of time. It demonstrates the importance of focusing on time and its politics in relation to race. And it underscores the significance of the whitewashing of the Neanderthal in current racial politics in Europe.

Notes

1. I would like to thank the organizers of the symposium "Code Narrative History: Critical Perspectives on Ancient DNA" in Stockholm, where a version of this chapter was delivered as a keynote address. I also thank the participants of this symposium for their comments and suggestions. I am grateful to the organizers, especially Daniel Strand, in their capacity as editors of this volume, for their feedback on various drafts of this chapter. The chapter has also benefitted from the feedback and suggestions by two anonymous reviewers. The analyses presented here are the result of collaborations with members of the RaceFaceID team, whom I thank for thinking together hard about this wild object called race. Finally, I thank the European Research Council for supporting my research through an ERC Consolidator Grant (FP7–617451-RaceFaceID-Race Matter: On the Absent Presence of Race in Forensic Identification).

2. Mr. 4% has, of course, received his name from the discovery that some contemporary human individuals have up to 4% Neanderthal DNA.

3. For a beautiful and important analysis of the racialization of the Neanderthal, the production of a racial type and a racial portrait, as depicted in the reconstructions of Egon von Eickstedt in Vienna, and of how these reconstructions in the 1920s shaped the popular imagination of race and its origins in prehistory, see Paul H. Lambers, Margit Berne, and Katrin Kremmler, "From Anatomy to Palaeo-Raciology: Two Neanderthal Reconstructions at the NHMW 1924/25," *Annalen des Naturhistorischen Museums in Wien: Serie A für Mineralogie und Petrographie, Geologie und Paläontologie, Anthropologie und Prähistorie* 123 (April 2022): 33–64. For a discussion of the portrayal of the Neanderthal by Boule and Kupta, see Marianne Sommer, "Mirror, Mirror on the Wall: Neanderthal as Image and 'Distortion' in Early 20th-Century French Science and Press," *Social Studies of Science* 36, no. 2 (200: 207–2406).

4. Chimamanda Ngozi Adichie, "The Danger of a Single Story," *Ted Talk*, July 2009, https://www.ted.com/talks/chimamanda_ngozi_adichie_the_danger_of_a_single_story#t-1796.

5. Here I am particularly referring to evolutionary theory and the ordering of species (and different kind of people) along the line of evolution.

6. Homi K. Bhabha, *The Location of Culture* (London: Routledge, 1994), 244.

7. Michel Serres and Bruno Latour, *Conversations on Science, Culture, and Time*, trans. Roxanne Lapidus (Ann Arbor: University of Michigan Press, 1995).

8. I spent half a year at Pääbo's lab as an anthropologist of science, where I conducted a laboratory ethnography focusing on human genetic diversity. See Amade M'charek, *The Human Genome Diversity Project: An Ethnography of Scientific Practice* (Cambridge: Cambridge University Press, 2005).

9. The ALF sequencer is a sequencing machine that detects target DNA fragments, because they carry a fluorescent label with them. In the case discussed here, these labels were added for the processing and copying of DNA in the PCR (polymerase chain reaction) machine.

10. Matthias Krings et al., "Neandertal DNA Sequences and the Origins of Modern Humans," *Cell* 90, no. 1 (1997): 19–30.

11. See Amade M'charek, "Race, Time and Folded Objects: The HeLa Error," *Theory, Culture & Society* 31, no. 6 (2014): 29–56. In this paper, I show how race is folded into the sequence and obscures its multiple origins. The original sequence was based on DNA from an unknown UK placenta, HeLa cells, as well as bovine DNA. The resequencing of the reference in 1991, however, has led to the exclusion of HeLa DNA, which originally stemmed from the African American woman Henrietta Lacks.

12. Rebecca L. Cann, Mark Stoneking, and Allan C. Wilson, "Mitochondrial DNA and Human Evolution," *Nature* 325, no. 6099 (1987): 31–36.

13. It should be noted that the authors of the study did not have access to the DNA of African populations, and that samples were actually taken from African American individuals, who thus represented African populations.

14. Irony in the sense of Donna Haraway: "Irony is about contradictions that do not resolve into larger wholes, even dialectically, about the tension of holding incompatible things together because both or all are necessary and true. Irony is about humor and serious play." See Donna Haraway, "A Cyborg Manifesto: Science, Technology, and Socialist Feminism in the Late 20th Century," in *Simians, Cyborgs, and Women: The Reinvention of Nature*, ed. Haraway (London: Free Association, 1991), 149–183. On the intricacies of Mitochondrial Eve, see Venla Oikkonen, "Mitochondrial Eve and the Affective Politics of Human Ancestry," *Signs* 40, no. 3 (2015): 747–772.

15. See Jane Gitschier, "All about Mitochondrial Eve: An Interview with Rebecca Cann," *PloS Genetics* 6, no. 5 (2010): 1–4.

16. For a helpful review, see Saioa López, Lucy van Dorp, and Garrett Hellenthal, "Human Dispersal Out of Africa: A Lasting Debate," *Evolutionary Bioinformatics* 11 (2015):

57–68. On the conversation among geneticists and paleontologists, see Svante Pääbo, *Neanderthal Man: In Search of Lost Genomes* (New York: Basic Books, 2014).

17. According to Pääbo, this is a paraphrase of a famous statement of the anthropologist Vincent Sarich, who worked in Allan Wilson's lab in Berkeley in the 1980s. It seems that Mark Stoneking might have borrowed it and used it in the interview with me in 1996. See Pääbo, *Neanderthal Man*, 95.

18. Krings et al., "Neandertal DNA Sequences," 27.

19. Richard Ed Green et al., "A Draft Sequence of the Neandertal Genome," *Science* 328, no. 5979 (2010): 710–722.

20. It is slowly becoming clear that the genetic material that modern humans received from the Neanderthals has played a crucial role in building resistance to viruses and bacteria. Perhaps this made human survival possible in Europe at the time. The presence of Neanderthal genes has also helped explain why some Covid patients have a very tough disease process, and why genes in turn protect people better against this virus. See Hugo Zeberg and Svante Pääbo, "The Major Genetic Risk Factor for Severe COVID-19 is Inherited from Neanderthals," *Nature* 587, no. 7835 (2020): 610–612.

21. Green et al., "Draft Sequence," 29.

22. John Hawks, "Accurate Depiction of Uncertainty in Ancient DNA Research: The Case of Neanderthal Ancestry in Africa," *Journal of Social Archaeology* 21, no. 2 (2021): 179–196.

23. David Reich quoted in Hawks, "Accurate Depiction of Uncertainty," 179.

24. For a discussion about the troubled history of genetics, see Daniel J. Kevles, *In the Name of Eugenics: Genetics and the Uses of Human Heredity* (Cambridge, MA: Harvard University Press, 1995). For the recent scholarship on race and genomics, see, for instance, Nadia Abu El-Haj, "The Genetic Reinscription of Race," *Annual Review of Anthropology* 36 (2007): 283–300; Duana Fullwiley, "The Molecularization of Race: Institutionalizing Racial Difference in Pharmacogenetics Practice," *Science as Culture* 16, no. 1 (2007): 1–30; Ian Whitmarsh and David S. Jones, eds., *What's the Use of Race? Modern Governance and the Biology of Difference* (Cambridge, MA: MIT Press, 2010); Alan H. Goodman, Yolanda T. Moses, and Joseph L. Jones, *Race: Are We So Different?* (Chichester: Wiley-Blackwell, 2012); Jonathan Kahn, *Race in a Bottle: The Story of BiDil and Racialized Medicine in the Genomic Age* (New York: Columbia University Press, 2013); Troy Duster, "A Post-Genomic Surprise: The Molecular Re-Inscription of Race in Science, Law, and Medicine," *British Journal of Sociology* 66, no. 1 (2015): 1–27; Daniel Strand, "0.01%: Genetics, Race and the Methodology of Differentiation," *Eurozine*, January 4, 2021, https://www.eurozine.com/0-01.

25. Siep Stuurman, *The Invention of Humanity: Equality and Cultural Difference in World History* (Cambridge, MA: Harvard University Press, 2017).

26. See Bhabha, *Location of Culture*; Charles W. Mills, "The Chronopolitics of Racial Time," *Time & Society* 29, no. 2 (2020): 297–317; Katharina Hunfeld, "The Coloniality of Time in the Global Justice Debate: De-centring Western Linear Temporality," *Journal of Global Ethics* 18, no.1 (2022): 100–117.

27. Anna Lowenhaupt Tsing, *The Mushroom at the End of the World: On the Possibility of Life in Capitalist Ruins* (Princeton, NJ: Princeton University Press, 2015).

28. Lowenhaupt Tsing, *Mushroom at the End of the World*, 22.

29. Serres and Latour, *Conversations on Science*, 58.

30. On the folding of time in objects and how that helps to produce race, see M'charek, "Race, Time and Folded Objects."

31. On the legacy and problems of race in physical and forensic anthropology, see Elizabeth A. DiGangi and Jonathan D. Bethard, "Uncloaking a Lost Cause: Decolonizing Ancestry Estimation in the United States," *American Journal of Physical Anthropology*, 175, no. 2 (2021): 422–436. On how this legacy plays out in genetic practice, see Roos Hopman and Amade M'charek, "Facing the Unknown Suspect: Forensic DNA Phenotyping and the Oscillation Between the Individual and the Collective," *BioSocieties* 15, no. 3 (2020): 1–25.

32. See Katerina Harvati and Terry Harrison, eds., *Neanderthals Revisited: New Approaches and Perspectives* (Dordrecht: Springer, 2006).

33. For an overview of this research, see the insightful Deutsche Welle documentary *Who Were the Neanderthals?* from 2021, produced by Rob Hope and Pascal Cruissot, https://www.youtube.com/watch?v=8p8tFcIQ8K4.

34. Nicolas Brown, dir., *Europe First Peoples*, PBS Nova, February 13, 2017, YouTube video, 54:42, https://www.youtube.com/watch?v=1587lxOA6sI.

35. On how the Neanderthal changed from initially more similar to a modern human to humanity's apish other in the early twentieth century, see Sommer, "Mirror, Mirror on the Wall."

36. My argument is akin to and inspired by Donna Haraway's important essay "Teddy Bear Patriarchy: Taxidermy in the Garden of Eden, New York City, 1908–1936," in *Primate Visions: Gender, Race, and Nature in the World of Modern Science* (London: Verso, 1989), 26–59. In this intriguing and powerful essay, Haraway analyzes how "nature," and the way it is displayed in the so-called African Hall at the American Museum of Natural History in New York, does not so much represent nature, as it can be found in Africa—"an immediate vision," as Carl Akeley would have it (in Haraway, "Teddy Bear Patriarchy," 36)—but rather reflects and reifies dominant ideas of class, race, and gender in the United States of the 1930s. To be sure, in contrast to my reading of the postcard, Haraway presents a thorough analysis of the museum, exhibitions, and key

figures (such as Carl Akeley), as well as the method of collecting and preserving (such as photography or taxidermy). Yet, both our analyses deal with the issue of time. "The African Hall was meant to be a time machine," Haraway suggests, but a linear one. By contrast, in my analysis of the postcard in the Neanderthal Museum in Mettmann, I zoom in on the multiplicity of time; not simply linearity, but also the folding and crumpling of time, in which distant moments in history and the present are superimposed in the "now."

37. M'charek, "Race, Time and Folded Objects."

38. The Turkana boy is the name given to an early hominid, a young boy of probably twelve years old, who lived some 1.6 million years ago. The finding of this skeleton in 1984 was a sensation, not only because it appeared to stem from such an archaic hominid, but also because his skeleton was complete. See Frank Brown et al., "Early *Homo Erectus* Skeleton from West Lake Turkana, Kenya," *Nature* 316, no. 6031 (1985): 788–792.

39. Susan Leigh Star, "Introduction: The Sociology of Science and Technology," *Social Problems* 35, no. 3 (1988): 197–205.

40. Paul Gilroy, "Race Ends Here," *Ethnic and Racial Studies* 21, no. 5 (1998): 838.

41. This theme is widely analyzed in critical race studies and cultural studies. See, for instance, Frantz Fanon, *Black Skin, White Masks* (New York: Grove, 1952); Stuart Hall, ed., *Representation: Cultural Representations and Signifying Practices* (London: Sage, 1997).

42. See also Deleuze and Guattari's argument on race and sameness, and how it leads to the bestialization of the nonsame. Gilles Deleuze and Felix Guattari, *A Thousand Plateaus: Capitalism and Schizophrenia* (Minneapolis: University of Minnesota Press, 1987).

43. Amade M'charek, Victor Toom, and Lisette Jong, "The Trouble with Race in Forensic Identification," *Science, Technology, & Human Values* 45, no. 5 (2020): 804–828.

44. Joyce C. Havstad, "Sensational Science, Archaic Hominin Genetics, and Amplified Inductive Risk," *Canadian Journal of Philosophy* 52, no. 3 (2022): 295. See also Elizabeth Jones's discussion of a field that is data-driven, but also celebrity-driven, with problematic consequences for how the field of aDNA has acquired its shape; Elizabeth D. Jones, "Ancient Genetics to Ancient Genomics: Celebrity and Credibility in Data-Driven Practice," *Biology and Philosophy* 34, no. 2 (2019): 1–35.

45. On the relation between affect and race, see Sara Ahmed, *The Cultural Politics of Emotion* (Edinburgh: University of Edinburgh Press, 2004).

46. Anna Källén et al., "Introduction: Transcending the aDNA Revolution," *Journal of Social Archaeology* 21, no. 2 (2021): 151.

47. Hawks, "Accurate Depiction of Uncertainty"; Lu Chen et al., "Identifying and Interpreting Apparent Neanderthal Ancestry in African Individuals," *Cell*, 180, no. 4 (2020): 677–687.

48. This happens to the point where white supremacists use the contribution of Neanderthal DNA in their DNA profiles as a marker for Europeanness and their belonging to the stronger "race." See Michael Cook, "I'm Glad I'm Part Neanderthal," *BioEdge*, October 22, 2016, https://bioedge.org/uncategorized/im-glad-im-part-neanderthal; Amy Harmon, "Why White Supremacists Are Chugging Milk (and Why Geneticists Are Alarmed)," *New York Times*, October 17, 2018.

6 The Lagertha Complex: Archaeogenomics and the Viking Stage

Andreas Nyblom

> Once you have seen Lagertha, it is hard to unsee her.
> —Judith Jesch, 2019[1]

On September 8, 2017, an article with the conspicuous title “A Female Viking Warrior Confirmed by Genomics” was published in the “Brief Communication” section of the *American Journal of Physical Anthropology* (*AJPA*).[2] It presented the results of a genetic sex determination of an individual buried with weapons in a chamber grave at the Viking Age site Birka in present-day Sweden. The article concluded that the individual, who had previously been assumed to have been male, was not only biologically female but the “first confirmed female high-ranking Viking warrior.”[3] The article went viral almost within hours and remains one of the most talked about research papers ever according to alternative metrics.[4] The article was published in close proximity to the airing of the fifth season of the popular History Channel series *Vikings*, and the individual, soon to be known worldwide as the “female Viking warrior,” came to be widely conflated with the lead female character of the show: the shieldmaiden Lagertha.[5]

Nine months earlier, on December 14, 2016, an episode of the docudrama *Real Vikings* had been released. It featured a meeting at the Swedish History Museum in Stockholm between Katheryn Winnick, the actor starring as Lagertha in *Vikings*, and three researchers in archaeology and osteology who were also authors of the scientific article later to be published in the *AJPA*. In front of the camera, Winnick and the researchers study the human remains and weaponry originally found in the chamber grave at Birka in 1878, subsequently stored at the museum. The production soon turns attention to the gender of the buried individual, and it is explained that it has previously been assumed to be male, owing to the traditional warrior equipment found in the grave. With the bones laid out on a table, the researchers explain confidently, while pointing to the remains of the pelvis, that they have evidence for it being female and that the person buried in the grave was "definitely a female warrior—someone who made her living on the battlefield." In excitement, Winnick bursts out: "So, this chick was a badass!" Leaning over the original artifacts from the grave, she grasps the hilt of a corroded sword and exclaims: "This is my sword. Oh, yeah! This is Lagertha's favorite weapon!" The scene ends with a sonorous voiceover which declares: "Finally, physical evidence verifies the legend of the shieldmaiden."[6]

The scene in *Real Vikings* was no doubt orchestrated to establish an intriguing analogy between the fictional character Lagertha and the real life and identity of the individual buried at Birka some thousand years before. Epitomizing the pop-feminist ambitions of the *Vikings* series—to challenge the stereotype of the Viking male by providing space for "women who wield weapons and women who wield power"[7]—it served simultaneously to authenticate the depiction of female warriors in *Vikings* and to visualize and dramatize knowledge claims in the academic field of archaeology. In what seemed like a win-win collaboration between entertainment and research, where the expertise and authority provided by the archaeologists was grafted onto the visually compelling imagery of Lagertha, fearlessly wielding her sword and shield on the battlefield, the ancient bones at the museum were brought to life as the remains of a true action heroine, a genuine shieldmaiden—a real Lagertha.

While science and entertainment are frequently assumed to be poles apart, here they were openly intertwined. The blockbuster article and the docudrama episode featured the same human remains from Birka, involved the same people, and made the same kind of claims and arguments, not only about the identity of the buried individual but more generally about the existence and characteristics of female Viking warriors as a social category. In an argument based on, first, an osteological assessment, and second, a genetic determination of the individual's biological sex, medieval legends about shieldmaidens and contemporary action heroines were somehow also confirmed as authentic representations of real-life individuals. In a most remarkable incarnation, the individual once buried in the Birka chamber grave came to converge with the figure of Lagertha, whose lineage extends from the twelfth-century imaginings of the Danish author Saxo Grammaticus to the popular *Vikings* series.

How are we to make sense of this complex taking shape around the figure of Lagertha, with its intimate intertwinement of science and entertainment, legend and genomics? What role did the researchers play in the realization of the "female Viking warrior" as a real Lagertha, and what role did the media play in the production of scientific knowledge? How, and to what effects, was aDNA brought into operation?

A Female Viking Warrior "Confirmed" by Genomics

As a scientific study, the article "A Female Viking Warrior Confirmed by Genomics" presents the results from aDNA and strontium isotope analyses of the human remains from grave Bj 581 at the Viking Age site Birka, located on an island in Lake Mälaren in central Sweden. An important Viking Age site for trade and commerce, Birka has been investigated by archaeologists since the nineteenth century. Originally excavated in 1878, the grave featured in the study includes not only the human skeleton but also assorted weapons and the remains of two horses. In the article, the authors identify this set of grave goods as "the complete equipment of a professional warrior," and hence describe Bj 581 as the epitome of a warrior grave.[8] The location of the grave in a prominent place near the garrison is taken as indicative of the social standing of the buried person. Furthermore, a full set of gaming pieces is understood as a sign of "knowledge of tactics and strategy, stressing the individual's role as a high-ranking officer."[9] Once the identity of the individual as a warrior—or even a high-ranking officer—has been put forward with traditional archaeological arguments, the actual scientific analysis, and the bulk of the scientific paper, revolve around the DNA and isotope analyses.

The genomic analysis is featured prominently, already in the title of the article, where its literal function is to confirm the "female Viking warrior." On closer inspection, however, it plays only a marginal role in the actual scientific analysis. Biological sex can be determined with a basic genetic analysis—by establishing the absence of a Y-chromosome—and does not require a full genome analysis. A genome-wide analysis, on the other hand, covers the entire nuclear and mitochondrial DNA of an organism. In aDNA studies of prehistoric individuals, such analyses are used to estimate ethnic or family relations and to find out if the individual had any genetically defined characteristics or rare medical conditions.

A genome-wide analysis was indeed performed on two samples from the human remains in Bj 581. First and foremost, it showed that the sampled bones belonged to the same individual. This is a significant result, since the grave had been excavated in 1878 and the human remains (which are now incomplete and lack the skull) were stored among other human remains at an institution that has since been reorganized and relocated. The genomic analysis, moreover, indicated a population affinity with present-day inhabitants of northern Europe. Within Sweden, it showed a stronger affinity with modern inhabitants of the southern and south-central parts than with those of the northern parts of the country. The strontium isotope analysis, which can indicate mobility between geographical regions throughout an individual's lifetime, was not conclusive but suggested that the individual buried in Bj 581 was born elsewhere and had moved to Birka.

However, none of these findings gained traction in the communication of the results that followed the publication of the article. And the article itself makes clear where the significance of the study lies. After accounting for the complicated scientific methodology and broader results of the DNA and strontium analyses, the authors conclude: "Hence the individual in grave Bj 581 is the first confirmed female high-ranking Viking warrior."[10] Moreover, this is said to "suggest that women, indeed, were able to be full members of male dominated spheres."[11]

Two curious claims are made in these statements. First, they set forth that the study could "confirm" that the buried individual had an in-life identity as a high-ranking warrior, although the genomic study established only biological sex and affinity to present-day populations. Second, they suggest that the study—although it included only a single individual—could say something in general about the position of women in Viking Age society.

Of course, neither of these claims is valid. More importantly, however, they point back to what seems to be the core objective of the study, which has little, if anything, to do with genomics and the analysis of aDNA. Rather, it seems that both the objective and principal results of this study had taken shape long before the publication of the scientific article, and long before the human remains were even sampled for aDNA. As indicated already in the *Real Vikings* scene, aired almost a year before the article was published, the objective was to demonstrate the real existence of a social and professional category of female warriors in the Viking Age, with recourse to legendary shieldmaidens. The analysis of aDNA brought nothing qualitative to this argument, since previous osteological assessments had already established the biological sex. Genetics acted solely as an agent of absolute confirmation—not only of the biological sex of the human remains but of the existence of professional female warriors in the Viking Age and of the high-ranking status of the individual buried in Bj 581. Like a magic wand, the word "genomics" seemed to have brought legendary shieldmaidens to real life.

A Spectacular Media Career

The publication of the article in the *AJPA* in September 2017 marked the beginning of a spectacular media career, which would turn the buried individual in Bj 581 into a global celebrity showcased in exhibitions, exploited in pornography, printed on t-shirts, and dramatized in documentaries, theater plays, and novels.[12] Presented as the "Viking High Ranking Birka Shield-Maiden," the individual—or rather the individual's genetic markers in combination with the mediatized celebrity image—was also used as a beacon for genetic ancestry tests on the website My True Ancestry. Highlighted as a "DNA Spotlight," the individual was promoted as an ancient ancestor with whom root-seeking consumers could connect and match their DNA.[13]

Only hours after its publication, the academic article had attracted massive media interest across the world.[14] The initial news headlines commonly combined the element of DNA as proof with the feminist implications of a female Viking warrior: "Gender Reveal: Ancient Viking Warrior Was a Woman, DNA Analysis Shows," "Famous Viking Warrior Was a Woman, DNA Reveals," and "New Science Shows High-Ranked Viking Warrior Was a Fierce Lady."[15]

According to the Altmetric attention score, which measures public spread and visibility of academic research, some 149 news outlets have to date reported on the *AJPA* article. It has been mentioned on a great number of blogs, Wikipedia and Facebook pages, and in thousands of tweets.[16] Of course, the overall popular appreciation of Vikings, fueled by books, films, and television series provided a fertile soil for the "female Viking warrior" to capture the public imagination. The results from a Google search of the title of the article abound with images of beautiful young women in various historical costumes. Many illustrations include helmets and armor, and words like "fierce" and "fearsome" are recurring. Frequent references are also made to Hollywood sheroes such as Xena Warrior Princess, Wonder Woman, and Daenerys Targaryen (from *Game of Thrones*).

Most common of all, however, are the allusions in text and imagery to Lagertha. As noted by archaeologist Howard Williams, Lagertha and the individual in grave Bj 581 became "recursively related as part of a wider cultural conversation that is set to run and run."[17] Not unlike the ways in which the small-bodied hominin *Homo floresiensis*, or the "Flores Hobbit," was imagined and made sense of when it was discovered in 2004 (relating in particular to Peter Jackson's recent film adaptation of *Lord of the Rings*), the "female Viking warrior" was configured within the scaffold of popular, fictional creations—an approach that was initiated and endorsed by the researchers themselves.[18]

In the media coverage, there were also abundant references to DNA as proof. These were often made in rhetorical combinations that are difficult to sustain from a scientific point of view, as in *Science Magazine*'s headline "DNA Proves *Fearsome* Viking Warrior Was a Woman."[19] While fearsomeness, or indeed a warrior occupation, is of course not inscribed in any strings of DNA, it is here, so to speak, evident by association. This should not, however, be regarded as a downstream invention by ignorant journalists. We see similar slippages to bolder claims in the academic article itself, and we see it expressed again by some of the authors reporting on their website that their research team has "uncovered a *fearsome* Viking warrior to be in fact a woman."[20] The leap to bolder claims seems to be characteristic for the recourse to DNA as evidence, by everyone involved in the communication around the individual from Bj 581.

Judging by the media response, the story appealed both to feminist aspirations of finding powerful women in history and to male heterosexual fantasies.[21] More precisely, the story about the individual buried in Bj 581 gained purchase in two distinct directions. On the one hand, it inspired applause in feminist media outlets and mainstream media reporting with feminist undertones. On the other, it spurred misogynist exclamations and hardcore pornography.

The feminist connection, which was present in the *AJPA* article as well as the episode of *Real Vikings*, was amplified in the subsequent media communication, where the "female Viking warrior" soon became a cudgel in polemic feminist debates. *The Guardian* called for a revision of male-centered Viking historiography, and *Huffington Post* deplored "sexism in research methods."[22] Less established media outlets made even bolder claims. A video from the producer Vocativ, for instance, presented the "female Viking warrior" within a medley of pop-cultural images of fighting women accompanied by bombastic music and subtitles claiming that “women kick ass” and have been “multi-tasking since at least the 8th century.”[23]

Since Vikings, as historian Katherine Lewis notes, have commonly been presented as “the epitome of an unbridled form of hypermasculinity predicated on physical strength . . . and callous brutality,” the idea of female Viking warriors, in fiction and research, comes as a significant and, to some, highly anticipated opportunity for discursive change.[24] In this context, the identification of a female individual in what has been described by one of the researchers behind the study as “the world’s ultimate warrior Viking grave,” was loaded with symbolic weight.[25] Eventually, the article even came to be associated with the global uprising against the abuse of women that ensued only a few weeks after its publication.[26] For instance, a Canadian playwright who later brought the “female Viking warrior” to Broadway claimed that the researchers had “rolled feminism, activism, Vikings and #MeToo up in one tasty, spicy, mind-blowing, intellectual taco.”[27] This connection was quite possibly spurred by a promotional video for *Vikings* in which Winnick/Lagertha delivered a #TimesUp speech from her throne in Kattegat, encouraging women to be warriors and queens.[28]

In the misogynistic direction, by contrast, the Norwegian Nazi apologist and neo-pagan Varg Vikernes questioned the results of the study on his YouTube channel by arguing that “it would not be logical to train women to become warriors” since women “are [physically] inferior” to men.[29] And on the Swedish online forum Flashback, self-styled historians suggested that the person buried in Bj 581 was in fact the soldiers’ favorite prostitute, honored with a warrior burial.[30] On a similar note, a dedicated porn site (which displays a DOI link to the *AJPA* article) features female actors personifying the “female Viking warrior” being subdued in a number of variations on sexual violence.[31]

The double vision of the “female Viking warrior” represented here—as fierce and powerful, on the one hand, and subordinate to the male gaze and sexual desire, on the other—is in some sense reflected in the academic attempt to frame the individual in Bj 581 and the figure of the shieldmaiden in a language of feminism, while the very origin of the fantasy of warrior women rests on male desires and anxieties.[32] Even the figure of Lagertha could be said to accommodate these obviously contradictory visions about the female Viking warrior. While Lagertha in *Vikings* has forcefully been put forth as an empowering character and a feminist role model, the original

Lathgertha, according to Viking studies scholar Judith Jesch, was rather a product of Saxo Grammaticus's "misogynist fantasy about warrior women."[33] Either way, both versions are undeniably products of male imagination.

The Prehistory of the "Female Viking Warrior"

Contrary to what the *AJPA* article from 2017 suggested and what news media subsequently reported, the "female Viking warrior" did not emerge as a result of genomics. The inflated narrative and composite identity embedded in the label "female Viking warrior" had already been articulated several years earlier, and in popular rather than academic contexts. While the DNA component of the study merely confirmed what several osteological assessments had indicated since the 1970s—that the biological sex of the individual in Bj 581 was female—none of these previous assessments had come with any explicit interpretation regarding the social identity of the individual. In scholarly settings, the individual's sex combined with the material context of the grave had merely been discussed as an "interesting and thought-provoking example" or "an interesting (and possibly controversial) find."[34] The full-blown "female Viking warrior" story—including assumptions about the individual's social gender, class, character, professional identity, and affinity to the shieldmaidens of Old Norse literature—was first presented in nonscientific contexts committed to the promotion of the popular TV series *Vikings*.

For instance, in a 2015 "Vikings Special" production entitled *Secrets of the Vikings*, the renowned Viking Age expert Neil Price (who would later be one of the authors of the *AJPA* article) presented the individual in Bj 581 as "a woman, buried with this absolute massive collection of weapons" in a grave that ought to be interpreted as "a burial of a shieldmaiden."[35] In combination with newly found images and figurines of women with weapons, Price claimed that the individual in Bj 581 added up to "a pretty compelling picture of what these warrior women may actually have looked like." Stressing that these findings were from the Viking Age itself—not from the later literary corpus of the sagas but "the Viking Age as it really was"—the production illustrated these findings with artistic reconstruction drawings and *Vikings* series footage of Kathryn Winnick as Lagertha, charging forward on horseback, shouting "Shield wall!"[36] The same suggestive presentation of the archaeological findings from Bj 581 was repeated a year later in the episode of *Real Vikings* discussed in the beginning of this chapter.

The popular productions around the TV series *Vikings* apparently provided scholars with an attractive platform and a dramatic license that allowed for speculative interpretations to be spelled out and potently illustrated. The article in the *AJPA* did not add any qualitative detail to the preexisting narrative; it merely worked as a scientific authorization of the hyperbolic story about the identity and character of the individual buried in Bj 581, and, by association, of the existence of real Viking Age shieldmaidens.

As could be expected, the *Vikings* production team was pleased to see their take on the Viking Age legitimized and reinforced by science. Within days of the publication of the article in 2017, the director of *Vikings* commented: "It's kind of wonderful to have the character of Lagertha validated in the show."[37] Later, both the director and Katheryn Winnick referred to the article as proof that the depiction of female warriors in *Vikings* was accurate and that shieldmaidens actually existed as a real social category in the Viking Age.[38]

Unpacking the Lagertha Complex

Its proponents have hailed archaeogenomics as a path to a more correct and scientific version of history, posing the "exquisite accuracy" of genomics against elements of storytelling and guesswork in traditional archaeological research.[39] In a particularly pregnant statement by archaeologist Kristian Kristiansen, aDNA is said to have opened "a new door to previously hidden absolute knowledge" that will "reduce the amount of qualified guessing" and reveal new stories about human history "without having to resort to storytelling."[40]

Considering what we know about the "female Viking warrior," such claims could at best be understood as promotional discourse. Instead of reducing the amount of storytelling and guesswork, we have seen how aDNA—or rather what has been termed the "DNA mystique" or the "social power of DNA"—has acted as leverage for inflated stories about social and professional roles and individual character in the Viking Age.[41] We have seen how a simple reference to ancient DNA has validated and subsumed narratives and images that cannot otherwise be academically substantiated, under the truth-affirming banner of genomics. As Marianne Sommer has said, this is symptomatic of an unresolved tension in aDNA research between a (genomic) esthetics of numbers and an (archaeological) esthetics of narrativity. The union of history writing and DNA, Sommer suggests, generates a conflict between, on the one hand, genetic knowledge, which, through its epistemic object and quantitative and technological approach is presented as particularly accurate and authentic, and, on the other hand, the ways in which that knowledge, in order to become meaningful, "needs to be rendered in a narrative, esthetically appealing way."[42]

In the *AJPA* article and in numerous interviews and documentaries preceding and following its publication, the authors elaborate on the identity, professional competence and personal character of "the female Viking warrior." These elaborations go far beyond any empirical evidence coming out of Bj 581. It is significant that the article begins by referring to medieval "narratives about fierce female Vikings fighting alongside men," and suggests that other scholars have been too quick to dismiss the women featured in these stories as mythological phenomena.[43] Correspondingly, it ends with an uncommented quotation from an Edda poem, written approximately two hundred years after the individual was buried at Birka:

> Then the high-born lady saw them play the wounding game,
> she resolved on a hard course and flung off her cloak;
> she took a naked sword and fought for her kinsmen's lives,
> she was handy at fighting, wherever she aimed her blows.[44]

This certainly implies that genomics had confirmed the truthfulness of medieval narratives, and that the individual in Bj 581 was a real-life shieldmaiden.[45]

As noted by sociologists Dorothy Nelkin and Susan Lindee, it is commonplace that DNA is presented as a conclusive solution to "historical questions that were once dependent for their resolution on records and testimonies from those alive at the time."[46] Obviously, the "DNA mystique" and the potential to frame unverifiable interpretations as conclusive facts may similarly tempt trained archaeologists to disregard well-established knowledge within the discipline concerning the perils of interpreting social roles from burial arrangements, and gender from chromosomal sex.[47]

While the individual in Bj 581 may have acted as a warrior in life, there is no scientific method by which we could ever find out, nor get to know exactly, what their social gender was, or what symbolic, personal, or functional significances were attributed to the grave goods at the time of burial. In fact, the compound "female-Viking-warrior" is likely to be fraught with suppositions regarding the Viking Age implications of each of these three denominations. Ancient DNA can neither verify nor disprove this or any other interpretation regarding the individual's in-life identity. The acceptability of the figure of the “female Viking warrior,” therefore, relied not on a scientific test but on the assertion and authority of genomics, as well as on the persuasive force of its presentation and cultural resonances.

The notion of female Viking warriors that informed the realization of narratives and images of the individual in Bj 581—from *Secrets of the Vikings* to *Real Vikings* and the article in the *AJPA*—was heavily indebted to the modern interpretation of the figure of the shieldmaiden as accounted for in medieval poetry and saga literature. The inference that the individual in Bj 581 was a “female Viking warrior” thus imposed an identity that drew on stories that were put into writing hundreds of years later, primarily by Christian men imagining a pagan past.[48] The combination of genomics and legend, science and fantasy, adheres to the conflicting esthetics identified by Sommer, and is also reminiscent of much earlier attempts to produce scientific knowledge about unknown prehistoric phenomena. A similar case is the convergence of myth and science in the nineteenth-century conceptualization of the dinosaur. As shown by film scholar John McGowan-Hartmann, the emergent science of paleontology coopted the ancient mythic figure of the dragon—as concept and image—into a scientific discourse that came to shape the understanding of dinosaurs and their nature. Paraphrasing McGowan-Hartmann’s outline of the paleontological resolution between dragon and dinosaur, the resolution between the shieldmaiden legend and the female individual buried with weapons would read: if there was such a thing as a shieldmaiden, it is here, and it is real. Not fantasy, but science. Not unknown, but known, and confirmed by the infallible science of genomics.[49]

The complex now surrounding the individual buried in Bj 581 can be further unpacked with help of archaeologist John Robb’s term “technologies of individuation.” Robb shows how the encounter with dead bodies in archaeology and bioanthropology “imposes a regime of depersonalization.”[50] After being provided with numbers or other impersonal designations, human remains are described, stored, catalogued, and exhibited as things or objects. For some of these remains, this is followed by a process of “repersonification,” whereby the human remains are clothed in a social persona. This “calls into operation a range of specialized technologies of individuation” that seek to recreate attributes commonly considered necessary for a social person, such as its sex, age, ethnicity, and individuating marks that reveal its unique history.[51] Various scientific methods are used to support these technologies of individuation, such as facial reconstructions and DNA analysis. According to

Robb, the ultimate goal of these archaeological technologies of individuation "is to assign a name, a history, a social persona."[52]

Attempting to answer questions such as what the person ate, what they looked like, what activities they performed, and how they died, archaeologists and forensic scientists tend to assume that the physical body constitutes the principal source of a person's individuation, commonly conflating biological sex with social gender and fitting chronological age into a normative biographical narrative. Processes of repersonification, therefore, call critical attention to how prehistoric figures are not simply vessels for ancient times but also constructions of modern imagination that are predicated on and tend to reinforce contemporary ideologies and notions about individuality, race, and gender.[53] Moreover, repersonalizations and reconstructions produce compelling images and narratives that inform future thinking and that are difficult to dislodge or unthink for researchers as well as publics.[54]

Owing to deliberate acts of repersonification by the researchers—in the *Vikings*-related productions, the scientific article, and the subsequent media communication—"the female Viking warrior," whose remains were previously known only by their relation to the grave with the impersonal label Bj 581, has now been assigned name(s), a biography, and a social persona. In interviews and dramatized documentaries, the researchers provide generous insights into their own ideas about the individual's life and personality. In the 2019 docudrama *The Viking Warrioress*, for example, Neil Price says that the "senior, female, Viking commander" was "presumably in charge of some *pretty nasty* things,"[55] while the lead author of the *AJPA* article, Charlotte Hedenstierna-Jonson, adds that she was "terrific in every sense of the word."[56] In *The Viking Warrior Queen*, a similar production from 2020, Hedenstierna-Jonson even speaks on behalf of the individual, suggesting that "she would have loved for us to be standing here today, talking about her, and talking about her achievements more than a thousand years later."[57]

Interesting with regard to repersonification are also the reconstruction drawings included in the *AJPA* article and in a follow-up paper published in the archaeological journal *Antiquity* in 2019.[58] Three reconstruction drawings are presented in these publications, and they were also included in the media packages distributed on publication. The first is an etching by Evald Hansen, originally published in a popular magazine in 1889, featuring the Bj 581 skeleton from above surrounded by the grave inventory, as if just uncovered by the excavator.[59] The second image is a commissioned artistic reconstruction drawing by illustrator Þórhallur Þráinsson picturing the individual at the time of the burial and showing a slender young woman in seated position, with soft facial features and fair hair in a ponytail.[60] The third image, included in the *Antiquity* article, is a page-size drawing by the artist Trancredi Valeri showing the individual "reconstructed as a female warrior of high status."[61] Pictured alive in a proud posture with arms crossed, surrounded by shields and weapons and the two horses, the "female Viking warrior" bears recognizably feminine features, with a slightly marked jaw, and long, dark, unbridled hair. Together, the three images form a triptych—a composite portrait by which the individual in Bj 581 is successively reinvented and brought back to life—from an anonymous and incomplete skeleton to a relatable and humanized subject: a full-fledged and independent warrior woman.

Since the skeleton is incomplete and the skull went missing in 1889, there is little evidence to support these visualizations. Apart from the use of original artifacts from Bj 581 as props in the in-life reconstruction, the drawings do not portray the actual individual but a generalized idea and image of the shieldmaiden, superimposed by the iconography of nineteenth-century romantic art and the visual presence of Lagertha in *Vikings*. As imaginative attempts to envision the in-life appearance of the individual buried in Bj 581, these reconstruction drawings come off as particularly strange when combined with the esthetics of numbers associated with genomics. As noted by archaeologist Simon James, "The only certain thing about any reconstruction drawing is that it is wrong."[62]

The visualizations of the "female Viking warrior" should not, however, be dismissed as mere illustrations or insignificant ornaments to the scientific facts. As noted by other scholars, reconstruction drawings constitute arguments in themselves and serve to reinforce particular interpretations.[63] Images cannot express ambivalence, interpretative uncertainty, or chains of assumptions; instead, they minimize or even eliminate ambiguity and support the impression that the past is known in its entirety.[64] In the case of the "female Viking warrior," we see reconstruction drawings combined, to extraordinary effect, with the symbolic truth-value of genomics. Drawings and genomics work as two separate strategies for reducing complexity and conveying certitude. Archaeologist Joan Gero has called critical attention to how such rhetorical strategies—"mechanisms of closure"—are used in archaeological research to conceal necessary and ethically important ambiguities in historical interpretation. The presentation of the results from the scientific study of the human remains from Bj 581, with images of complete living women and allusions to the absolute determining power of genomics, serves to create an aura of certainty around the findings—or, as Gero puts it, "to produce a knowledge product that is unassailable and unambiguous."[65] By naming their preferred understanding of the individual in Bj 581 a "genomic reinterpretation,"[66] the researchers present the "female Viking warrior" not as a result of various considerations, assumptions, and efforts to repersonalize the individual, but as an unambiguous and impersonal reading of machined data—as if merely extracted from the bones and made available through full-genome sequencing.[67]

The Allure of Closure and Attention

The central position awarded to DNA and genomics in the academic articles about the skeleton in Bj 581, as in the media coverage more generally, was not coincidental. We have seen how the researchers had invested in and committed to the shieldmaiden-inspired interpretation of the "female Viking warrior" years before the genetic analysis was performed. Like the *Real Vikings* episode aspired to settle "once and for all" the question about the reality of shieldmaidens, the scientific study employed genomics in order to "solve the issue"—that is, to ward off any disbelief and ambiguity regarding the "female Viking warrior" interpretation.[68] Science has indeed been recognized as "the most potent instrument of persuasion in our culture,"[69] but attention has also been called to the persuasive capability of images, narratives, and popularizations and their roles in the construction of scientific knowledge.[70] While these resources were put to use in abundance in the making of the "female Viking warrior," the work of the researchers has been framed as a purely scientific endeavor, removed from any instances of meaning-making and interpretation—as if the "female Viking warrior" was merely found or discovered. This dovetails with what sociologists of science have noted about the factness of facts: that they, as Amade M'charek puts it, depend on "their ability to disconnect themselves from the practices that helped produce them."[71] By purposefully distancing the accomplishment of the "female Viking warrior" from the sphere of popularization and the esthetics of narrativity it ultimately relied on, the knowledge claims could come off as more certain and authoritative.

This strategy is particularly apparent in the second academic article in *Antiquity*, where the researchers initially reflect on the public attention that was generated by the first article in the *AJPA*. Despite the already established connection to Lagertha, and the fact that the article comprised a catalog of components that could be expected to create headlines—DNA, Vikings, an individual hero figure, legendary tales, female empowerment, violence, and weapons—the researchers imply that the "level of interest" took them by surprise.[72] Obviously turning a blind eye to their own efforts to bring the "female Viking warrior" to life, they explicitly distance their research from pop-cultural renderings of Vikings, which are dismissed as a problematic legacy and a "tangle of history, myth and cliché."[73] Finally, in an attempt to further downplay the significance of their own interpretive work, outreach, and agency, it is implied that the massive global attention that was bestowed on their research was owing merely to the grave itself, or "the genomic data" alone.[74]

Considering that this concerns one of the most successful research papers ever in terms of public outreach, these accounts do not come across as entirely sincere. One commentator has indeed suggested that the article in the *AJPA* had been "designed for maximum worldwide public impact."[75] In many ways, the case of the "female Viking warrior" presents itself as something of a textbook example of what has been termed a "mediatization of science"—involving, for example, the presentation of results in the media prior to peer review and scientific publication, and an increasing entwinement of scientific, political, and popular discourses.[76]

The field of aDNA research appears to have been particularly adaptive to the imperatives of visibility and public outreach in science. Studying the history of aDNA research, historian of science Elizabeth Jones has argued that this field can be considered a "celebrity science," since considerations of celebrity and public attention tend to shape the kind of research that gets funded and pursued. With its propensity for sensational knowledge claims, archaeogenetics thrives in the media limelight.[77] This is particularly true of the kind of aDNA research to which the "female Viking warrior" was subject. This line of research is characterized by its preoccupation with, and production of, celebrity in a more literal and traditional sense, through biographical inquiries into the lives and identities of prehistoric individuals.

While this branch of research has been dismissed as inferior and populist—as something of a "forensic version of tabloid history" rather than serious research[78]—a changing rationale for science communication that puts a high premium on media visibility and public attention has made celebrity-oriented research attractive for competitive academics.[79] With mummies, Vikings, and famous individuals amounting to nearly 70 percent of the press coverage of bioarchaeological research, bioarchaeologists Christopher Stojanowski and William Duncan suggest that these insights should form the basis for a research agenda that would "draw the public to our discipline."[80] Putting center stage what John Robb critically discusses as technologies of individuation, Stojanowski and Duncan propose that research should attempt to "establish emotional connections to the past" by focusing on individuals.[81] To tell the stories of these individuals, and to bring them to life as relational persons with names and faces, they argue, will "maximize our potential in public arenas."[82]

Conclusion

If anything, the case of the "female Viking warrior" and the massive media attention it acquired attest to Stojanowski and Duncan's observation. Being the most widely exposed output from the field of aDNA research, however, one may ask what it tells about the research field it has so amply brought awareness to. As we have seen, genomics and aDNA played only marginal roles as analytical tools and empirical evidence. Rather than an outcome of a genomic analysis of "empirically testable Viking Age reality,"[83] as the researchers would have it, the "female Viking warrior" was accomplished through stories told and images drawn of how this individual—with recourse to supposedly comparable figures in Old Norse texts and contemporary popular culture—lived out their existence. Like Ötzi the Iceman and other prehistoric media celebrities, the "female Viking warrior" appears to have been approached from the very beginning, not as a research project but as a person with a story, provoking a research agenda whose core objective was to repersonalize and resocialize the previously dehumanized skeletal remains.[84] In this respect, ancient DNA worked mainly as a resource for embedding these interpretations and imaginative realizations in a language of scientific authority and objectivity. While heavily dependent on an esthetics of narrativity, and in some respects even on what could be described as "real person fan-fiction," the "female Viking warrior" was filtered through the esthetics of numbers associated with genomics.[85] As scholar of science and technology Andreas Gunnarsson puts it, genomics here served as something of a narrative utility tool for "enhancing the credibility of the fantastical."[86]

As made clear by the intense debate following the publication of "A Female Viking Warrior Confirmed by Genomics," the confident conclusion that the individual in Bj 581 was "the first confirmed female high-ranking Viking warrior" was conceivable only if countless ambiguities, uncertainties, and alternative interpretations were removed from consideration.[87] The very ambition, one may add, to scientifically "confirm" and "determine"[88] the complex social identity of a 1000-year-old set of human remains, could either appear to have been inspired by the selection criteria of the media or be seen as the effect of an "objectionable hubris,"[89] rather than any "transdisciplinary wisdom"[90] gathered in aDNA research. Social identities, after all, cannot simply be deduced from biological data and objects left behind, nor pinned down as if operating on a continuum from the more to the less likely.[91] Rather than being the "most incontestable" example of a female Viking warrior, as suggested by an enthusiastic archaeologist, it could well be argued that it is one of the most disputable, precisely on behalf of these pretentions at scientific closure.[92]

Apart from it being empirically and ethically questionable to attempt to impose a comprehensive identity on the individual in Bj 581—who, for all we know, may still have identified as a Christian man with an inclination for amusement and games, as suggested by the original excavator—the desire for closure and determination does not sit well with the study's concurrent ambitions for female restoration and empowerment.[93] If anything, feminist scholars have sought to resist a scientific discourse of finality in favor of the partly understood, paying tribute to "technologies of humility" rather than mechanisms of closure.[94] The kind of feminism powered by ancient genomics that transformed the individual in Bj 581 into a real Lagertha appears to have been guided primarily by present-day concerns about representation and by aspirations to reinvigorate the image of the Viking Age. Not actually "confirmed by genomics," the "female Viking warrior" was rather accomplished by something that it is tempting to designate as "bygonics." Effectively blurring the lines between the empirical Viking Age and its contemporary representation in popular culture, the case of the "female Viking warrior" presents itself as the ultimate confirmation, not of any historical reality, but of a prophesy made by one of the researchers in the *Real Vikings* episode: "We are going to see female warriors taking their place on the Viking stage."

Notes

1. Judith Jesch, "Viking 'Warrior Women,'" *History Extra*, March 4, 2019, https://www.historyextra.com/period/viking/birka-warrior-woman-vikings-female-argument-judith-jesch.

2. Charlotte Hedenstierna-Jonson et al., "A Female Viking Warrior Confirmed by Genomics," *American Journal of Physical Anthropology* 164, no. 4 (2017): 853–860.

3. Hedenstierna-Jonson et al., "Female Viking Warrior," 857.

4. Anna Källén et al., "Archaeogenetics in Popular Media: Contemporary Implications of Ancient DNA," *Current Swedish Archaeology* 27, no. 1 (2019): 69–91. Altmetric tracks the online activity around scholarly outputs, for example, tweets, news stories, and mentions on Wikipedia. The scientific article was number 43 on Altmetric's 2017 top 100 list of the most discussed journal articles that year. See "The Altmetric Top 100," Altmetric, accessed December 16, 2022, https://www.altmetric.com/top100/2017.

5. Shieldmaiden is a literary term for women taking part in battles. Shieldmaidens are found in medieval literature such as the Poetic Edda and the writings of Saxo Grammaticus. This literature features Old Norse culture (in the Scandinavian or Icelandic Viking Age, AD 800–1050), and it is debated among scholars to what extent they refer to real-world events and to what extent they are mythological representations of oral history narratives or the authors' own fantasies.

6. *Real Vikings*, season 1, episode 3, "Viking Women," directed by Rebecca Snow, aired December 14, 2016, on History Channel. Historical consultant to the series was professor of archaeology Neil Price—one of the researchers in the scene and one of the authors of the *AJPA* article.

7. *Real Vikings*; Sarah Banet-Weiser, "Postfeminism and Popular Feminism," *Feminist Media History* 4, no. 2 (2018): 152–156.

8. Hedenstierna-Jonson et al., "Female Viking Warrior," 854.

9. Hedenstierna-Jonson et al., "Female Viking Warrior," 854.

10. Hedenstierna-Jonson et al., "Female Viking Warrior," 857.

11. Hedenstierna-Jonson et al., "Female Viking Warrior," 858.

12. See the exhibition "Buried at Birka," Birka Museum, 2020, https://www.birkavikingastaden.se/en/attraction/new-exhibition-buried-at-birka. For an example of its use in pornography see Källén et al., "Archaeogenetics in Popular Media," 83. T-shirts are for sale in the Birka Museum shop. Documentaries include *The Viking Warrioress* (*La Guerrière de Birka*), directed by Gautier Dubois and Aleksandar Dzerdz, 2019; and *Viking Warrior Women*, directed by Stuart Strickson, aired December 3, 2019, on National Geographic. In the theater is the play written and directed by

Melanie Teichroeb, *Shield Maiden*, 2018. For a novel based on the article, see Nancy Marie Brown, *The Real Valkyrie: The Hidden History of Viking Warrior Women* (New York: St. Martin's, 2021).

13. "DNA Spotlight: High Ranking Birka Shield-Maiden," My True Ancestry, https://mytrueancestry.com/en/spotlights/birka.

14. Källén et al., "Archaeogenetics in Popular Media," 76.

15. Sofia Lotto Persio, "Gender Reveal: Ancient Viking Warrior Was a Woman, DNA Analysis Shows," *Newsweek*, September 11, 2017; Michael Greshko, "Famous Viking Warrior Was a Woman, DNA Reveals," *National Geographic*, September 12, 2017; Lianna Remigio, "New Science Shows High-Ranked Viking Warrior Was a Fierce Lady," *Bust*, September 12, 2017, https://bust.com/feminism/193441-viking-remains-uncovered-to-be-a-fierce-lady-warrior.html.

16. "Altmetric Attention Score," Altmetric, https://wiley.altmetric.com/details/24937638.

17. Howard Williams, "Viking Warrior Women: An Archaeodeath Response, Part 10," *Archaeodeath*, August 1, 2019, https://howardwilliamsblog.wordpress.com/2019/08/01/viking-warrior-women-an-archaeodeath-response-part-10/.

18. Murray Goulden, "Hobbits, Hunters and Hydrology: Images of a 'Missing Link,' and Its Scientific Communication," *Public Understanding of Science* 22, no. 5 (2013): 575–589.

19. Michael Price, "DNA Proves Fearsome Viking Warrior Was a Woman," *Science Magazine*, September 8, 2017; emphasis added.

20. "The Atlas. News and Publications" *Atlas Project*, accessed October 13, 2021, https://web.archive.org/web/20211013183529/http://theatlas.se; emphasis added.

21. Simon Trafford, "Hyper-Masculinity vs Viking Warrior Women: Pop Culture Vikings and Gender," *Just nu och för hemskt länge sedan*, January 11, 2019, https://blogg.mah.se/historiskastudier/2019/01/11/hyper-masculinity-vs-viking-warrior-women-pop-culture-vikings-and-gender.

22. Paula Cocozza, "Does New DNA Evidence Prove that There Were Female Viking Warlords?" *The Guardian*, September 12, 2017; Alanna Vagianos, "DNA Test Reveals Powerful Viking Warrior Was Actually a Woman," *Huffington Post*, September 11, 2017, https://www.huffpost.com/entry/dna-test-reveals-powerful-viking-warrior-was-actually-a-woman_n_59b68b72e4b0b5e531078e5b.

23. "DNA Confirms There Were Kick Ass Female Viking Warriors," Vocativ, September 12, 2017, Youtube video, 1:33, https://www.youtube.com/watch?v=vOp-7Sc5NNg.

24. Katherine J. Lewis, "'What Does a Man Do?' Representing and Performing Masculinity," in *Vikings and the Vikings: Essays on Television's History Channel Series*, ed. Paul Hardwick and Kate Lister (Jefferson, NC: McFarland, 2019), 59.

25. Louise Nordström, "Viking Warrior Found in Sweden Was a Woman, Researchers Confirm," *The Local*, September 8, 2017, https://www.thelocal.se/20170908/confirmed-viking-warrior-was-a-woman/.

26. The article was published on September 8, 2017, and what was to become known as the MeToo movement was initiated by actress Alyssa Milano on October 15.

27. Melfroh, "Feminism, Activism, Vikings, #MeToo," *Shield Maiden*, July 29, 2019, https://shieldmaidenplay.com/feminism-activism-vikings-metoo/?utm_source=rss&utm_medium=rss&utm_campaign=feminism-activism-vikings-metoo.

28. Ruth Kinane, "*Vikings* Channels the Time's Up Movement in New Promo," *Entertainment Weekly*, January 10, 2018, https://ew.com/tv/2018/01/10/vikings-times-up-promo/.

29. Källén et al., "Archaeogenetics in Popular Media," 82.

30. Källén et al., "Archaeogenetics in Popular Media," 82.

31. Källén et al., "Archaeogenetics in Popular Media," 83.

32. Helen Watanabe-O'Kelly, *Beauty or Beast? The Woman Warrior in the German Imagination* (Oxford: Oxford University Press, 2010); Patrick Geary, *Women at the Beginning: Origin Myths from the Amazons to the Virgin Mary* (Princeton, NJ: Princeton University Press, 2006).

33. Judith Jesch, *Women in the Viking Age* (New York: Boydell, 1991), 180.

34. Charlotte Hedenstierna-Jonson and Anna Kjellström, "The Urban Woman: On the Role and Identity of Women in Birka," in *Kvinner i vikingtid/Vikingatidens kvinnor*, ed. Nancy Coleman and Nanna Løkka (Oslo: Scandinavian Academic Press, 2014), 189; Anna Kjellström, "People in Transition: Life in the Mälaren Valley from an Osteological Perspective," in *Shetland and the Viking World: Papers from the Proceedings of the 17th Viking Congress 2013*, ed. Val Turner, Olwyn Owen, and Doreen Waugh (Lerwick: Shetland Heritage, 2016), 198.

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36. "Secrets of the Vikings." In the video, the reconstruction drawing by Þorhallur Þrainsson included in the 2017 article is interspersed with these claims about the identity of the individual.

37. Michael Starr, "History's 'Vikings' Lets Women Get in on the Action," *New York Post*, September 19, 2017.

38. Lewis, "What Does a Man Do?," 67.

39. David Reich, "How Genetics is Changing Our Understanding of 'Race,'" *New York Times*, March 23, 2018.

40. Kristian Kristiansen, “Towards a New Paradigm? The Third Science Revolution and its Possible Consequences in Archaeology,” *Current Swedish Archaeology* 22, no. 1 (2014): 27.

41. Dorothy Nelkin and M. Susan Lindee, *The DNA Mystique: The Gene as a Cultural Icon* (Ann Arbor: University of Michigan Press, 2004); Alondra Nelson, *The Social Life of DNA: Race, Reparations and Reconciliation after the Genome* (Boston, MA: Beacon, 2016).

42. Marianne Sommer, “DNA and Cultures of Remembrance: Anthropological Genetics, Biohistories and Biosocialities,” *BioSocieties* 5, no. 3 (2010): 372.

43. Hedenstierna-Jonson et al., “Female Viking Warrior,” 853.

44. Hedenstierna-Jonson et al., “Female Viking Warrior,” 858. The quote is from the poem “Atlamál” in the Poetic Edda, believed to have been written in the twelfth century.

45. See also James W. McAllister, “Scientists’ Reuse of Old Empirical Data: Epistemological Aspects,” *Philosophy of Science* 85, no. 5 (2018): 755–766.

46. Nelkin and Lindee, *DNA Mystique*, xxii.

47. See, for example, Mike Parker Pearson, *The Archaeology of Death and Burial* (College Station: Texas A&M University Press, 2000); Pamela Geller, “Brave Old World: Ancient DNA Testing and Sex Determination,” in *Exploring Sex and Gender in Bioarchaeology*, ed. Sabrina Agarwal and Julie Wesp (Albuquerque: University of New Mexico Press, 2017), 70–98.

48. Jesch, *Women in the Viking Age*, 180.

49. John McGowan-Hartmann, “Shadow of the Dragon: The Convergence of Myth and Science in Nineteenth Century Paleontological Imagery,” *Journal of Social History* 47, no. 1 (2013): 56. McGowan-Hartmann’s summary reads: “If there is such a thing as a dragon, it is here. And it is real. Not fantasy, science; not unknown, known; ancient, but revealed by modern knowledge; an important field of study, and a little scary, in an entertaining sort of way.”

50. John Robb, “Towards a Critical Ötziography: Inventing Prehistoric Bodies,” in *Social Bodies*, ed. Helen Lambert and Maryon McDonald (Oxford: Berghahn, 2009), 104.

51. Robb, “Towards a Critical Ötziography,” 105.

52. Robb, “Towards a Critical Ötziography,” 106.

53. Robb, “Towards a Critical Ötziography.” See also Nina Nordström, “The Immortals: Prehistoric Individuals as Ideological and Therapeutic Tools in Our Time,” in *Archaeologists and the Dead: Mortuary Archaeology in Contemporary Society*, ed. Howard Williams and Melanie Giles (Oxford: Oxford University Press, 2016), 204–232; Amade

M'charek, "Beyond Fact or Fiction: On the Materiality of Race in Practice," *Cultural Anthropology* 28, no. 3 (2005): 420–442.

54. Robb, "Towards a Critical Ötziography," 112.

55. *Viking Warrioress*, statement by Neil Price. Emphasis in original.

56. *Viking Warrioress*, statement by Charlotte Hedenstierna-Jonson.

57. *Secrets of the Dead,* season 18, episode 4, "Viking Warrior Queen," directed by Alexandar Dzerdz and Gautier Dubois, released July 7, 2020, on PBS. Statement by Charlotte Hedenstierna-Jonson, who was also acting as historical consultant for the production.

58. Neil Price et al., "Viking Warrior Women? Reassessing Birka Chamber Grave Bj.581," *Antiquity* 93, no. 367 (2019): 181–198.

59. Hedenstierna-Jonson et al., "Female Viking Warrior," 854.

60. "Supporting Information 2," in Hedenstierna-Jonson et al., "Female Viking Warrior," 20, https://onlinelibrary.wiley.com/action/downloadSupplement?doi=10.1002%2Fajpa.23308&file=ajpa23308-sup-0002-suppinfo2.docx.

61. Price et al., "Viking Warrior Women?," 193.

62. Julie Solometo and Joshua Moss, "Picturing the Past: Gender in *National Geographic* Reconstructions of Prehistoric Life," *American Antiquity* 78, no. 1 (2013): 124.

63. Stephanie Moser, "The Visual Language of Archaeology: A Case Study of the Neanderthals," *Antiquity* 66, no. 253 (1992): 831–844.

64. Solometo and Moss, "Picturing the Past," 124.

65. Joan Gero, "Honoring Ambiguity/Problematizing Certitude," *Journal of Archaeological Method and Theory* 14, no. 3 (2007): 320.

66. "Supplementary material," in Price et al., "Viking Warrior Women?" 23, https://static.cambridge.org/content/id/urn:cambridge.org:id:article:S0003598X18002582/resource/name/S0003598X18002582sup001.pdf.

67. See Gero on "machining data" as one of several strategies for stabilizing evidence and producing knowledge that appears unambiguous. Gero, "Honoring Ambiguity," 320–321.

68. "Viking Women," *Real Vikings*. Hedenstierna-Jonson et al., "A Female Viking Warrior," 853: the abstract states that "An earlier osteological classification of the individual as female was considered controversial in a historical and archaeological context. A genomic confirmation of the biological sex of the individual was considered necessary to solve the issue."

69. Roger Cooter and Stephen Pumfrey, "Separate Spheres and Public Places: Reflections on the History of Science Popularization and Science in Popular Culture," *History of Science* 32, no. 3 (1994): 237.

70. David A. Kirby, “Science Consultants, Fictional Films, and Scientific Practice,” *Social Studies of Science* 33, no. 2 (2003): 231–268; José van Dijck, “Reading the Human Genome Narrative,” *Science as Culture* 5, no. 2 (1995): 217–247.

71. M’charek, “Beyond Fact or Fiction,” 436.

72. Price et al., “Viking Warrior Women?” 182.

73. Price et al., “Viking Warrior Women?” 182.

74. Price at al., “Viking Warrior Women?” 181, 182.

75. Judith Jesch, “Some Further Discussion of the Article on Bj 581,” *Norse and Viking Ramblings*, September 18, 2017, http://norseandviking.blogspot.com/2017/09/some-further-discussion-of-article-on.html.

76. Simone Rödder, “Reassessing the Concept of a Medialization of Science: A Story from the ‘Book of Life,’” *Public Understanding of Science* 18, no. 4 (2009): 452–463.

77. Elizabeth D. Jones, “Ancient Genetics to Ancient Genomics: Celebrity and Credibility in Data-Driven Practice,” *Biology and Philosophy* 34, no. 27 (2019): 1–35.

78. Nelkin and Lindee, *DNA Mystique*, xxii. See also Jones, “Ancient Genetics to Ancient Genomics,” 7–14.

79. Frank Marcinkowski and Matthias Kohring, “The Changing Rationale of Science Communication: A Challenge to Scientific Autonomy,” *Journal of Science Communication* 13, no. 3 (2014): 1–8.

80. Christopher M. Stojanowski and William N. Duncan, “Engaging Bodies in the Public Imagination: Bioarchaeology as Social Science, and Humanities,” *American Journal of Human Biology* 27, no. 1 (2015): 52, 57.

81. Stojanowski and Duncan, “Engaging Bodies,” 57.

82. Stojanowski and Duncan, “Engaging Bodies,” 51.

83. “Supplementary material,” in Price et al., “Viking Warrior Women?” 21, https://static.cambridge.org/content/id/urn:cambridge.org:id:article:S0003598X18002582/resource/name/S0003598X18002582sup001.pdf.

84. Robb, “Towards a Critical Ötziography,” 112.

85. Melanie Piper, “Real Body, Fake Person: Recontextualizing Celebrity Bodies in Fandom and Film,” *Transformative Works and Cultures* 20 (2015), https://journal.transformativeworks.org/index.php/twc/article/view/664/542.

86. Andreas Gunnarsson, *Unleashing Science Popularization: Studies on Science as Popular Culture* (Gothenburg: University of Gothenburg, 2012), 4.

87. For an overview of academic and popular responses to the “female Viking warrior,” see archaeologist Howard Williams’s blog *Archaeodeath*, https://howardwilliamsblog.wordpress.com.

88. Hedenstierna-Jonson et al., “Female Viking Warrior,” 855. The authors state that “a female warrior of this importance has never been determined.”

89. Priscilla Wald, “Future Perfect: Grammar, Genes, and Geography,” *New Literary History*, 31, no. 4 (2000): 681.

90. Jane E. Buikstra and Katelyn L. Bolhofer, “Bioarchaeologists Speak Out: An Introduction,” in *Bioarchaeologists Speak Out: Deep Time Perspectives on Contemporary Issues*, ed. Jane E. Buikstra (Cham: Springer, 2019), 2.

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92. Persio, “Gender Reveal.”

93. Hjalmar Stolpe, “Ett och annat om Björkö i Mälaren,” *Ny Illustrerad Tidning*, December 21, 1889.

94. Donna Haraway, “Situated Knowledges: The Science Question in Feminism and the Privilege of Partial Perspective,” *Feminist Studies* 14, no. 3 (1988): 575–599; Sheila Jasanoff, “Technologies of Humility,” *Nature* 450, no. 7166 (2007): 33; Gero, “Honoring Ambiguity.”

7 Ancient DNA and the Politics of Ethnicity in Neo-Nationalist China

Magnus Fiskesjö

The imposition of conventional national, ethnic, or other labels as a way to classify human DNA data inevitably creates a dilemma for ancient DNA (aDNA) studies, for genetics generally, and for our understanding of history. Some scholars have discussed this problem, yet they often leave out the case of China entirely.[1] Some have proposed solutions such as the use of geographical terms that do not correspond to—and therefore can avoid getting mixed up with—today's political entities.[2] In 2021, a group of scholars proposed a set of ethics rules for aDNA studies.[3] However, they left out the issue of naming, perhaps not fully grasping the dangers involved, given that the manipulation of ethnicities in genetics is often heavily politicized, not least in authoritarian countries like China.

Frequently left out of these discussions around the labeling of populations in aDNA research is the fundamental point that while human biological differences and variations are real, it is we who splice the continuum of human difference and name entities as separate and distinct. This act of naming is a social act carried out in social context, and typically in a situation of power inequality.

While some form of classification for genetic data is necessary, the use of ethnonyms or similar names to categorize genetic clusters often creates the false impression of self-evident "natural" identities that seamlessly coincide with contemporary concepts, such as, for example, "China."[4] This problem is exacerbated today by the powerful trend toward embracing identities as the primary lens through which to see the world. The new nationalisms that grow out of this trend also influence researchers how to frame and narrate their research.

The repertoire of names used in aDNA research often derives from implicit frames of reference that draw on tradition, scholarly practice, and habit. But these names can also be explicitly mandated by authorities that monopolize the power to define social identities. This chapter focuses on contemporary China, where there is a state-mandated framing of identities, policed by government authorities and dictating the image of a "China" that has dominated its region since ancient times. This places heavy, inescapable constraints on how past and present human groups must be named and discussed. These constraints impact significantly on aDNA research, which like all science in China must conform to the nationalist ideas embraced by the current one-party state. These constraints are often not understood or acknowledged in Western accounts of aDNA research in China—such as the ones I cite here—which generally go along with them, and fail to recognize how they frame and constrain the research. My sample size of aDNA research on China is not large, but I believe that when considered in the context of today's aggressive Chinese nationalism and how it affects our view of the past, these initial findings are suggestive.

Before I discuss China and the consequences of the new Chinese nationalism for archaeology and aDNA studies in this region, a few general observations should be made that are relevant to aDNA studies more broadly. One consequence of the act of naming is the implication that the named phenomena possess a coherence and stability. This can mask both their complexity, their change over time, and their process of formation. We end up assuming that all phenomena are fixed with a core essence, and we may even assume that only that which can be precisely measured, delineated, and identified is real at all.[5]

The Denisovans, first identified in Russia and recently confirmed as having lived in East and Southeast Asia, provide a powerful example of how the act of naming ancient people can mislead us badly and make us forget the process through which they are created. The Denisovans, hominids related to both Neanderthals and modern humans, were given their name after the Siberian site of their discovery, the Denisova Cave in the Altai Mountains. A few bones and teeth provided recoverable genetic material, which first enabled their identification and classification as a species separate from other relatives. The species was recently confirmed by aDNA from another skeletal fragment, as well as from soil samples from a cave on Chinese territory.[6] Further discoveries of Denisovan-like DNA in present-day people in Papua New Guinea, the Philippines, and elsewhere have suggested an underlying, yet unmapped, history of interaction with *Homo sapiens* comparable to our drawn-out interaction with the Neanderthals, who similarly "live on" inside us.[7]

Many scientists know that these discoveries mask a story of evolutionary change that is more complex and extensive than we are yet able to understand. From the moment the Denisovans were named and their story was told by science writers, however, they came to be understood in society at large as a single, coherent group of people, wandering from Central Asia all the way to Island Southeast Asia, an "elusive bunch" moving in to sleep with the natives.[8] Scientists may be clear that we have limited knowledge, and know only that between Siberia, the Philippines, and Papua New Guinea exchanges of genetic material occurred over many tens of thousands of years. However, an image emerges, not of complex patterns of change, but of groups of people packing their bags to move across the landscape.

This is an example of how modern-day concepts of people as ethnicities shape our understanding of the distant past, even though ethnicity as such may not even be salient or relevant for the times when the Denisovans lived. We can be sure, however, that they did not call themselves Denisovans—just as the ancient inhabitants of what is today China did not think of themselves as living in China, regardless of what today's rulers of China would like us to think.

The Origins of China's New "Genetic" Nationalism

China's recent turn toward an aggressive new—and increasingly genetically defined—nationalism is the latest chapter in a long struggle over the identity of China the nation and the Chinese people after the fall of the last empire. To understand the place of aDNA in current Chinese nationalism, it is necessary to recap this history.

As a political entity, China can be traced back to the second millennium BCE, to the early Bronze Age kingdoms in what is today northern China that were based on agriculture, mining, and war. These kingdoms were overcome by the first large conquest empire in the third century BCE, which created a structure that has been resuscitated again and again over the last two millennia. This suggests a continuity that is partly due to the continuing survival of the written language of the Bronze Age and imperial classics, deployed even when "alien" or "barbarian" dynasties came in to take over and revive the empire.[9]

Until 1912, China was, in other words, not a nation but a conquest empire. It claimed to rule the world, "all under heaven." The key tenets of imperial ideology were not about race or ethnicity. Instead, non-Chinese were regarded as inferior barbarians who would all eventually submit to Chinese rule.[10] After Republican Chinese revolutionaries overthrew the last dynasty in 1911–1912, they grappled with how China could become a modern unified nation-state like Japan and the countries of Europe, which all claimed a majority ethnicity coinciding with the state: the nation-state.[11] For many Chinese intellectuals, China now became a "race-nation,"[12] in which the older imperial idea of innate civilizational superiority was merged with European-derived notions of a superior "race" in charge—the "Chinese race."[13] Some Chinese nationalist intellectuals (including the most famous Republican, Sun Yat-sen) advocated turning the empire into a pure, unified state without recognition for the diverse peoples that inhabited it.[14] They also touted the Yellow Emperor, a late-nineteenth century invention, as an ancestor of the Han Chinese. The Han "group," which today counts as the dominant ethnic group in China, was actually invented in its present form only in the late nineteenth century, as part of the nationalist drive that copied ideas about ethnicity and modern ethnopolitics from Japan and Europe. In the 1950s, the "Han Chinese" label was designed to comprise over 90 percent of the population, despite the huge internal differences—including linguistic ones.[15] Most international geneticists and others don't know this history, and habitually go along with the Chinese fiction that the Han Chinese is an ancient people existing in its present form since ancient times, and now claimed to be "the world's largest ethnic group."[16]

The Chinese communists promised in the 1930s that if they came to power, each of the peoples conquered by the past empires would be allowed to separate from China to form independent countries. This included Tibet, the Uyghurs in "Xinjiang" (China's "New Frontier" in Central Asia, conquered in the eighteenth century) and other peoples. But when they got into power in 1949, the Communists reneged on the promise, instead introducing a Soviet-inspired model with nominal autonomy for "ethnic minorities" (*shaoshu minzu*). These groups were, in reality, subjected to Han Chinese rule and heavy-handed cultural assimilation, in obvious continuity with the empire, but now with a nationalist dimension.[17]

The new official "truth" was that the modern nation China had always existed its current, modern size.[18] Moreover, the Communist regime insisted that despite the distinctive non-Chinese languages and cultures of the non-Han ethnic minorities, they too had always been part of a single, mysteriously united, Chinese ethnicity (*Zhonghua minzu*). In this "Chinese super-nation," the Han were counted as the dominant faction, and all peoples present on today's map of China were seen as having always been destined to merge into this entity, guided in this "development" by the innately superior Han.[19]

When this idea was fashioned from the 1950s onward, it could still only be vaguely justified in terms of genealogy, history, and archaeology. Genetics could not yet be used to prove such links or serve as a tool of Chinese statecraft, as it is today. Instead, so-called ethnohistorians stepped up to reread the Chinese classics in order to show how all the various peoples named there really corresponded to modern-day ethnicities (which find their meaning in contributing to the formation of China).[20]

When modern archaeology came to China in the early twentieth century, Chinese archaeologists continued the quest to reconfirm the classics and assemble a new revised story of an autochthonous Chinese civilization.[21] But excavations yielded voluminous discoveries of previously unknown and nameless prehistoric people who had lived across the East Asian mainland during Neolithic times. At first, this presented a difficult challenge for the orthodox conception of China. Where had these peoples come from? However, by the mid-twentieth century, Chinese archaeologists synthesized a new national (pre)history according to which autochthonous Neolithic peoples across East Asia all merged into the ethnically Han Chinese nation.[22] Preferably, the "Chinese" even formed a distinct branch of human evolution—an effort to avoid the idea that the Chinese, like everyone else, might be descendants of migrants from Africa.[23]

Even more important, however, is the glorification of the "rejuvenated" nation and the past empires, which now dominates official discourse in China.[24] This stands in direct conflict with earlier communist ideas about inequality, exploitation, and class struggle. The solution has been to drop class struggle and focus on the glory of China.

Needless to say, the whole theory of an Ur-Chinese race-nation that expanded and swallowed up others because of its superior virtue, embodied by the emperors, is false and misleading. When the Chinese ethnohistorians and archaeologists interpreted the movement of named ethnic groups on their map as proof of the real migrations of peoples, they ignored the fact that the history they traced was not one of migrations, but mostly of the Chinese empires expanding by force and conquering others. What the empire actually did was to recycle its set of names for the barbarians of each cardinal direction and shift the labels to new, yet-to-be conquered peoples.[25] This is one of the most striking examples anywhere of how human populations and the ethnic labels imposed on them are not the same thing—and this despite the long-standing Chinese obsession with the "rectification of names," that is, uniting the name and the reality it supposedly refers to.[26]

Enter the New Genetics

The modern-era Chinese nationalist longing for national purity and unity was adopted by the Communist Party leaders in the 2010s.[27] In 2017, the long-running project of assimilating the non-Chinese—inherited from the empire's ideology of civilization—was aggressively accelerated with the forced assimilation of the Uyghurs in the Xinjiang region, a wide-ranging campaign with atrocities that already meets the definition of genocide.[28]

This genocide, which today very much frames the current practice of genetics, archaeology, and other sciences in China, is carried out by the full machinery of the Chinese state, which combines and uses new technologies for a surveillance program unprecedented in history. This includes AI-driven face recognition, records of the iris, voice, gait, blood type and fingerprints, the massive collection of DNA from the entire population, as well as QR-coding homes and tracking phones.[29] The collected information is being used to detain massive numbers of people in camps and forced-labor factories, while children are confiscated in the hundreds of thousands and cut off from their family and culture.[30] Also, large numbers of Uyghur women have been sterilized by force.[31]

How is the genetic information used and how does it relate to the state's orthodox version of Chinese identity? One obvious use is the immediate practical use of racial profiling of Uyghurs and other Central Asian people in order to identify and classify them, so they can be targeted with coercive and destructive measures.

The Chinese government has never explicitly stated precisely what other purposes the accumulation of the massive data-banks of genomic information will serve. Even so, the gathering of DNA is also increasingly done on people in the Han Chinese majority in a compulsory or semimandatory manner on a mass scale across China. The collecting of DNA now intentionally targets ordinary citizens' patrilineal connections, traced over several generations, by harvesting male Y-chromosome genetic data, which is then incorporated into the world's largest database of such information.[32] While the ultimate purpose remains unclear, it may mirror the goals apparently pursued by the regime in the areas inhabited by ethnic minorities: to accurately delineate, catalog, and identify individuals over time, with a certain time depth, so as to be able to manipulate or eliminate undesirable units of the broader population.

The first time I heard of the new, expansive DNA collection was in the incident of a young Chinese man who had created an app to help connect people whose social media messages had been deleted by the authorities. He was quickly sought out at home by the police, who forced him to sign a statement that he would never do such a thing again, and took his blood and DNA without explanation.[33]

The Chinese state's DNA database forms part of the build-up of precrime policing, which can combine DNA-based identification with face recognition and personal history for an instant, real-time identification. The technologies are developed by the burgeoning Chinese genomic and surveillance industries, and with the aid of Western counterpart companies, universities, and investors.[34] It surely also has to do with the nascent "social credit" system, by which ordinary Chinese people—not members of the party elite—are constantly ranked.[35] There are also credible reports that the Chinese regime actively collects DNA on foreigners and harvests vast amounts of personal information abroad. This DNA information can be seen as a tool of global racial profiling that will enable the use of ethnic or "racial" characteristics in the Chinese regime's biopolitical management of people worldwide.[36]

Ancient DNA, China, and the "World's Largest Ethnic Group"

Since its beginnings in China, genetics has been used to try to describe and delineate the nation and its constituent peoples in order to control them and, in the case of the non-Chinese ethnicities, construct a narrative about their necessary, subservient relation to the nation's majority group.[37] Huge volumes of research have been put out in this vein—from earlier descriptive studies of ethnic distinctions (exemplified by the curious body of literature on the dermatoglyphics or fingerprint patterns of minorities) to the current, more sophisticated and AI-engineered study of human DNA variation by ethnicity.[38]

For this chapter, the two most important aspects of this research are, first, the potential challenge of aDNA to the orthodoxy of Chinese national identity and how this challenge is met in Chinese research and, second, how the story of aDNA is being incorporated into the state narrative mounted to erase the Uyghurs and other targeted minorities.

Recent breakthroughs in genetics and ancient genomics promise new possibilities for the delineation, identification, and possible manipulation of ethnic groups. The stunning successes in collecting and analyzing the DNA from living people, which has been used to build deep "family trees" of populations going from the present back into history,[39] as well as the successful extraction and analysis of DNA from ancient remains—all of this might have presented a challenge to the state orthodoxy of Chinese identity. Yet, this orthodoxy seems to be holding up in the same way that it withstood the potentially devastating archaeological discoveries of an unknown, pluralistic Neolithic, which, as mentioned above, was nevertheless coopted into the narrative of an eternal, dominant "China."

Recent aDNA research in China is framed according to the reigning view of an unstoppable, "natural" expansion of the ancestors of the (superior Han) Chinese, who merged and created a "China" millennia before one existed in written history. Chinese archaeogeneticists are successfully continuing the twentieth-century efforts to extend the concept of China backward in time.[40] Instead of the pottery traditions used in earlier archaeology, these scientists build on new genetic data that suggest a similar process of how a Han Chinese genome merged together.

One representative and much-cited piece has Melinda Yang, a scholar of Chinese origin based in the United States, as its main author.[41] It draws on genetic material from "26 ancient individuals from northern and southern East Asia spanning 9500 to 300 years ago," and seizes on how the diversity of an earlier Neolithic decreases through a dramatic "admixture" process which implies the unification of a China-to-be.[42] This argument is underpinned by the constant reference to the sites of the samples as derived from "China." While the geographical term "East Asia" is sometimes used, the article mostly speaks in terms of northern and southern China, as if the ancient south (East Asia south of the Yangtze River) was already Chinese, even though the conquest of this region and the destruction of its previous cultures actually took place in Neolithic and Bronze Age times. This is one of many examples of how contemporary Chinese archaeogenetics projects the term "China" backward in time, not just as a shorthand, but to suggest it existed—a move that we find repeated elsewhere in the world, for similar reasons and in similar nationalistic contexts.[43]

In the article by Yang and colleagues, we see recently published aDNA data marshaled as confirmation of what earlier population genetics studies of living groups have already suggested: while today's southern Chinese sometimes carry the same genetic variants of those speakers of Austronesian languages who dispersed from today's China into the Pacific and beyond, the Austronesian cultures south of the Yangtze were destroyed and replaced during prehistory.[44] Austronesian speakers may have been the first East Asian rice-growing people in the Yangtze valley—but their entire language family and their cultures are now completely extinct in mainland China. All that remains are a few obscure loanwords in Chinese.[45] Their languages survive today only because the language family spread first to Taiwan and from there to the Philippines, the Pacific, much of Southeast Asia, and even Madagascar. On the mainland, the story is one of Chinese-speaking peoples' displacement and assimilation of older southern cultures in the south region from the Yangtze and southward, which in prehistoric times was more like an extension of the diversity of Southeast Asia.

Against this background, it is fascinating to see how the new research by the team headed by Melinda Yang is presented to confirm the genetic homogenization of "China's South." While Yang's article uses terms like "human population shifts" and does not contain any explicit statements that the text is about the creation of China, a news release from the American Association for the Advancement of Science jumped to the conclusion that the article "reveals [the] genetic history of China" through aDNA.[46] In making this claim, the association goes along with the Chinese researchers' language and with much common practice. The news release speaks of the great replacement in what is today southern China only as a matter of how "northern populations spread southward, transforming southern China's Austronesian genetic ancestry," which in turn "gave rise to modern population genetics."[47] This is a dressed-up way of saying that modern China emerged from the displacement and assimilation of more ancient southerners.

Other ancient DNA studies are even clearer in their objective of reconfirming the ancestry of China and its dominant people today—the Han Chinese—as the "World's Largest Ethnic Group."[48] In a paper written by population geneticist Charleston Wen-Kai Chiang and colleagues, the ancient coherence and expansion of the Han people are attributed to "their advantage in agriculture and technology," which led their population "to become the largest ethnic group today in China."[49] This is stated about an identity that was actually constructed in the late nineteenth century in response to European nationalist ideas about unitary nations and national origins. We now see it affirmed—and "confirmed"—by the prestige of genomic science.

Many geneticists who write these treatises are sophisticated scientists who are conversant with the methods and theories in their field. Yet, they cannot easily escape the dilemma inherent in how their research is framed conceptually, as they are dependent on terms such as "China," "Han Chinese," "minorities," and so on. Thus, there is a widespread lack of attention to the potential problems inherent in this type of research.

I suggest that this situation results from two main factors. The first is the inertia of inherited concepts, names, and labels that scholars recycle and apply without thinking. This issue is not unique to China; it exists in other parts of the world, where names and labels are only recently coming under debate. The second factor is more important and insidious. For the reasons I have explained above, political leaders as well as nationalist academics in China will frequently declare what is the "correct" approach to archaeology and genetics. Scholars cannot go against such declarations. In the current climate, there is a shrinking space for public debate and it is unthinkable for a scholar to publish unorthodox ideas or a radical rethinking of a field. Instead, scholars pursue research within the parameters set by government authorities and policies—and this is so even for scholars based outside of China, who can be denied visas if they show themselves too unorthodox.

As archaeologist and anthropologist Erika Evasdottir has described in her 2004 book *Obedient Autonomy*, archaeologists, just like geneticists and other scientists in China, try to maintain some creative space within these parameters.[50] Concretely, this means that in order to preserve limited freedom to pursue their own favorite issues, archaeologists seldom violate the tenets set down by officialdom regarding the sensitive questions of how China came to be, Chinese identity, and so forth. This is especially the case now that China's top party leader—as we will see below—has personally laid out an agenda on archaeology, culture, and history.

In the case of aDNA, the leading Chinese geneticist Fu Qiaomei is an outstanding example of this "obedient autonomy."[51] In China, she is sometimes featured on state television, cheerfully discussing topics such as "the genetic histories of the Chinese." Here, she brilliantly navigates the set limits while presenting the new research on admixture events in high antiquity that created the Chinese people, lending this axiom new scientific authority.

The space available in China for public debate and criticism has been cut drastically under the current General Secretary of the Communist Party, Xi Jinping. Since Xi came to power in 2012, he has systematically reasserted and increased the party's control and censorship of all media and all publishing. He is directly responsible for the atrocious policies in Xinjiang, which he has publicly described as "totally correct."[52] His top priority is making China great again, and he therefore takes a keen interest not only in armaments and aircraft carriers, but also in archaeology and history. While Xi does not get into specifics of genetics, he appropriates the term "DNA" (used interchangeably with the Chinese word for gene, *jiyin*) to speak of the "DNA" of the Chinese nation—an unexplained but scientific-sounding and therefore seemingly authoritative abstraction of the nation's enduring essence.[53]

In November 2020, President Xi published an article in his own name, disseminated throughout official media, where he mobilizes "DNA" to speak of the achievements of the Chinese nation across the millennia, which Xi also specifies as archaeology's task to describe and glorify.[54] He enshrines detailed accounts of archaeological findings and promotes a deeply essentialist idea of a "rejuvenated" China, "the Chinese nation's undying, everlasting, never-fading cultural DNA" (*Zhonghua minzu sheng sheng bu xi, chang sheng bu shuai de wenhua jiyin*).[55]

Such pronouncements cannot be openly contradicted by anyone. Just as in Mao's and Stalin's time, they also have an increasing tendency to be copied and integrated into the writings of every scientist as part of an openly and unapologetically politicized science.

There is an inherent tension between the conditions for Chinese scholars operating in China, and those on the outside who can theoretically still critique these Chinese constraints and the state orthodoxy about history. This tension enters a grey zone in situations where, for example, Chinese scholars undertake genetic research in China but are based abroad, or where they have foreign coauthors. As for non-Chinese scholars, their awareness of the nature and consequences of contemporary Chinese nationalism will vary greatly. If they lack sufficient awareness and/or are not fully engaged with the work, they may find themselves inadvertently signing off on or copying not just the essentialized Chinese ethnonationalism, with its framing and vocabulary for talking about its ancestry, but even the general secretary's guidance, and the genetics abuse in Xinjiang.[56] If they should refuse to obey the party line, or dare speak against it, they may be blocked from China.

The Incoherent Other

In this penultimate section, I return to the use of aDNA in the erasure of unwanted ethnicities, and its role in the current Chinese government's project of unifying the Chinese nation to make it "rejuvenated." Here I seek to show that, in great contrast with how aDNA has been used to reconfirm the perceived unity and development of the dominant Han Chinese as the world's largest ethnic group (as discussed above), ethnic minorities are, at the same time, shown as "always already" incoherent and ultimately nonviable. Their inevitable fate is therefore to be assimilated into the unified Chinese nation.

This interpretation of aDNA research in China is no surprise. As we have seen, archaeologists have long been instructed to interpret their findings to promote the glorious history of the nation. Indeed, at the outset of the current genocide in Xinjiang, officials renewed their call on archaeologists to prove in their work that the region has been part of China "since ancient times."[57] The officials already know that in the nationalist climate in China, it would be difficult, if not impossible, for any archaeologist to publish anything that contradicts the narrative of the state (or its leader) about the antiquity and glory of China. In this vein, "minorities" are invariably confirmed as fading appendages who at most can get a nod for having contributed to China's greatness.

But there is more. The minorities must also be described as inherently incoherent: they do not coalesce into glorious nations. Not only was Xinjiang always Chinese—a statement plainly at variance with the truth—but the peoples who live there now and yearn for genuine autonomy must themselves be described as historical failures.

The tone for this project has been set by the central government itself in one of the many "white papers" issued on Xinjiang.[58] This is a fascinating, if repugnant, text that reiterates the state narrative on the formation of China, and in the process even presents the imperial-era Chinese set of terms for the barbarians of the four directions as real, actual "ethnic groups."[59] This is another example of how the alternate reality created by the state's effort to interpret and name the past is presented as an uncontestable historical fact. On Xinjiang, the paper insists not only that the central Asian region has been a part of China since ancient times, but that any and all of the independent kingdoms (of which there were many) that have ever existed historically in that region "were all local regimes within the territory of China; they were never independent countries." In particular, the paper states that there was never a "so-called" modern East Turkistan republic (although such a republic was indeed twice set up in the 1930s and 1940s): "Xinjiang Has Never Been 'East Turkistan.'"[60]

As for Islam, which is widely prohibited and persecuted as part of the genocidal program in the region, the religion is described as having been forced on the people by outsiders, rather than being the choice of the local Uyghurs themselves. Moreover, the paper argues that the people who are called "Uyghurs" today were formed by various migrations and mergers, including "the Han people."[61] That is, the "Uyghur"—today a people of at least twelve million, with a long history of writing, literature, and other distinct cultural achievements—is not really a coherent thing.

As if on cue, new aDNA research can be seen to affirm these guidelines from the powers that be. This research claims that the peoples who have lived in this region, unlike the Han Chinese, never coalesced into enduring nations. Instead, they are mixed, without achieving an essential, Chinese-styled "unity." For example, one recent article by anthropologist Wenjun Wang and colleagues aims to "understand the genetic history of Xinjiang."[62] It draws on aDNA from 237 samples in the region, suggesting that this shows past "intense admixture with high genetic diversity" and that "future studies with ancient genomic data will reveal more admixture patterns in this region," that is to say, not cohesion, as in the case of China.[63] I believe this can only be read as portraying diversity as hopelessly splintered and not viable, because not "united."

In genetics proper, genetic diversity as such is not necessarily infused with such politics. It can even be an indicator of antiquity, since a life-form with a long history in a place has had more time to diversify. But I submit that here, outside of the genetic definition, diversity is being used to signify weakness, and mixture disunity. As we have seen, the preferred Chinese story, seemingly confirmed by the new archaeogenetics, is an amalgamation from the center, whose ancestry is ascribed to the core of that center. In this light, the findings of genetic disunity ("diversity") in the region of the Uyghurs is not coincidental—rather, they are the direct or indirect result of policy directives to scholars.

In another similar example, geneticist Qidi Feng and colleagues speak of a "complex scenario of ancestral origins and admixture history" in the midst of "massive migrations" in ancient times, as part of the (splintered) genetic history of the Uyghur people who today live in the Xinjiang region.[64] Back in 2010, Chunxiang Li and colleagues wrote about the "West-East admixed population" that supposedly characterizes Xinjiang—a move that I understand as emphasizing that the Uyghur nation does not stand on its own as a coherent entity, but wavers between West and East.[65] And in 2015, Shi-Zhi Gao and colleagues emphasized that Xinjiang is (unfortunately) a "crossroads," but (thankfully) experienced the in-migration of ancient Chinese people already in the Bronze Age.[66]

None of this is coincidental. The findings are meant to show that humans in the Xinjiang region have never arrived at anything like coherence or unity. The thrust of these studies is that the region's people have been unable to achieve an independent existence, at best existing as fleeting, temporary historical appendages to the body of an enduring China. This is the result desired by state officials, produced within the official framing provided by the state, and aided by foreign scientists and publishers who relay it without comment or without examining the life of the labels in use.

Finally, the most recent example is the curious battle over the Tarim mummies. These comprise a series of human remains found in the deserts of today's Uyghur region, dating back to the second and first millennia BCE and having features that have historically been interpreted as "European." This has even led some scholars to argue that the mummified people were the forebears of speakers of Tocharian, an Indo-European language also attested from the region.[67]

But now, a series of Chinese and international geneticists have extracted aDNA from these mummies and analyzed it, concluding that these individuals were not "Westerners," "Europeans," or "Eurasians," but "Asian."[68] The term "Asian" is obviously chosen as a convenient contrast to the labeling of the remains as "European" or "Eurasians." Regardless of the validity of the genetics assessments themselves, it is difficult to see the formulations of these conclusions as other than tendentious affirmations of the labels "non-Western," and "Asian," which affiliate the remains of humans who predate such concepts with the modern peoples defined by them. This is done as if to provide these ancient humans with an avenue into the families of peoples that—like Uyghurs and others—would later be absorbed into a powerful China.

Here, it is not only the term "China," but also "Eurasian" and "Asian," that stand out. With these terms, the international team may perhaps have only geographical considerations in mind, as if they were unaware of how all of these labels are loaded with contemporary significance. None of the presentations of the findings by the original authors or science journalists raise the issue of naming, and none consider what the ideological motivations or repercussions for the terminological choices made may be.[69] In its report on the archaeogenetic analysis of the mummies, the Hong Kong–based, pro-China newspaper *South China Morning Post* chose the triumphant headline "Xinjiang Mummies' Origins Closer to Home than We Thought," emphasizing that an authoritative "international team" had found that these mummies were not "Westerners" but "Asians."[70] In the article, these term are not used as neutral terms, but as distinctly contemporary ethnic concepts alive with controversy in the context of the Chinese claim to dominance.

Conclusions

We do not know the motives behind the Chinese authorities' mass collecting of DNA data from Uyghur and Chinese people. It is possible that they go beyond known aspects of surveillance, biopolitical management, and sorting for the genocide in Xinjiang, which itself is meant to purify the rejuvenated Chinese race-nation.

Regardless, the pursuit of DNA collection from the living is sure to be accompanied by continued research into aDNA, which itself will continue to be directed by the same party-state policy goals of making China great once again. My prediction is that the state narrative of an ancient and magically coherent China will continue to be promoted with new findings from aDNA research. By the same token, the other peoples and cultures that have inhabited East Asia will continue to be demoted and depicted as merely passive appendages to the body of this enduring "China." This is an abusive use of the power of naming, which has enormous significance: bolstering the Chinese regime's nationalist identity claims today, by way of bolstering its bid to fully control the past, as well.

Around the world, non-Chinese geneticists, editors, and other actors involved in the dissemination of aDNA studies in China often seek to be "respectful" of Chinese colleagues. In doing so, they may not understand the politics of archaeology and history in China, and are likely to be coopted into the unquestioned support of the Chinese government's agenda. This state of affairs is likely to continue unless the Chinese use and abuse of DNA, and of the power of naming, come into focus and receive the attention that they deserve. If not, it is likely that the same abuse of "essential" national identities projected into the past—so as to dominate that past, the present, and the future by way of that past—will continue in other parts of the world as well.

Notes

1. Daniel Strand, "0.01%: Genetics, Race and the Methodology of Differentiation," *Eurozine*, January 4, 2021, https://www.eurozine.com/0-01; David Reich, *Who We Are and How We Got Here: Ancient DNA and the New Science of the Human Past* (Oxford: Oxford University Press, 2018); Susanne E. Hakenbeck, "Genetics, Archaeology and the Far Right: An Unholy Trinity," *World Archaeology* 51, no. 4 (2019): 517–527; Anna Källén, "De första svenskarna: Arkeogenetik och historisk identitet," *Fronesis*, no. 66–67 (2019): 110–123. See also Jonatan Kurzwelly and Malin S. Wilckens, "Calcified Identities: Persisting Essentialism in Academic Collections of Human Remains," *Anthropological Theory* 23, no. 1 (2023): 100–122. An exception is Margaret Sleeboom-Faulkner, "How to Define a Population: Cultural Politics and Population Genetics in the People's Republic of China and the Republic of China," *BioSocieties* 1, no. 4 (2006): 399–419.

2. See, for example, Stefanie Eisenmann et al., "Reconciling Material Cultures in Archaeology with Genetic Data: The Nomenclature of Clusters Emerging from Archaeogenomic Analysis," *Nature Scientific Reports* 8 (2018), https://www.nature.com/articles/s41598-018-31123-z.

3. Songül Alpaslan-Roodenberg et al., "Ethics of DNA Research on Human Remains: Five Globally Applicable Guidelines," *Nature* 599, no. 7883 (2021): 41–46.

4. Compare in this volume Marianne Sommer and Ruth Amstutz, chapter 2.

5. See David Graeber's discussion about the British-Indian realist philosopher of science Roy Bhaskar. David Graeber, *Toward an Anthropological Theory of Value: The False Coin of Our Own Dreams* (New York: Palgrave/St. Martin's, 2001), 51–53.

6. Dongju Zhang et al., "Denisovan DNA in Late Pleistocene Sediments from Baishiya Karst Cave on the Tibetan Plateau," *Science* 370, no. 6516 (2020): 584–587; Ann Gibbons, "DNA Tracks Mysterious Denisovans to Chinese Cave, Just before Modern Humans Arrived Nearby," *Science Magazine*, October 29, 2020.

7. Maximilian Larena et al., "Philippine Ayta Possess the Highest Level of Denisovan Ancestry in the World," *Current Biology* 31, no. 19 (2021): 1–12.

8. Bruce Bower, "An Indigenous People in the Philippines Have the Most Denisovan DNA," *Science News*, August 12, 2021, https://www.sciencenews.org/article/indigenous-people-philippines-denisovan-dna-genetics.

9. As in the well-known examples of the outsider Qin invading the Central Plains kingdoms and setting up the First Empire; later also the Mongols; and the Manchus of the last dynasty that ended in 1911.

10. Magnus Fiskesjö, "The Legacy of the Chinese Empires: Beyond 'the West and the Rest,'" *Education about Asia* 22, no. 1 (2017): 6–10.

11. Magnus Fiskesjö, "Rescuing the Empire: Chinese Nation-Building in the Twentieth Century," *European Journal of East Asian Studies* 5, no. 1 (2006): 15–44.

12. Stephan Feuchtwang, "The Chinese Race-Nation," *Anthropology Today* 9, no. 1 (1993): 14–15.

13. Yuehtsen Juliette Chung, *Struggle for National Survival: Chinese Eugenics in Sino-Japanese contexts, 1896–1945* (New York: Routledge, 2002); Yinghong Cheng, *Discourses of Race and Rising China* (Cham: Palgrave Macmillan, 2019); Magnus Fiskesjö, "Racism with Chinese Characteristics: How China's Imperial Legacy Underpins State Racism and Violence in Xinjiang." China Channel, *Los Angeles Review of Books China Channel*, January 22, 2021, https://chinachannel.lareviewofbooks.org/2021/01/22/chinese-racism/.

14. John Fitzgerald, *Awakening China: Politics, Culture, and Class in the Nationalist Revolution* (Stanford, CA: Stanford University Press, 1996).

15. Thomas Mullaney et al., eds. *Critical Han Studies: The History, Representation, and Identity of China's Majority* (Berkeley: University of California Press, 2012).

16. See, for example, Charleston Wen-Kai Chiang et al., "A Comprehensive Map of Genetic Variation in the World's Largest Ethnic Group—Han Chinese," *Molecular Biology and Evolution* 35, no. 11 (2018): 2736–2750.

17. Fiskesjö, "Rescuing the Empire," 15–44.

18. Such "truths" are set out in the Chinese government's "white papers." See, for example, Information Office of the State Council of the Peoples Republic of China, "National Minorities Policy and Its Practice in China," Office of the Chargé d'Affaires of the People's Republic of China in the Republic of Lithuania, http://lt.china-office.gov.cn/eng/zt/zfbps/200405/t20040530_2910831.htm.

19. See Fiskesjö, "Rescuing the Empire"; Fiskesjö, "Legacy of the Chinese Empires," 6–10. One of the most influential Chinese formulations of this merger of everyone into the Zhonghua (Chinese) is Xiaotong Fei, *Zhonghua minzu duoyuan yiti geju* [The pattern of China's nationalities: Multiple origins, single form] (Beijing: Zhongyang minzu daxue, 1989).

20. The term *minzu shi* (ethnohistory) refers to a major genre in Chinese scholarship that has little or nothing to do with ethnohistory as understood in other parts of the world, namely history from the ethnic point of view. Instead, it consists mainly of the search to match Chinese historical texts with current ethnicities. While there is no good introduction to the genre in other languages, in Chinese, see Jianmin Wang, *Zhongguo minzuxue shi*, vol. 1, 1903–1949, vol. 2, 1950–1997 (Kunming: Yunnan Educational Publishers, 1997–1998). The book mainly focuses on ethnology, but also discusses Chinese-style ethnohistory.

21. Magnus Fiskesjö, "Chinese Autochthony and the Eurasian Context: Archaeology, Mythmaking and Johan Gunnar Andersson's 'Western Origins,'" in *Fitful Histories and Unruly Publics: Rethinking Temporality and Community in Eurasian Archaeology*, ed. Kathryn O. Weber, Emma Hite, and Adam T. Smith (Leiden: Brill, 2016), 303–320.

22. Tao Wang, "Establishing the Chinese Archaeological School: Su Bingqi and Contemporary Chinese Archaeology," *Antiquity* 71, no. 271 (1997): 31–39. This addition of several thousand years of Neolithic prehistory to the China story is the basis of today's official political mantra about "5,000 years of Chinese history" (though written history only extends to about 1200 BCE).

23. The new global paleoanthropology suggested that even Chinese people ultimately derived from Africans, something that is still largely unacceptable to Chinese people, despite Chinese geneticists at Fudan University confirming that it is in fact true.

24. Fiskesjö, "Rescuing the Empire"; Fiskesjö, "Legacy of the Chinese Empires."

25. On these issues, see Ming-ke Wang, "The Ch'iang of Ancient China through the Han Dynasty: Ecological Frontiers and Ethnic Boundaries" (PhD diss, Harvard University, 1992), and his masterful Chinese book on the subject, *Hua-Xia bianyuan: Lishi jiyi yu zuqun rentong* [The frontiers of Hua-Xia: Historical memory and ethnic identity] (Taipei: Yunchen wenhua, 1997). See Magnus Fiskesjö, "On the 'Raw' and the 'Cooked' Barbarians of Imperial China," *Inner Asia* 1, no. 2 (1999): 139–168.

26. John Makeham, "Zheng ming (Rectification of Names)," in *Encyclopedia of Confucianism*, ed. Xinzhong Yao (London: RoutledgeCurzon, 2003), 813–814.

27. Kenneth Dean and Brian Massumi, *First and Last Emperors: The Absolute State and the Body of the Despot* (Brooklyn, NY: Autonomedia, 1992).

28. A comprehensive overview is found in "The Uyghur Genocide: An Examination of China's Breaches of the 1948 Genocide Convention," *Newlines Institute for Strategy and Policy*, Policy Report, March 8, 2021, https://newlinesinstitute.org/uyghurs/the-uyghur-genocide-an-examination-of-chinas-breaches-of-the-1948-genocide-convention. More sources, including the collection and use of DNA, is found in my frequently updated online Uyghur bibliography, http://uhrp.org/bibliography.

29. Mark Munsterhjelm, "Scientists Are Aiding Apartheid in China," *Just Security*, June 18, 2019, https://www.justsecurity.org/64605/scientists-are-aiding-apartheid-in

-china; James Leibold and Emile Dirks, "Genomic Surveillance: Inside China's DNA Dragnet," Australian Strategic Policy Institute, 2020, https://www.aspistrategist.org.au/genomic-surveillance-inside-chinas-dna-dragnet; "China: Police DNA Database Threatens Privacy," Human Rights Watch, May 15, 2017, https://www.hrw.org/news/2017/05/15/china-police-dna-database-threatens-privacy. See also Sui-Lee Wee, "China Is Collecting DNA from Tens of Millions of Men and Boys, Using U.S. Equipment," *New York Times*, June 17, 2020.

30. Darren Byler, "The Xinjiang Data Police," *Noema*, October 8, 2020, https://www.noemamag.com/the-xinjiang-data-police; Yael Grauer, "Revealed: Massive Chinese Police Database," *The Intercept*, January 29, 2021, https://theintercept.com/2021/01/29/china-uyghur-muslim-surveillance-police. On the procedures inside the concentration camps, see Magnus Fiskesjö, "Forced Confessions as Identity Conversion in China's Concentration Camps," *Monde Chinois* 62 (2020): 28–43; Darren Byler, *In the Camps: China's High-Tech Penal Colony* (New York: Columbia Global Reports, 2021).

31. Since it was conclusively documented in 2019–2020, the systematic mass sterilizations have convinced many to declare the Chinese government's acts in Xinjiang a genocide under the United Nations Convention of 1948. On these actions, see Nathan Ruser and James Leibold, "Family De-planning: The Coercive Campaign to Drive Down Indigenous Birth-Rates in Xinjiang," Australian Strategic Policy Institute, 2021; Rukiye Turdush and Magnus Fiskesjö, "Dossier: Uyghur Women in China's Genocide," *Genocide Studies and Prevention: An International Journal* 15 no. 1 (2021): 22–43.

32. Leibold and Dirks, "Genomic Surveillance."

33. Nathan Vanderklippe, "China Steps up Internet Censorship of Criticism of Xi Jinping," *Globe and Mail*, March 11, 2018.

34. Munsterhjelm, "Scientists Are Aiding Apartheid in China."

35. See Katie Canales and Aaron Mok, "China's 'Social Credit' System Ranks Citizens and Punishes Them with Throttled Internet Speeds and Flight Bans if the Communist Party Deems Them Untrustworthy," *Business Insider*, November 28, 2022, https://www.businessinsider.com/china-social-credit-system-punishments-and-rewards-explained-2018-4.

36. See the controversy over the worldwide harvesting of genomic information by Chinese state-sponsored biotech company BGI. Kirsty Needham and Clare Baldwin, "China's Gene Giant Harvests Data from Millions of Women," *Reuters*, July 7, 2021, https://www.reuters.com/investigates/special-report/health-china-bgi-dna/; Joby Warrick and Cate Brown, "China's Quest for Human Genetic Data Spurs Fears of a DNA Arms Race," *Washington Post*, September 21, 2023.

37. For a history of genetics in China generally (but before archaeogenetics), see Tan Jiazhen and Zhao Gongmin, eds., *Zhongguo yichuanxue shi* [History of genetics

in China] (Shanghai: Shanghai keji jiaoyu, 2002); Laurence Schneider, *Biology and Revolution in Twentieth-Century China* (Lanham, MD: Rowman & Littlefield, 2003).

38. See, for instance, Hai-Guo Zhang et al., "Dermatoglyphics from All Chinese Ethnic Groups Reveal Geographic Patterning," *PLoS One* 5, no. 1 (2010): 1–12.

39. HUGO Pan-Asian SNP Consortium et al., "Mapping Human Genetic Diversity in Asia," *Science* 326, no. 5959 (2009): 1541–1545. See also Dennis Normile, "SNP Study Supports Southern Migration Route to Asia," *Science* 326, no. 5959 (December 2009): 1470. A similar approach using contemporary DNA data from around the world has been commercialized by companies that pretend to be able to determine individual ancestry based on personal samples. See, for instance, Daniel Strand and Anna Källén, "I Am a Viking! DNA, Popular Culture and the Construction of Geneticized Identity," *New Genetics and Society* 40, no. 4 (2021): 520–540.

40. In "Chinese archaeogeneticists," I include both Chinese geneticists in China and ethnic Chinese scholars abroad working in the same vein, as is strongly encouraged by the nationalist home regime. In line with the regime's new racist idea of the Chinese nation, anyone of "Chinese blood" is urged to serve its interests, regardless of citizenship. This pressure is often difficult to resist, including for scholars who still hope to have access to China and risk being denied as punishment for their disloyalty.

41. Melinda A. Yang et al., "Ancient DNA Indicates Human Population Shifts and Admixture in Northern and Southern China," *Science* 369, no. 6501 (2020): 282–288; see also Melinda A. Yang, "Ancient DNA Is Revealing the Genetic Landscape of People Who First Settled East Asia," *The Conversation*, September 15, 2020, https://theconversation.com/ancient-dna-is-revealing-the-genetic-landscape-of-people-who-first-settled-east-asia-139458; American Association for the Advancement of Science (AAAS), "Ancient DNA Reveals Genetic History of China," EurekAlert!, May 14, 2020, https://www.eurekalert.org/news-releases/708044.

42. Yang et al., "Ancient DNA Indicates Human Population Shifts," 282.

43. For a similar case in Israel, see Megan Gannon, "When Ancient DNA Gets Politicized," *Smithsonian Magazine*, July 12, 2019, https://www.smithsonianmag.com/history/when-ancient-dna-gets-politicized-180972639/.

44. There is a large literature on these issues and on the current consensus on Austronesian history and migration. Large tracts are summarized in Geoffrey K. Chambers and Hisham A. Edinur, "Reconstruction of the Austronesian Diaspora in the Era of Genomics," *Human Biology* 92, no. 4 (2020): 247–263. See also Terry Melton, "Genetic Evidence for the Proto-Austronesian Homeland in Asia: mtDNA and Nuclear DNA Variation in Taiwanese Aboriginal Tribes," *American Journal of Human Genetics* 63, no. 6 (1998): 1807–1823; Elizabeth Matisoo-Smith, "Tracking Austronesian Expansion into the Pacific via the Paper Mulberry Plant," *Proceedings of the National Academy of Sciences* 112, no. 44 (2015): 13432–13433.

45. Jerry Norman and Tsu-Lin Mei, “The Austroasiatics in Ancient South China: Some Lexical Evidence,” *Monumenta Serica: Journal of Oriental Studies* 32, no. 1 (1976): 274–301.

46. AAAS, “Ancient DNA Reveals Genetic History.”

47. AAAS, “Ancient DNA Reveals Genetic History.”

48. Chiang et al., “Comprehensive Map,” 2736.

49. Chiang et al., “Comprehensive Map,” 2736.

50. Erika E. S. Evasdottir, *Obedient Autonomy: Chinese Intellectuals and the Achievement of Orderly Life* (Vancouver: University of British Columbia Press, 2004).

51. Professor Fu is also a coauthor on one of the papers I have discussed above. See Yang et al., “Ancient DNA Indicates Human Population Shifts.”

52. Chris Buckley, “Brushing Off Criticism, China’s Xi Calls Policies in Xinjiang ‘Totally Correct,’” *New York Times*, September 26, 2020.

53. “DNA” and “gene” are obviously not the same thing, but the Chinese term for DNA is too complex to be used by politicians in this way. Thus, the acronym DNA and the Chinese word for gene, *jiyin*, are used interchangeably, as if they referred to the same thing: a buried code that preserves and transmits an essence. The compound literally means “fundamental cause” or “driver.” Like many modern Chinese terms in science, it may have been first coined in Japan.

54. Jinping Xi, “Jianshe zhongguo tese Zhongguo fengge Zhongguo qipai de kaoguxue. Geng hao renshi yuanyuan liuchang boda jingshen de Zhonghua wenming” [Build an archaeology with Chinese characteristics, Chinese style, and Chinese spirit: Better investigate the ancient, grand, and profound Chinese civilization], *Xinhua Net*, November 30, 2020, http://www.xinhuanet.com/politics/2020-11/30/c_1126803588.htm. See also the official party newspaper *Guangming Ribao*’s article in the same month, setting out the official truth on these matters: “Cong kaogu faxian kan baqian nian yilai zaoqi zhongguo de wenhua jiyin” [Looking at the cultural genes of early China in the past 8,000 years from archaeological discoveries], *Xinhua Net*, November 4, 2020, http://www.xinhuanet.com/politics/2020-11/04/c_1126695556.htm.

55. Xi, “Jianshe zhongguo.”

56. See note 41 above. In reality, complicity and self-censorship are widespread, and therefore do not often come to light.

57. Bai Tiantian, “Official Urges Archeologists to Prove Xinjiang Part of China since Ancient Times,” *Global Times*, March 23, 2017. On the policies, see Jilil Kashgary and Kurban Niyaz, “Chinese Research on Xinjiang Mummies Seen as Promoting Revisionist History,” *Radio Free Asia*, June 11, 2022, https://www.rfa.org/english/news/uyghur/melting-pot-06032022104308.html.

58. As indicated in note 18 above, the so-called white papers are the government's statements of the official truth on matters of history, the ownership of Tibet, and so on.

59. State Council Information Office of the People's Republic of China, *Historical Matters Concerning Xinjiang* (Beijing: Foreign Languages Press, 2019).

60. State Council Information Office, *Historical Matters*.

61. State Council Information Office, *Historical Matters*.

62. Wenjun Wang et al., "Ancient Xinjiang Mitogenomes Reveal Intense Admixture with High Genetic Diversity," *Science Advances* 7, no. 14 (2021): 1. This research comes from the new aDNA laboratory at the Institute for Vertebrate Paleontology and Paleoanthropology in Beijing. While the institute has long languished among the paucity of human fossils found in China, it has been reinvigorated with its new mission in genetics and, especially, aDNA. Like all research institutions in China, it is closely controlled by the ruling Communist Party.

63. Wang et al., "Ancient Xinjiang Mitogenomes," 9.

64. Qidi Feng et al., "Genetic History of Xinjiang's Uyghurs Suggests Bronze Age Multiple-Way Contacts in Eurasia," *Molecular Biology and Evolution* 34, no. 10 (2017): 2572.

65. Chunxiang Li et al., "Evidence that a West-East Admixed Population Lived in the Tarim Basin as Early as the Early Bronze Age," *BMC Biology* 8, no. 15 (2010): 1–12.

66. Shi-Zhu Gao et al., "Ancient DNA Reveals a Migration of the Ancient Di-Qiang Populations into Xinjiang as Early as the Early Bronze Age," *American Journal of Physical Anthropology* 157, no. 1 (2015): 71–80.

67. See, for instance, James Patrick Mallory and Victor H. Mair, *The Tarim Mummies: Ancient China and the Mystery of the Earliest Peoples from the West* (London: Thames & Hudson, 2000). This book was written before the emergence of archaeogenomics. There have been many criticisms of these arguments, taking issue with the authors' naming of the mummy populations as "Westerners" or "Europeans."

68. Fan Zhang et al., "The Genomic Origins of the Bronze Age Tarim Basin Mummies," *Nature* 599, no. 7884 (2021): 256–261.

69. Bruce Bower, "DNA from Mysterious Asian Mummies Reveals Their Surprising Ancestry," *Science News*, October 27, 2021, https://www.sciencenews.org/article/ancient-dna-asian-mummies-bronze-age-ancestry-mystery; Holly Chik, "Xinjiang Mummies' Origins Closer to Home than We Thought, Study Finds," *South China Morning Post*, October 27, 2021.

70. Chik, "Xinjiang Mummies' Origins."

8 Concluding Commentary

K. Ann Horsburgh

A great deal of ink has been spilled over the problems exhibited by researchers attempting to incorporate ancient DNA (aDNA) data into anthropological models of prehistory. The problems are both ethical and interpretive. Several of the chapters in this volume have compellingly and comprehensively discussed the ethical violations abundantly seen in aDNA research. They show that since there continue to be significant professional rewards for rapid and sensational publication—a phenomenon explored in detail in Andreas Nyblom's chapter on the fuss surrounding the "the female Viking warrior"—and few professional consequences for riding roughshod over ethical standards and the concerns of descendant and stakeholder communities, researchers will continue to make their own culture-bound value judgments. The research community itself must decide whether the ethical requirements of engaging in aDNA research should have teeth, by whom those teeth should be wielded, and what kinds of wounds those teeth should inflict.

I want to thank the editors of this volume for the opportunity to provide this commentary. I will use the space available to me to discuss two phenomena related to anthropological aDNA research: one relevant to the community of scholars interested in molecular approaches to the past, and one relevant to both public understandings of the kinds of research discussed in this book and to the ways in which scholars untrained in genetics understand the data generated. First, however, I would like to be explicit about my positionality in this space, because the peculiarities of my academic background significantly shape my views on the current state of affairs. I am a molecular anthropologist trained in the four-field Americanist tradition, in which the subdisciplines of biological anthropology, archaeology, linguistics, and sociocultural anthropology sit together under the umbrella of anthropology. I was trained in this way first in my home country of Aotearoa New Zealand, which—by virtue of a historical quirk—follows an Americanist anthropology rather than the British anthropology more typical of Commonwealth countries, and then later in the United States. While I hold undergraduate degrees in both anthropology and the biological sciences, all my advanced training is in anthropology, not biology. I came to molecular anthropology having read while in high school popular accounts of Allan Wilson's and Vince Sarich's immunological research devoted to dating the evolutionary split between humans and the rest of the great apes, and of Rebecca Cann's PhD research, which resulted in the naming of Mitochondrial Eve.

The vast majority of the research in which I have been involved has used modern and ancient DNA of both human ancestors and nonhuman animals in Africa and the islands of the Pacific Ocean. In the last few years, however, my research interests have substantially shifted. Laboratory skills are significantly transferable, and I am now using molecular approaches to interrogate the complex interactions between human health and cultural and social phenomena, like those discussed in Venla Oikkonen's chapter about how pathogens in the thawing permafrost alter our conceptions about the future. I am therefore an insider. I have spent many years generating aDNA data, and I love the lab. But I am an insider with one foot out the door. It is from this vantage point, then, that I first want to comment on a category error that is a routine part of discussions of the use and misuse of aDNA data in reconstructions of prehistory, and second, to discuss the relationship between the public's love affair with anthropologically relevant aDNA and the meteoric rise of direct-to-consumer (DTC) genomics.

A Category Error

The category error is routinely made in the discussion of interdisciplinarity and transdisciplinarity in the generation and interpretation of aDNA data in anthropological contexts. The category error is that which frames this kind of research as necessarily a collaboration between anthropologists/archaeologists and geneticists. As shown in Charlotte Mulcare and Mélanie Pruvost's chapter about the problematic nature of interdisciplinarity in aDNA studies, the discussion is typically framed around the divergent norms of anthropologists trained in the social sciences and geneticists trained in the life sciences. These differences are said to result in difficulties in communication, nonalignment of priorities, and failures to understand the nuances and complexities of data generated in a different discipline. All these things are indeed difficult, and it is certainly true that the largest, best-funded aDNA laboratories are run by geneticists. However, discussions framed in this way render invisible the many anthropologists who run aDNA laboratories.

The reasons why archaeologists prefer to collaborate with geneticists rather than molecular anthropologists (or anthropological geneticists) are both real and understandable.[1] Geneticists specializing in aDNA tend to work in departments of biological sciences (which come with a variety of names) or medical schools. They have considerably lower teaching loads than people based in anthropology departments, and therefore have more time available for research activities. They are also almost universally better resourced than people in social science departments, both in terms of the support services provided and in terms of research money. Collaborating with geneticists, then, is simply easier than collaborating with molecular anthropologists.

Meanwhile, archaeologists lamenting the lack of real engagement by geneticists are commonplace. Frequent complaints are heard about geneticists ignoring the input of social scientists, and even about manuscripts being published without the archaeologists seeing (never mind approving) the text. I have a great deal of sympathy for archaeologists who are frustrated with the ways in which genetic data are interpreted, but they are not powerless here. If proper, thoughtful, fully contextualized interpretation of anthropologically relevant genetic data matters to them, then there are two sensible courses of action. They can continue to collaborate with geneticists but make their full participation in interpretation and make the writing of the resulting papers a condition of facilitating access to archaeological remains. Archaeologists and the curators of collections have considerable power to dictate terms and demand meaningful collaborations. The field will be better off if they begin wielding that power more widely.

The other option open to archaeologists is to collaborate with anthropologists rather than biologists. This is the more difficult road. Vanishingly few molecular anthropologists have standing budgets, and even fewer have the armies of postdoctoral fellows and laboratory technicians enjoyed by the largest and best-funded genetics labs. This approach requires winning grants before work can begin. It also requires an appreciation that with a smaller workforce come necessarily slower results. I am not an archaeologist, but I do suggest that archaeologists might find collaborations with other anthropologists rewarding, despite the inherent challenges.

Collaborations across disciplines, or even subdisciplines, is necessarily time-consuming if it is to be done well. Much of the archaeological dissatisfaction in the interpretations of ancient DNA data stems from the difficulties in communication across disciplines, particularly around the uncertainties and messiness inherent in archaeological data. Genetic data from archaeological sources, which make up most of the data discussed in this volume, are also necessarily messy.[2] Many aDNA researchers describe what they do in the laboratory as experiments. While aDNA lab work does have the veneer of the experimental, it is by necessity a historical science, not an experimental one.[3] While some biologists are trained in the historical sciences (e.g., paleontology), most are not, and geneticists are especially unlikely to be. As the shared social science training of archaeologists and molecular anthropologists includes a common training in the (pre)historical, they can begin their collaborations with a shared appreciation of the methods, limitations, and complexities of historical data.

Molecular Chauvinism

As demonstrated by several chapters in this volume, and perhaps most clearly in Magnus Fiskesjö's chapter on the political abuse of archaeogenetic research in China, aDNA data are published by people incentivized to go beyond their data and make grand—but unsupported—claims. These claims are then understood by both producers and consumers of genetic data with a bias I have elsewhere named "molecular chauvinism."[4] Molecular chauvinism is the tendency to treat genetic data as though they are untarnished by the messiness attendant on other data in the social sciences and, consequently, to privilege them over other kinds of data. The implicit assumption is that the distance between data and interpretation is shorter and less complicated, and so the interpretation is more likely to be accurate. You need only contemplate the claim of geneticist David Reich that "human genome variation has surpassed the traditional toolkit of archaeology—the study of the artifacts left behind by past societies—in what it can reveal of changes in human populations in the deep past" to be convinced that I am not overstating the case here.[5]

Ancient DNA data are consumed by people largely untrained in genetics, embedded in a culture excited about the possibilities of personalized medicine and captivated by recreational DTC genomics. The Human Genome

Project was completed in 2003 and it was supposed to usher in a healthcare revolution in which we would all benefit from personalized medicine tailored to the specifics of our individual genomes.[6] While the tangible health benefits flowing from genome sequencing have been few and far between, the public enthusiasm for genetic data has shown no sign of abating.

One of the largest DTC recreational genomics companies, 23andMe, was founded only three years after the completion of the Human Genome Project. It was followed by Ancestry DNA in 2012. By 2018, the global market value for DTC genomics reached US $830 million, and it is anticipated that by 2025, the global DTC genomics market will value more than US $2.5 billion.[7] People spit in tubes and hand over money because of a perception that the results they obtain from these companies are meaningful. As Daniel Strand and Anna Källén observe in the introduction to this volume, the popular discourse on DNA has long reproduced the assumption that our genes offer a source of truth about who we "really" are. So pervasive is the notion that our essential selves are to be found in our DNA that is has become a metaphor for realness—characteristic X is "baked into our DNA." In a way, this idea also comes to the fore in Amade M'charek's chapter about the changing representations of the Neanderthal: as soon as it is proved that modern humans share DNA with Neanderthals, this hominin group ceases to be portrayed as a monkey or a troglodyte and is instead depicted as "one of us."

The meteoric rise of DTC companies and their broad uptake by the general public for both ancestry estimation and detection of health-related variants exacerbate a tendency toward genetic determinist thinking that is planted in peoples' thinking in high school biology classes about Gregor Mendel. You could be forgiven for thinking that we are quite good at examining DNA sequences and predicting important phenotypic traits. We use human characteristics to teach Mendelian inheritance in both high school and at the university. We teach that, for example, the ability to roll your tongue is dominant over the inability, and so if you have TT or Tt combinations of alleles you will be able to roll your tongue and will be unable to roll your tongue only if you have tt alleles. We further teach that if two tongue rolling Tt people have children, about a quarter of their kids will be tt and thus unable to roll their tongues. Unfortunately for this favorite of the classroom, tongue rolling ability does not work like that at all. Instead, it is likely influenced by multiple genes, and there is probably a significant environmental influence as well.[8]

The nongenetic component of tongue rolling ability points to the fact that the actions of genes are influenced by the environments in which they find themselves; but further, the actions of genes are impacted by the genomes in which they find themselves. To illustrate this point, consider another favorite of the classroom, which is indeed inherited in a Mendelian fashion: the ABO blood system. At the end of the long arm of chromosome 9 is a gene which encodes an enzyme that comes in three alleles.[9] If the A allele is present, a sugar called N-acetylgalactosamine is added as a fifth sugar on the surface of the red blood cell. If the B allele is present, then the sugar galactose is added to the existing string of four sugars. The O allele is nonfunctional, and so does nothing. Thus, if you have inherited an O allele from each of your parents, you have no fifth sugar on any of your red blood cells and have type O blood. When considered in this way, it is then easy to see both why A and B alleles are dominant to O, and why A and B alleles are co-dominant to each other.

Genes do not, however, act is isolation. They act in functional biological organisms, as part of nested physiological pathways. There is another gene, on the long arm of chromosome 19, which is relevant to a person's ABO status. This gene (FUT1) similarly encodes an enzyme which moves sugars around.[10] In most people, the enzyme encoded by FUT1 adds the sugar fucose to a string of three sugars on red blood cells. In people who inherited the recessive, nonfunctional version of this gene (genotype hh), that sugar is never added. People carrying this combination of alleles have what is known as the Bombay phenotype. It does not matter what alleles are carried at the ABO gene, because those enzymes have no substrate upon which to act. Regardless of the alleles carried at ABO, a person with the Bombay phenotype will have functionally O-type blood.[11] There are no reported health effects associated with the Bombay phenotype, until someone needs a blood transfusion. Transfused with typical O-type blood with red blood cells with four sugars on their surfaces, the alleles of the ABO system suddenly have a task they can complete, and add fifth sugars to the newly transfused red blood cells. The patient's system now recognizing the transfused blood as nonself launches an aggressive immune response.[12]

The ABO system, then, is a very straightforward Mendelian system. Except when it is not. Genes are obviously important in the building of bodies, but the relationships between genes and traits are not simple or unidirectional and almost never involve single genes and single characteristics. We know much more about the genetics of disorder than we do about the genetics of the average, so genetic disease is a useful place to think about the relationships between genotype and phenotype. Of the diseases we know to show patterns of inheritance, only about 2 percent show patterns consistent with simple Mendelian inheritance.[13] The rest are influenced by many genes interacting in complex reticulated networks with each other and with other contributors to the developmental system, including the environment and nongenetic inheritance.[14] Their influence is probabilistic, not deterministic.

Final Thoughts

Despite grandiose claims to the contrary, aDNA data have not, and will not, revolutionize reconstructions of the past. Certainly, there has been a dramatic increase in the volume of genetic data relevant to reconstructions of prehistory, but our powers of interpretation have lagged behind the truly impressive improvements in laboratory-based techniques for DNA recovery and analysis.

Further, genetic data are meaningful only to the extent to which they articulate with other kinds of data, which means that engagement across specialties has to be careful, equitable, and undertaken with a humility about the boundaries of one's own knowledge and a respect for the epistemological rigor in diverse disciplines. As suggested by Stewart B. Koyiyumptewa and Chip Colwell's chapter about the conflicts between paleogeneticists and Indigenous groups in the United States, a productive future for aDNA research hinges on an engagement with descendant communities and their inclusion as core members of research teams, drivers of research agendas, and lead investigators.

Finally, the field of aDNA studies would benefit enormously from a recalibration of its core mission and its core values. If the research community is interested in accurate, nuanced, and rich reconstructions of the past, we need to stop reaching for the flashy press release, slow down, and truly grapple with the intricacies of synthesizing multiple, complex datasets. As made clear in Marianne Sommer and Ruth Amstutz's chapter about the graphic representations employed in aDNA research, complex historical processes must not be reduced to simple figures or models.

As this volume has shown, it is simultaneously true that the revolutionary nature of aDNA research for the reconstruction of prehistory has been overblown and that aDNA can contribute meaningfully to our understandings of the past. The contributors to this volume are largely not practitioners of aDNA research. The book is generally critical of aDNA research as it is currently practiced, even when the authors are primary producers of aDNA data. Nonetheless, the contributors herein engage with the field because, done carefully, slowly, with respect for ancestors, with respect for descendant communities, and with care for complexities of social science data, the discipline can contribute significantly to the work of prehistorians. Ancient DNA research will be greatly enriched if the scholars at the bench take seriously the work done by the authors of *Critical Perspectives on Ancient DNA*.

Notes

1. I strongly prefer "molecular anthropologist" over "anthropological geneticist" for the kinds of researchers I'm talking about because they are primarily anthropologists with a molecular toolkit rather than geneticists who happen to focus on humans. Thus, for a molecular anthropologist, anthropology is the core, not the modifier. My perspective on this point is not widely shared, and many researchers who earned PhDs in anthropology, hold positions in departments of anthropology, and address anthropological questions with molecular data call themselves anthropological geneticists.

2. Ancient DNA data can also be generated from paleontological remains that do not derive from archaeological contexts, but this volume focuses on archaeological contexts and questions.

3. See Carol E. Cleland, "Methodological and Epistemic Differences between Historical Science and Experimental Science," *Philosophy of Science* 69, no. 3 (2002): 474–496.

4. See K. Ann Horsburgh, "Molecular Anthropology: The Judicial Use of Genetic Data in Archaeology," *Journal of Archaeological Science* 56 (2015): 141–145.

5. David Reich, *Who We Are and How We Got Here: Ancient DNA and the New Science of the Human Past* (Oxford: Oxford University Press, 2018), xx.

6. See Francis Collins and David Galas, "A New Five-Year Plan for the US Human Genome Project," *Science* 262, no. 5130 (1993): 43–46.

7. National Academies of Sciences, Engineering, and Medicine, *Exploring the Current Landscape of Consumer Genomics: Proceedings of a Workshop* (Washington, DC: National Academies Press, 2020), 11.

8. See John J. Reedy, Thomas Szczes, and Thomas D. Downs, "Tongue Rolling among Twins," *Journal of Heredity* 62, no. 2 (1971): 125–127; Nicholas G. Martin, "No

Evidence for a Genetic Basis of Tongue Rolling or Hand Clasping," *Journal of Heredity* 66, no. 3 (1975): 179–180; Taku Komai, "Notes on Lingual Gymnastics: Frequency of Tongue Rollers and Pedigrees of Tied Tongues in Japan," *Journal of Heredity* 42, no. 6 (1951): 293–297; Alfred Henry Sturtevant, *A History of Genetics* (New York: Harper & Row, 1965). It is also worth noting that teaching genetics in this way, with fundamental errors in facts, is an effective way to lead high school and undergraduate students to suspect that their social father is not their biological father; a phenomenon we euphemize as a "nonpaternity event." Regardless of what we call it, leading teenagers to doubt the identities of their biological fathers is a terrible thing to do to people, and it is an especially terrible thing to do based on bad biological information. For a discussion about this, see John McDonald, *Myths of Human Genetics* (Baltimore, MD: Sparky House, 2011).

9. See Marion E. Reid and Christine Lomas-Francis, *The Blood Group Antigen FactsBook* (New York: Elsevier Academic, 2004).

10. See Yoshiro Koda et al., "Missense Mutation of FUT1 and Deletion of FUT2 Are Responsible for Indian Bombay Phenotype of ABO Blood Group System," *Biochemical and Biophysical Research Communications* 238, no. 1 (1997): 21–25; R. J. Kelly et al., "Molecular Basis for H Blood Group Deficiency in Bombay (Oh) and Para-Bombay Individuals," *Proceedings of the National Academy of Sciences* 91, no. 113 (1994): 5843–5847; Florence F. Wagner and Willy A. Flegel, "Polymorphism of the h Allele and the Population Frequency of Sporadic Nonfunctional Alleles," *Transfusion* 37, no. 3 (1997): 284–290.

11. See Reid and Lomas-Francis, *Blood Group Antigen FactsBook*.

12. See Sheetal Malhotra et al., "Acute Hemolytic Transfusion Reaction in a Patient with Bombay Phenotype: Implications for ABO Grouping," *Indian Journal of Hematology and Blood Transfusion* 30 (2014): 108–110.

13. See Eva Jablonka and Marion J. Lamb, *Evolution in Four Dimensions: Genetic, Epigenetic, Behavioral, and Symbolic Variation in the History of Life* (Cambridge, MA: MIT Press, 2006).

14. See James DiFrisco and Johannes Jaeger, "Beyond Networks: Mechanism and Process in Evo-devo," *Biology and Philosophy* 34 (2019): 1–24.

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