



Article

Ancient human DNA: A history of hype (then and now)

Journal of Social Archaeology

2021, Vol. 21(2) 236–255

© The Author(s) 2021



Article reuse guidelines:

sagepub.com/journals-permissions

DOI: 10.1177/14696053211990115

journals.sagepub.com/home/jsa



Elizabeth D Jones

Department of Forestry and Environmental Resources,
North Carolina State University, USA

Elsbeth Bösl

Department of Social Sciences and Public Affairs, Historical
Institute, Bundeswehr University Munich, Germany

Abstract

In this article on the history of ancient DNA research, we argue that the innovation of next-generation sequencing (NGS) of the early 2000s has ushered in a second hype cycle much like the first hype cycle the field experienced in the 1990s with the advent of the polymerase chain reaction (PCR). While the first hype cycle centered around the search for the oldest DNA, the field's current optimism today promotes the rhetoric of revolution surrounding the study of ancient human genomes. This is evidenced from written sources and personal interviews with researchers who feel the vast amount of data, the conclusions being made from this data, and the ever-increasing celebrity status of the field are perhaps moving too fast for their own good. Here, we use the concept of contamination, in both a literal and figurative understanding of the term, to explore the field's continuities and disparities. We also argue that a number of additional, figurative interpretations of "contamination" are useful for navigating the current debate between geneticists and archaeologists regarding the origin, evolution, and migration of ancient humans across space and time. Our historical outlook on aDNA's disciplinary

Corresponding author:

Elizabeth Jones, Forestry and Environmental Resources, North Carolina State University, Raleigh, NC, USA.

Email: elizabeth_jones@ncsu.edu

development, we suggest, is necessary to accurately appreciate the state of the field, how it came to be, and where it might go in the future.

Keywords

Ancient DNA, ancient humans, hype cycle, contamination, celebrity, history of science

Introduction

Since its birth in the 1980s, the field of ancient DNA (aDNA) research has been propelled by state-of-the-art technological innovations and high-impact journal publications and media coverage, especially as the growth of the field coincided with the release of *Jurassic Park*, a major blockbuster movie. Although those scientists in search of dinosaur DNA represented only a small subset of the overall aDNA community, the hype that surrounded the search for the oldest DNA in the 1990s was critical to the development of the discipline and its current state today. As the field grew under the influence of press and public interest, it became a multidisciplinary one including researchers from paleontology, botany, and epidemiology to molecular biology and archaeology. Such researchers from different scientific backgrounds came together in the common pursuit of DNA from old material to learn more about evolutionary history.

Recently, archaeologists and geneticists have taken center stage in their search for DNA from ancient humans. Combining the expertise of practitioners from various disciplines to study a subject as complex as human history is promising, not least because it enhances the limited epistemological resources of archaeology. Ancient DNA findings allow for new insights into an inaccessible dimension of the past. As such, researchers are generating bold stories of our origin and evolution. But this is all exceedingly controversial. There is much conflict over epistemology, evidential hierarchies, and scientific authority. Meanwhile, the public is often presented with success stories where DNA features as an objective and decisive source of truth about the past. However, archaeologists and historians are skeptical of this seemingly unbridled confidence in aDNA data and the historical narratives being produced from it.

The field of aDNA research has experienced episodes of confidence in this new approach to fossil studies along with equally intense skepticism about the scientists' potential to deliver on initial promises. Over the decades, the field has followed a similar trajectory to that of other scientific ideas and technological innovations (Collar et al., 2015; Fenn and Raskino, 2008; Bösl, 2017). This trajectory – “the hype cycle” – characterizes the lifespan of an idea or innovation as a series of highs and lows associated with scientific or technological opportunities. This cycle is described as moving from an initial trigger to a peak of expectations, often followed by a trough of disillusionment, then a slope of enlightenment and plateau of productivity.

We argue that the innovation of next-generation sequencing (NGS) of the early 2000s has ushered in a second hype cycle much like the first hype cycle that the field experienced in the 1990s with the advent of the polymerase chain reaction (PCR). While the first hype cycle centered around the search for the oldest DNA, mainly dinosaur DNA, the field's current optimism today promotes the rhetoric of revolution surrounding the study of ancient humans. We approach this argument as historians of science, drawing on extensive evidence from historical documents, contemporary articles, and original interviews with scientists involved in the field of aDNA research.

Here, we draw on the concept of contamination to explore continuities and disparities between the field's past and current hype cycles. Over the years, aDNA researchers became concerned about contamination in a literal and figurative sense. In the former, contamination related to potential exposure to modern DNA, an issue heightened by the degraded and delicate composition of ancient genetic sequences. In the latter, contamination referred to what some viewed as disproportionate media attention surrounding the field that could have adverse effects on its credibility. Today, given what researchers and reporters call the ancient genomics revolution, we argue for contamination as an extended metaphor to help make sense of debates over aDNA research as an approach to studying human evolutionary history.

In the past 10 years, the field's current hype cycle has triggered massive epistemological changes and controversial debates between what might be roughly construed as the sciences and humanities. Based on our reading of this debate, we argue that a growing number of researchers from geneticists to archaeologists are concerned with two further and figurative understandings of contamination. First, some worry about purist and simplistic narratives of human history as told through genetic evidence that downplay or deny the reality that human populations are the result of what has been referred to as "contaminated diversity" through the cross-fertilization of people over time and space (Tsing, 2015). Second, some worry about the challenges of truly interdisciplinary research – what we refer to as "disciplinary contamination" – through the mixing and misunderstanding of methods in genetics and archaeology (Booth, 2019). In analyzing historical and contemporary material involving aDNA research, we argue that our perspective on the discipline's development is necessary to accurately appreciate the state of the field, how it came to be, and where it might go in the future, especially in the midst of hype and ensuing controversy.

1990s: The first hype cycle

In the late 1980s and early 1990s, a small group of researchers began to test the limits of DNA preservation in ancient and extinct material with a new molecular biological technique called the polymerase chain reaction (PCR) (Mullis and Faloona, 1987). The advantage of PCR was its automatic amplification of DNA. This took the mental and physical strain out of the previously manual

process of cloning which rendered the extraction of ancient and degraded DNA possible but extremely difficult. In 1984, for example, Alan Wilson, a foremost evolutionary biologist of the day, along with colleagues at University of California, Berkeley, demonstrated the first successful experiment to recover DNA from a 140-year-old *Equus quagga*, an extinct zebra-like relative of the horse (Higuchi et al., 1984). Other studies suggested it was possible to go farther back in time. For example, Svante Pääbo – a graduate student at Uppsala University in Sweden – provided some of the first evidence for recovering DNA from ancient Egyptian mummies (Pääbo, 1985). For the first time, studying ancient molecules was possible, but this new line of research needed technological improvements to ensure its accuracy and efficiency. PCR, developed shortly after these studies, provided that opportunity. PCR could create billions of copies of DNA sequences from only a few strands of DNA, which is often the case with aDNA sequences.

With PCR's innovation, researchers raced to sequence the first and the oldest DNA from some of the world's most iconic creatures. Crucially, Michael Crichton's 1990 book and Stephen Spielberg's 1993 movie *Jurassic Park* coincided with these events, and its instantaneous worldwide popularity situated aDNA research and its scientists in the spotlight. In the early 1990s, the hype around the search for DNA from fossils took form as two different but not unrelated expectations: (1) that scientists could recover multi-million-year-old DNA and (2) that they could one day use that DNA to resurrect extinct creatures such as dinosaurs.

Following *Jurassic Park*'s 1990 publication, two research teams in the US set out in a race to extract and sequence multi-million-year-old DNA. In 1993, George Poinar, along with his son Hendrik Poinar and colleague Raul Cano, claimed to have recovered DNA from a 125–135-million-year-old amber-encased weevil, announcing it as the oldest DNA ever recovered (Cano et al., 1993). *Nature* published the paper on June 10, 1993 – one day after the *Jurassic Park* movie premiere and one day before its release in theaters across the United States. *The New York Times* noted the timing as well as parallels between the research findings and movie premise: “The report of the achievement is being published today in the British journal *Nature*, one day before the opening of ‘Jurassic Park,’ a much-publicized movie based on the notion of cloning extinct dinosaurs from their surviving DNA [...]” (Browne, 1993). The scientists involved in this work took other measures to align their discovery with *Jurassic Park*'s fame. According to the *Los Angeles Times*, Hendrik Poinar set up shop in the movie theater lobby on the opening weekend of *Jurassic Park*, selling bits and pieces of amber in hopes of raising funding for future research (King, 1993). In this case, these scientists saw *Jurassic Park*'s popularity as a chance to promote their own image, as well as the overall image of aDNA research, by advertising their work amidst the movie's release.

In the wake of *Jurassic Park*, the UK Natural Environmental Research Council funded the Ancient Biomolecules Initiatives, which included funds to test this *Jurassic Park* hypothesis (Smith, 1995). In London, researchers undertook a

comprehensive study to try to recover DNA from fifteen samples of amber insects, each from different resin types and time periods. After performing DNA extractions and PCR amplifications, they carried out negative controls and conducted phylogenetic analyses to check for aDNA authenticity. Despite extensive experiments, however, they were unsuccessful and in every instance “failed to recover any authentic ancient insect DNA” (Austin et al., 1997: 470). The *Jurassic Park* hypothesis appeared debunked.

Although the scientists searching for multi-million-year-old DNA were only a small subset of the overall community, the whole of the field was affected by the high-profile nature of their claims and the equally high-profile response to their refutation. This led to a dramatic drop in public and professional confidence in the field’s credibility. Some scientists believed that extraordinary claims should be accompanied by extraordinary evidence in order to prevent erroneous and what many viewed as publicly embarrassing results.

By the end of the 1990s, aDNA researchers were concerned about contamination in a literal sense. This referred to unintentional and problematic exposure of modern DNA. Ancient DNA sequences, for example, were easily contaminated by environmental, bacterial, or recent human DNA introduced to a specimen over time or through handling in a museum collection or lab. This issue was heightened because of the degraded and damaged composition of aDNA, which resulted in fragmented genetic sequences. Therefore, it was difficult for researchers to determine what DNA sequences belonged to the actual specimen under study. This question of aDNA authenticity was a major problem for scientists.

In response, two aDNA researchers – Alan Cooper and Hendrik Poinar (who had published on multi-million-year-old DNA from amber insects) – co-authored a paper in *Science*, titled “Ancient DNA: Do it Right or Not at All” (Cooper and Poinar, 2000). In it, they argued for the adoption of nine criteria for doing aDNA in order to avoid such pitfalls. Although standards for aDNA authenticity had been suggested before, and while some scientists seemed to embrace those standards, they felt others ignored them. Cooper and Poinar even argued that editors and reviewers of high-profile journals continued to publish work without proper protocols, thus partly blaming them for failing to enforce criteria that would legitimize the practice. One of the criteria they argued for was the physical separation of the “Ancient DNA Lab” from other labs. This lab became a space by which scientists measured the credibility of research results within this community, especially in the aftermath of disillusionment (Interviews: Burger; Grupe; Hummel). The field’s credibility was at stake, and aDNA authenticity was a prerequisite on which both the success of the field and the reputation of practitioners promoting it depended.

Scientists also felt the need to address the hype and influence of celebrity. Some felt it undermined their credibility. This was especially the case when public expectations of what aDNA researchers could accomplish became misaligned with reality. Some researchers, for example, viewed the hype around multi-million-year-old DNA as a figurative source of contamination and believed that disproportionate

or undeserved media interest had the adverse effect of contaminating their credibility. This was because select studies that suffered from contamination or the irreproducibility of results had been published in high-impact journals, such as *Nature* and *Science*, and broadcasted publicly.

However, their relationship with the media was complicated at best. Just as media attention was perceived to challenge the young field, it empowered it too. The media was vital to the field's growth in terms of its initial formation and overall identity. The press consistently publicized the nascent science, but scientists also purposefully fashioned their own opportunities for attention which helped influence publication timing, grant funding, research agendas, and professional recruitment (Jones, 2019, 2022). In the early years, hype was performative in that it generated interest and guided activity that led to the experimentation of novel ideas in order to establish evidence for their value (Borup et al., 2006; Brown, 2003). Indeed, it is often pragmatic to engage in hype to attract public attention and further funding. Sociologist Nik Brown (2003) captured this tension between hope and hype, explaining that while hype plays a role in generating activity and sustaining interest in new technologies and their applications, hype can lead to overshoot, which can result in damaged reputations of not just individuals but of whole research fields. Researchers faced this dilemma at the turn of the century.

The prospect of using aDNA techniques as applied to archaeology, anthropology, and epidemiology was enticing. However, contamination was even more of an issue when it came to working on ancient humans since authentic sequences were difficult to distinguish from contaminants. PCR exacerbated the issue of contamination because of its high sensitivity, often amplifying exogenous DNA in the PCR reaction because it was often better preserved than endogenous DNA. The obtained sequences could appear reliable but in fact be false positives. Skepticism around the ability to reliably recover authentic and ancient DNA sequences from humans arose early in the field, especially as a number of studies claimed it was possible. Erika Hagelberg et al. (1989), for example, were among the first to extract DNA from human bones ranging from hundreds to thousands of years old. *Nature* published their discovery. At the time, recalled one interviewee, "people had no idea whether DNA survived in bone, and if it did what to do with it or how to get it out in the first place" (Interviewee 11).

Pääbo, an early and vocal leader in the field, was an immediate skeptic. In 1990, a select group of researchers gathered together for the Biomolecular Palaeontology Community Meeting at the University of Glasgow (Natural Environment Research Council, 1990). As one researcher remembered it: "Svante Pääbo, very famously at the meeting, stood up and said, 'Of course you can't get DNA from bone!' – just before Erika Hagelberg stood up and said, 'Here's my results on DNA from bone'" (Interviewee 9). Another researcher recalled a similar situation: "Svante had [...] some very public fights with her in conferences [...] saying it was all shit" (Interviewee 32). This disagreement came down to contamination and the difficulty of proving aDNA authenticity. This early conflict certainly slowed research in this arena during this time, but it did not deter it completely.

In fact, several practitioners attempted to use aDNA sequences to learn about human evolution, populations, migrations, diet, and disease, as well as to determine the sex, age, and kinship of past people. For example, researchers from the UK to France, Germany, Israel, and the US investigated the preservation and extraction of DNA in ancient humans (Hänni et al., 1990; Hummel and Herrmann, 1991; Stone and Stoneking, 1993; Vigilant et al., 1989). Practitioners also published on evidence of early diseases in ancient humans (Baron et al., 1996; Spigelman and Lemma, 1993). Together, these works suggested the success of aDNA data in archaeological, anthropological, and epidemiological contexts, but contamination, again, was a concern. Cooper, a chief critic of the field, spoke out against it at an aDNA conference in the late 1990s. “Cooper [...] stood up and instead of talking about the work he was doing, he talked about how *rubbish* the field was and how human aDNA was becoming completely discredited” (Interviewee 4). This interviewee explained, “[...] [I]t needed to be done [...]. We’d just listened to four talks by people who [...] said, ‘We’ve done this’ and ‘We’ve done that.’ Is it actually genuinely true?” (Interviewee 4).

In the field, a number of influential researchers such as Cooper and Pääbo continued to pursue aDNA from a variety of material but through a rigid focus on methodology in direct response to prior studies on ancient humans and multi-million-year-old specimens. In making a name for themselves through their research programs, subsequent publications, and overall power, they secured access to rare and highly valuable samples, despite the challenges of contamination. Paradoxically, Pääbo (a former critic of ancient human DNA) was the first to receive remains of the original Neanderthal specimen for aDNA study (2014).

In 1997, Pääbo’s team reported the recovery of mitochondrial (mtDNA) Neanderthal DNA (Krings et al., 1997). When compared to recent mtDNA of primates and modern humans, distinct differences appeared. This was interpreted as evidence that Neanderthals had lived, then died, without contributing their DNA to modern humans. It also suggested that modern humans had their origin not in Europe, but in Africa, which substantiated the controversial Out-of-Africa hypothesis. Since the mtDNA results only gave insights into maternal lines, they did not entirely eliminate the possibility of a genetic contribution from extinct Neanderthals to extant humans. These findings added heat to an already heated debate on “one of the longest-standing questions in palaeoanthropology” (Harvati and Harrison, 2006; Weaver and Roseman, 2005). Tomas Lindahl, an expert in the chemical behavior of DNA and early critic of the field, actually endorsed the study for its soundness, calling it “the greatest achievement so far in the field of ancient DNA research” (Lewin, 1997: 43).

Overall, this study claimed that palaeogenetics had a more authoritative role in studying human history vis-à-vis those who worked with nonmolecular methods in more traditional disciplines such as archaeology, anthropology, and primatology. DNA from fossil material was argued by both scientists and media reporters to provide more reliable data compared to traditional archaeological evidence. To further showcase the power of aDNA data, Pääbo and his lab set out to sequence

much larger parts of the genome to at long last determine our relatedness to extinct Neanderthals.

2000s: The second hype cycle

At the turn of the century, the standards employed to avoid contamination and confirm authenticity were somewhat overshadowed by the innovation of a new technology called next-generation sequencing (NGS) (Margulies et al., 2005). While PCR required specific DNA fragments of sufficient length to be present in a sample, NGS was capable of sequencing every DNA fragment present. As a result of NGS, researchers could now recover millions of sequences at higher yield and in a fraction of the time. This allowed better estimation of the percentage of endogenous and exogenous DNA by searching for signatures of molecular degradation or post-mortem damage characteristic of authentically ancient DNA. Consequently, the technology did not remove the problem of contamination, but it did reframe the concerns. One scientist put it this way: “So, now it’s not only a question of having controls [. . .]. You can actually look at your data and determine whether you have a contamination problem or not, right?” (Interviewee 7). With the advent of NGS, researchers were quick to adopt the technology to overcome some of the previous limitations and contamination issues associated with PCR (Poinar et al., 2006). In doing so, scientists sought to establish aDNA’s legitimacy.

In 2006, Pääbo – now in Leipzig, Germany – announced with a press release that his lab at the Max Planck Institute for Evolutionary Anthropology and 454 Life Sciences Corporation would be the first to sequence the entire Neanderthal genome in just two years’ time (Max Planck Society, 2006). Four years after the announcement, Pääbo and his team finally finished the Neanderthal Genome Project (Green et al., 2010). The effort, conducted by over 50 scientists at a cost of approximately €5 million, successfully sequenced 4 billion base pairs of Neanderthal DNA (Callaway, 2010). Scientists, for the first time, declared they had data to answer questions about Neanderthal evolutionary history. However, it was not just the data that was important but the ability to analyze it that was critical. The combination of this genomic data and statistical methods, developed by Harvard University geneticist David Reich and his lab, allowed them to detect signals of admixture between early humans and Neanderthals.

With genomic sequences, scientists inferred that early humans interbred with the Neanderthals before going extinct 30,000 years ago. However, the evidence suggested that Neanderthals only interbred with a particular human population, those who had traveled out of Africa into Eurasia. By comparing the Neanderthal genome with present-day human genomes, they determined Neanderthals shared more similarities with present-day non-African populations than with present-day African populations. “The next time you’re tempted to call someone a Neanderthal, you might want to take a look in the mirror,” reported *National Geographic*. “According to a new DNA study, most humans have a little

Neanderthal in them – at least 1 to 4 percent of a person’s genetic makeup” (Than, 2010).

As aDNA researchers began to adopt NGS, they ushered in a new era of exploration and raced to sequence the first genomic data from ancient plants, animals, diseases, humans, and even famous historical figures like King Richard III (Bos et al., 2011; Gilbert et al., 2008; King et al., 2014; Rasmussen et al., 2010; Willerslev et al., 2014). Meanwhile, other research shed light on the behavior of early humans, including Mesolithic and Neolithic hunter-gatherers, while also exploring transformations in human cultural practices such as milk consumption (Bramanti et al., 2009; Burger et al., 2007; Haak et al., 2005; Skoglund et al., 2012; Warinner et al., 2014). Practitioners also sequenced the first genomic data from a Denisovan, a formerly unknown extinct hominin species whose identity as a distinct archaic human species was uniquely obtained exclusively from DNA extracted from a small finger bone, as no extensive fossil record existed (Krause et al., 2010; Reich et al., 2010). According to scientists and journalists, these works suggested a revolution in our understanding of human history (Gibbons, 2015; Stoneking and Krause, 2011). This race for the first, the oldest, or the most human genomes shared striking similarities to the 1990s’ hunt for the first or the oldest DNA.

However, one key difference between the PCR and NGS eras was that practitioners went from having little to almost too much data. High-throughput sequencing technologies could produce large amounts of data that required researchers to seek or learn computational and statistical skills to interrogate it (Interviews: Krause and Haak; Burger). From a field dominated by the laboratory scientist, aDNA research was moving into the realm of the bioinformatician: “Processing is completely different because before I could still look at each sequence by eye and edit them by hand, but now we have [. . .] billions of sequences and you have to do everything by bioinformatics” (Interviewee 15). According to practitioners, the growing availability of samples combined with the increasing ability to sequence genomes rapidly superseded their aptitude to analyse the data. It could supersede the question asked of the data, too. “People are going *over* the top because they can – just sequencing the living crap out of absolutely everything,” remarked another researcher. “So, we’re in this kind of exploration phase again, where it’s like, ‘Grab as much data as you possibly can, hire a great bioinformaticist, and then start asking questions in the resulting data sets’” (Interviewee 22). After a nearly 30-year history, it appeared that researchers had entered another era of experimentation as they tested the limits of NGS.

In interviews with aDNA researchers, some suggested that the innovation of NGS of the early 2000s has ushered in a second hype cycle much like the one they experienced in the 1990s with PCR. “It’s almost like the very early days of ancient DNA when you could get a *Nature* paper by saying, ‘Ancient DNA recovered from extinct thylacine or quagga or Egyptian mummy or mammoth or whatever.’” This same interviewee said, “It didn’t really matter what the answer was. It was just the fact that you could do it. And I think that’s possibly what’s driving a lot of the

ancient DNA community at the moment [...]” (Interviewee 25). Meanwhile, some saw this as a race to sequence the first ancient human genomes. “[S]everal really big names in ancient DNA, they jumped onto the human train,” remarked one researcher. “Scientists *know* that there are certain types of analyses that the media would go *more crazy* about than others, right? [...]” (Interviewee 38). The race for the first or oldest genomes is reminiscent of the race for the first or oldest DNA.

Furthermore, some felt the vast amount of data, the conclusions being made from this data, and the ever-increasing celebrity status of the field are perhaps moving too fast for their own good. “[...] We have entered into another phase [...] where everybody thinks it’s just so fucking amazing, right? [...] I think they will be super surprised in 10 years from now – five or 10 years from now – in terms of a lot of those claims will need to be modified! And I think that we haven’t by any means understood the limitations of what we are actually doing with genomics” (Interviewee 7). The ancient genomics era was similar to the ancient genetics phase of the 1990s in terms of its exciting potential and exploratory nature, but the issue has shifted: “The problem is another kind now. [...] It’s the way you do the data analysis and it’s the interpretations you are taking from that data analysis” (Interviewee 7; Interview: Krause and Haak).

At its most extreme, aDNA research, scientists argued, can be seen as data mining in terms of producing data and describing its patterns without a specified hypothesis (Millar and Lambert, 2019). This has been regarded as a deviation from the hypothesis-based approach many scientists say they practice. Given the nature of aDNA research, scientists often adopt a material-based rather than inductive approach as hypotheses rarely can be built a priori and then be tested on the results. For a few, this approach was far from desirable and even problematic (Interviews: Meier; Burger). However, in reality, scientists – aDNA researchers included – use multiple approaches simultaneously and iteratively, assessing the achievability of research results against the accessibility to technology, samples, funding, and prestige to be gained (Jones, 2019). This data-driven or material-driven strategy was often pragmatic and common in an exploratory phase of research, especially when researchers were testing the possibilities of new technologies as is often the case in any hype cycle.

One interviewee likened the present state of the discipline to its early phase of research in the 1990s. “[T]his research discipline has developed the way that all [...] new scientific disciplines develop, in that you have an initial, wonderful discovery, you have lots of hype and high expectations, and then you come down to it with a bump, and then you do the hard work of working out what it all means and what you can really do [...]” For this scientist, the community had undergone a first hype cycle and was now embarking on a second: “I think with these next-generation sequencing techniques we have to do it all again; come down to it with a bump, and sort out what we can and can’t do. So, I think it’s cyclical” (Interviewee 5). What was distinctly different, however, about this phase of the discipline’s development was that the implications for this sort of hype, and the

consequences of such failed or misaligned expectations, were more serious than ever. While much hype of the 1990s was focused on the *discovery* of multi-million-year-old DNA, the current hype cycle is focused on the *interpretation and presentation* of DNA from ancient humans that sometimes offers the public an inaccurate impression that genetic evidence can conclusively and consistently solve archaeological problems.

High stakes: Disciplinary debates and public understanding of human history

The newfound access to ancient human DNA on a large scale and its increasing application to questions about human history has caused discomfort among some archaeologists and geneticists. The issues and arguments are multifaceted. Further, the sides that these researchers find themselves on are not wholly binary. However, we suggest that the concept of contamination, taken as an extended metaphor, is helpful in highlighting two overarching points of contention related to the idea of (1) “contaminated diversity” and (2) “disciplinary contamination.”

First, some worry about purist and simplistic narratives of human history as told through genetic evidence that downplay or deny the complexity of human evolutionary history. For example, archaeologists (as well as historians) question the extent to which socio-cultural categories neatly correspond to genetic and biological categories. They highlight the variety of epistemological and political risks in trying to make connections between them (Frieman and Hofmann, 2019; Furholt, 2019; Hakenbeck, 2019). Here, they are concerned about biodeterminism and reducing complex concepts of identity and belonging to biological explanations. This is most problematic when scientists claim that genetic events are correlated to historical population movement, cultural change, and ancestry. Some aDNA studies, for example, present cultures as bounded social groups of homogeneous biological descent. For archaeologists, this perception evokes less-than-desirable memories of Gustav Kossinna’s contention that archaeological cultures were distinct and bounded entities and that changes in culture come through migration. Such ideas were used to legitimize the German Nazi political philosophy and following World War II researchers distanced themselves from this view of human culture. Consequently, archaeologists view neat and tidy stories of human history as a setback reflecting outdated biodeterministic perspectives (Heyd, 2017).

After decades of internal disciplinary struggles within the humanities over concepts such as culture, ethnicity, and migration, these scholars have arrived at more nuanced understanding of human history (Furholt, 2020; Samida and Eggert, 2013). Today, it is generally agreed that identities are negotiated and consolidated through discursive formations and cultural symbols and are therefore historical and variable (Díaz-Andreu et al., 2014). Archaeologists use archaeological cultures as a concept to map the diffusion of artefact types (Brather, 2016; Burmeister,

2016). Archaeologist Daniela Hofmann explained how the current application of ancient genomics to understand the Neolithic Transition, for example, poses an unnecessary challenge to the field: “It seems that as a discipline, we are being asked to go back to an explanatory paradigm we have long left behind and to equate an archaeological culture with a new population. This throwback is shaking our ambition to be a sophisticated, humanities-aligned discipline, and archaeologists rightly refuse to give up the theoretical insights of many decades of research” (Hofmann, 2015: 457).

Archaeologists Rachel Crellin and Oliver Harris point out the irony of the practice of aDNA research, one that relies on extreme protocols to ensure the purity of samples in the lab, and how some practitioners’ interpretation of the ancient genetic data sometimes, although not always, presents a purist picture of the past (2020: 46). In reality, ancient and modern human populations are often the product of what Anna Tsing termed “contaminated diversity” through the cross-fertilization of people over time. Tsing put it best this way, explaining that “everyone carries with them a history of contamination; purity is not an option” (Crellin and Harris, 2020: 50; Tsing, 2015: 27). To be fair, there are select aDNA studies that have argued this, thus supporting this argument, but the concern for simplified, sensationalized narratives remains.

Second, some worry about the challenges of truly interdisciplinary research, or what we refer to as “disciplinary contamination,” through the mixing and misunderstanding of methods in genetics and archaeology. As Thomas Booth (an archaeologist working alongside geneticists) perceptively noted, the discord between the two resides in epistemological differences, resulting in misunderstandings of process, sample sizes, and evidence all the way to the interpretation of results and research publication conventions (2019).

One component of this issue regards different perspectives on evidential hierarchy. Some geneticists have asserted with great vehemence the hard evidence of genetic sequences, thus openly or unconsciously devaluing archaeological and historical sources as less reliable evidence. For archaeologists, unbridled confidence in genetic evidence appears to compete with the humanities-focused disciplinary methods that draw on material culture to ritual practices as documented through the archaeological record. DNA from a constructivist point of view is not infallible, but it is often labeled as such by the media and even other scientists. Instead, some argue that geneticists, archaeologists, anthropologists, and historians alike must understand how their methods and data can complement rather than compete with or trump one another. DNA adds to the discussion while archaeology, history, and linguistics provide the context in the first place. To be sure, archaeologists are receptive to new methods and data, and many have forged strong beneficial relationships with geneticists, using various data to reveal the complexity of humankind. Yet the potential to combine genetic data with archaeological and historical evidence is far from straightforward. To date, truly interdisciplinary projects are scarce and some archaeologists fear that their role in the ancient genomics revolution is being reduced, making them mere contributors of samples

and context instead of being valued as collaborators. While some aDNA publications acknowledge and integrate current research in archaeology and history, their numbers are limited (Booth, 2020).

Science studies scholars call for researchers in all disciplines to recognize that the past is part of a complex ongoing socio-cultural setting and that science is never pure or uncontaminated by the social and political landscape (Egorova, 2010). Historians of science have pointed out that current discourses are part of that setting and research on past identities is in many ways related to the construction of identities in the present. It is hardly possible to divorce the biological from the cultural because there are always underlying assumptions regarding issues of race, gender, ethnicity, and identity (Blakey, 2020; Lipphardt, 2019; Marks, 2017). To Furholt, it is naïve to assume, as David Reich does, that aDNA research has the potential to speak to race without necessarily being racist (Furholt, 2020; Reich, 2018). Reich denied that his work was a form of scientific racism, arguing that genetics actually transcends the social or cultural category of race concepts while dealing only with the biological facts of it. As historian of science Jenny Reardon put it, “As much as biologists have tried over the last several decades to constrict race to apolitical scientific purposes, the use of race is never neutral. It is always tied to questions with political and social salience” (Reardon, 2004).

These concerns are heightened because of the very publicized nature of this line of research and the tendency of media reporters to tell a clean and simple story that sometimes does not do justice to the complexity of the research (Nilsson Stutz, 2018; Samida, 2020). According to Stefanie Samida (2019), press coverage on aDNA studies is very homogenous with hardly any articles that are critical or even draw on any other historical sources. As Ion argued in the case of King Richard III, for example, the media emphasized the role of DNA in identifying the skeleton over other lines of evidence that were equally if not more important (2017). These narratives appear to enhance geneticists’ credibility to the public but devalue archaeological and historical evidence.

Additionally, a number of media communications reinforce outdated narratives of human history. Furholt, for example, articulated the concern this way: “[. . .] [I]t is disconcerting that many of the narratives put forward, especially in the popular media [. . .], convey the impression that we as archaeologists would support a view of prehistory that is made up of closed ethnic groups of people, defined by a uniform and differential culture and biology, who fight each other, extinguish each other and take each other’s women [. . .]” (2020). Archaeologist Anna Källén and colleagues noted similar patterns in their analysis of the Birka “warrior” in that the scientific research article was communicated to the public by drawing on popular narratives and current political debates (Hedenstierna-Jonson et al., 2017; Källén et al., 2019; Price et al., 2019). Likewise, others demonstrated how aDNA research on population migration across Europe has been exploited by far-right groups with racist, nationalistic, and political agendas (Lidén and Eriksson, 2013; Frieman and Hofmann, 2019). Additionally, there are major concerns about research that generalizes ancient human behaviour from just one

or a few samples. Such studies often focus on topics of kinship, gender, and health and can be prone to embracing aspects of scientific sexism, homophobia, or ableism via biodeterministic reasoning, which is problematic (Shuttleworth and Meekosha, 2017). As Frieman and Hofmann argued (2019), the blame for such misappropriation of aDNA research cannot be placed on one person or group, be it the press or the public. Scientists must actively engage with the implications (intended or unintended) of their work, especially given the media attention surrounding it.

Much hype that has followed the field since its birth comes down to a reductionist understanding that DNA on its own can both create the complexity of human life and explain how it came to be. As science communications scholar Dorothy Nelkin argued, this view of DNA as the “bible” or “blueprint of life” dates back to the 1970s, when scientists in the new field of recombinant DNA research launched a serious media campaign to hype their work as well as combat criticisms of genetic engineering. Nelkin argued that scientists have learned how to position their science in a favorable framework, using rhetorical strategies to better achieve public support and funding (Nelkin, 1995: 130). Although pragmatic, this becomes problematic when DNA is privileged by scientists and depicted to the public as a conclusive or superior form of evidence. “These narratives are accepted by the public, by some aDNA specialists and by some archaeologists as basic facts against which other kinds of evidence can be weighed,” explained Crellin and Harris. “They are explicitly held up as something archaeology must be tested against [...] and not the other way around [...]” (Crellin and Harris 2020: 41).

Crucially, this discord between archaeologists and geneticists can be a springboard for dialogue rather than division. Important to note is that while the research itself is cause for debate, so are the ways in which the aDNA findings are presented to both the scientific community and public. As some have suggested, critical reflection on ancient genomic research should be pursued by those scientists internal to the practice itself (Hakenbeck, 2019). In light of the second hype cycle of the current NGS era, practitioners need to reflect on how to better ensure their research is not only methodically and theoretically sound but also ethically conducted and responsibly communicated to the public. In other words, researchers who conduct this type of work and communicate it through the media with the advantage of the field’s every-increasing celebrity status must also be prepared to address the potential politicization of their findings. This monumental effort requires discussion amongst geneticists, archaeologists, ethicists, historians, and science studies scholars, as well as media and communication studies scholars.

Conclusion

Throughout the 1990s and the first hype cycle of the PCR era, aDNA researchers were concerned about the literal contamination of aDNA sequences from

exogenous DNA sources. They were also worried about a more figurative source of contamination via hype and disproportionate media attention. While there is certainly continuity between the hype cycles of the PCR and the NGS eras respectively, there is a distinct difference. In this second hype cycle, the optimism around the search for aDNA is far less about the novelty and controversy surrounding the preservation of DNA from ancient specimens (and speculative potential for dinosaur resurrection) and more about rewriting human evolutionary history. Further, contamination concerns in the ancient genomic revolution extend beyond the confines of the lab in terms of scientists' efforts to generate authentic DNA sequences and reproducible results. They also extend beyond scientists' direct and indirect efforts to manage hype in order to produce enough interest, activity, and funding behind their work while avoiding overshoot and potential disillusionment.

In this paper, we argued that "contamination" is productive as an extended metaphor for understanding the current controversy within genetics and archaeology over the use of aDNA to answer perennial questions about human origins, evolution, migration, and culture. This multifaceted debate is evident through scholarship critiquing some, but not all, aDNA researchers for what some view as (1) purist and simplified narratives of human history and (2) disciplinary differences related to epistemology and evidence that seem to minimize traditional archaeological methods and data. These two overarching points of contention reflect a concern for how the interpretation and presentation of aDNA data may "contaminate" the credibility of archaeology. Yet this is more than a quarrel between disciplinary traditions. The work at stake – all of which is highly publicized and sensationalized – has grave consequences for the public understanding of humanity. In the business of writing and rewriting human evolutionary history, researchers (despite discipline) must recognize how their work may contain explicit, implicit, or unintended claims of consequence to past and current notions of political, cultural, and national identities. This responsibility also extends to media personnel as communication conduits to the broader public.

Acknowledgements

The authors are grateful to Anna Källén and colleagues for the opportunity to publish in this special issue. They also thank the reviewers for their insightful comments that have made this paper stronger.

Declaration of conflicting interests

The author(s) declared no potential conflicts of interest with respect to the research, authorship, and/or publication of this article.

Funding

The author(s) received no financial support for the research, authorship, and/or publication of this article.

References

- Austin JJ, Ross AJ, Smith AB, et al. (1997) Problems of reproducibility – Does geologically ancient DNA survive in amber-preserved insects? *Proceedings of the Royal Society, Series B, Biological Sciences* 264(1381): 467–474.
- Baron H, Hummel S and Herrmann B (1996) *Mycobacterium tuberculosis* complex DNA in ancient human bones. *Journal of Archaeological Science* 23(5): 667–671.
- Blakey ML (2020) On the biodeterministic imagination. *Archaeological Dialogues* 27(1): 1–16.
- Booth T (2019) A stranger in a strange land: A perspective on archaeological responses to the palaeogenetic revolution from an archaeologist working amongst palaeogeneticists. *World Archaeology* 51(4): 586–601.
- Booth T (2020) Imagined biodeterminism. *Archaeological Dialogues* 27(1): 16–19.
- Borup M, Brown N, Konrad K, et al. (2006) The sociology of expectations in science and technology. *Technology Analysis & Strategic Management* 18(3–4): 285–298.
- Bos KI, Schuenemann VJ, Golding GB, et al. (2011) A draft genome of *Yersinia pestis* from victims of the Black Death. *Nature* 478(7370): 506–610.
- Bösl E (2017) *Doing Ancient DNA: Zur Wissenschaftsgeschichte Der aDNA-Forschung [Doing Ancient DNA: Ancient DNA Research from the Perspective of the History of Science]*. Bielefeld: Transcript.
- Bramanti B, Thomas MG, Haak W, et al. (2009) Genetic discontinuity between local hunter-gatherers and Central Europe's first farmers. *Science* 326(5949): 137–140.
- Brather S (2016) New questions instead of old answers: Archaeological expectations of aDNA analysis. *Medieval Worlds* 4: 22–41.
- Brown N (2003) Hope against hype – Accountability in biopasts, presents, and futures. *Science & Technology Studies* 16(2): 3–21.
- Browne MW (1993) DNA from the age of dinosaurs is found. *The New York Times*, 10 June. Available at: www.nytimes.com/1993/06/10/us/dna-from-the-age-of-dinosaurs-is-found.html (accessed 18 January 2021).
- Burger J, Kirchner M, Bramanti B, et al. (2007) Absence of the lactase-persistence-associated allele in early Neolithic Europeans. *Proceedings of the National Academy of Sciences of the United States of America* 104(10): 3736–3741.
- Burmeister S (2016) Archaeological research on migration as a multidisciplinary challenge. *Medieval Worlds* 4: 42–64.
- Callaway E (2010) Neanderthal genome reveals interbreeding with humans. *New Scientist*, 6 May. Available at: <https://www.newscientist.com/article/dn18869-neanderthal-genome-reveals-interbreeding-with-humans> (accessed 27 January 2021).
- Cano RJ, Poinar HN, Pieniazek NJ, et al. (1993) Amplification and sequencing of DNA from a 120–135-million-year-old weevil. *Nature* 363(6429): 536–538.
- Collar A, Coward F, Brughmans T, et al. (2015) Networks in archaeology: Phenomena, abstraction, representation. *Journal of Archaeological Method and Theory* 22(1): 1–32.
- Cooper A and Poinar HN (2000) Ancient DNA: Do it right or not at all. *Science* 289(5482): 1139.
- Crellin R and Harris OJT (2020) Beyond binaries: Interrogating ancient DNA. *Archaeological Dialogues* 27(1): 37–56.
- Díaz-Andreu M, Lucy S, Babić S, et al. (eds) (2014) *The Archaeology of Identity: Approaches to Gender, Age, Status, Ethnicity and Religion*. London: Routledge.

- Egorova Y (2010) DNA evidence? The impact of genetic research on historical debates. *BioSocieties* 5(3): 348–365.
- Fenn J and Raskino M (2008) *Mastering the Hype Cycle: How to Choose the Right Innovation at the Right Time*. Boston, MA: Harvard Business Press.
- Frieman C and Hofmann D (2019) Present pasts in the archaeology of genetics, identity, and migration in Europe: A critical essay. *World Archaeology* 51(4): 528–545.
- Furholt M (2019) De-contaminating the aDNA-archaeology dialogue on mobility and migration: Discussing the culture-historical legacy. *Current Swedish Archaeology* 27: 53–26.
- Furholt M (2020) Biodeterminism and pseudo-objectivity as obstacles for the emerging field of archaeogenetics. *Archaeological Dialogues* 27(1): 23–25.
- Gibbons A (2015) Revolution in human evolution. *Science* 349(6246): 362–366.
- Gilbert MTP, Kivisild T, Grønnow B, et al. (2008) Paleo-Eskimo mtDNA genome reveals matrilineal discontinuity in Greenland. *Science* 320(5884): 1787–1789.
- Green RE, Krause J, Briggs AW, et al. (2010) A draft sequence of the Neandertal genome. *Science* 328(5979): 710–722.
- Haak W, Forster P, Bramanti B, et al. (2005) Ancient DNA from the first European farmers in 7500-year-old Neolithic sites. *Science* 310(5750): 1016–1018.
- Hagelberg E, Sykes B and Hedges R (1989) Ancient bone DNA amplified. *Nature* 342(6249): 485.
- Hakenbeck S (2019) Genetics, archaeology and the far right: An unholy trinity. *World Archaeology* 51(4): 517–527.
- Hänni C, Laudet V, Sakka M, et al. (1990) Amplification of mitochondrial DNA fragments from ancient human teeth and bones. *Comptes Rendus de l'Académie des Sciences. Serie III, Sciences de La Vie* 310(9): 365–370.
- Harvati K and Harrison T (2006) Neanderthals revisited. In: Harvati K and Harrison T (eds) *Neanderthals Revisited: New Approaches and Perspectives*. Dordrecht: Springer, pp. 1–7.
- Hedenstierna-Jonson C, Kellström A, Zachrisson T, et al. (2017) A female Viking warrior confirmed by genomics. *American Journal of Physical Anthropology* 164(4): 853–860.
- Heyd V (2017) Kossinna's smile. *Antiquity* 91(356): 348–359.
- Higuchi R, Bowman B, Freiberger M, et al. (1984) DNA sequences from the quagga, an extinct member of the horse family. *Nature* 312(5991): 282–284.
- Hofmann D (2015) What have genetics ever done for us? The implications of aDNA data for interpreting identity in Early Neolithic Central Europe. *European Journal of Archaeology* 18(3): 454–476.
- Hummel S and Herrmann B (1991) Y-chromosome-specific DNA amplified in ancient human bone. *Die Naturwissenschaften* 78(6): 266–267.
- Ion A (2017) How interdisciplinary is interdisciplinary? Revisiting the impact of aDNA research for the archaeology of human remains. *Current Swedish Archaeology* 25: 87–108.
- Jones ED (2019) Ancient genetics to ancient genomics: Celebrity and credibility in data-driven practice. *Biology and Philosophy* 34(27): 1–35.
- Jones ED (2022) *Ancient DNA: The History and Celebrity of a Science*. New Haven, CT: Yale University Press.
- Källén A, Mulcare C, Nyblom A, et al. (2019) Archaeogenetics in popular media: Contemporary implications of ancient DNA. *Current Swedish Archaeology* 27: 69–91.

- King PH (1993) Step right up and see the science. *Los Angeles Times*, 16 June. Available at: http://articles.latimes.com/1993-06-16/news/mn-3654_1_dna-research (accessed 18 January 2021).
- King TE, Gonzalez Fortes G, Balaesque P, et al. (2014) Identification of the remains of King Richard III. *Nature Communications* 5(December): 5631.
- Krause J, Fu Q, Good JM, et al. (2010) The complete mitochondrial DNA genome of an unknown hominin from Southern Siberia. *Nature* 464(7290): 894–897.
- Krings M, Stone A, Schmitz RW, et al. (1997) Neandertal DNA sequences and the origin of modern humans. *Cell* 90(1): 19–30.
- Lewin R (1997) Back from the dead. *New Scientist*, 18 October. Available at: <https://www.newscientist.com/article/mg15621045-300-back-from-the-dead/> (accessed 27 January 2021).
- Lidén K and Eriksson G (2013) Archaeology vs. archaeological science: Do we have a case? *Current Swedish Archaeology* 21: 11–20.
- Lipphardt V (2019) Über den allzu sorglosen umgang mit population labels und sampling schemes [On the very careless use of population labels and sampling schemes]. *NTM* 27: 167–177.
- Margulies M, Egholm M, Altman WE, et al. (2005) Genome sequencing in microfabricated high-density picolitre reactors. *Nature* 437(7057): 376–380.
- Marks J (2017) *Is Science Racist? Debating Race*. Cambridge: Polity.
- Max Planck Society (2006) Neandertal genome to be deciphered. Press release, 20 July. Available at: www.mpg.de/534422/pressRelease20060720 (accessed 18 January 2021).
- Millar CD and Lambert DM (2019) Archaeogenetics and human evolution: The ontogeny of a biological discipline. *World Archaeology* 51(4): 546–559.
- Mullis KB and Faloona FA (1987) Specific synthesis of DNA in vitro via a polymerase-catalyzed chain reaction. *Methods in Enzymology* 155: 335–350.
- Natural Environment Research Council (1990) *Special Topic in Biomolecular Palaeontology Community Meeting Programme*. Glasgow. Elizabeth Jones Personal Collection.
- Nelkin D (1995) *Selling Science: How the Press Covers Science and Technology*. New York: WH Freeman and Company.
- Nilsson Stutz L (2018) A future for archaeology: In defense of an intellectually engaged, collaborative and confident archaeology. *Norwegian Archaeological Review* 51(1–2): 48–56.
- Pääbo S (1985) Molecular cloning of ancient Egyptian mummy DNA. *Nature* 314(6012): 644–645.
- Pääbo S (2014) *Neanderthal Man: In Search of Lost Genomes*. New York: Basic Books.
- Poinar HN, Schwarz C, Qi J, et al. (2006) Metagenomics to paleogenomics: Large-scale sequencing of mammoth DNA. *Science* 311(5759): 392–394.
- Price N, Hedenstierna-Jonson C, Zachrisson T, et al. (2019) Viking warrior women? Reassessing Birka chamber grave Bj. 581. *Antiquity* 93(367): 181–198.
- Rasmussen M, Li Y, Lindgreen S, et al. (2010) Ancient human genome sequence of an extinct Palaeo-Eskimo. *Nature* 463(7282): 757–762.
- Reardon J (2004) *Race to the Finish: Identity and Governance in an Age of Genomics*. Princeton, NJ: Princeton University Press.
- Reich D (2018) *Who We Are and How We Got Here: Ancient DNA and the New Science of the Human Past*. Oxford: Oxford University Press.

- Reich D, Green RE, Kircher M, et al. (2010) Genetic history of an archaic hominin group from Denisova Cave in Siberia. *Nature* 468(7327): 1053–1060.
- Samida S (2019) Archaeology in times of scientific omnipresence. In: Brather-Walter S (ed) *Archaeology, History and Biosciences: Interdisciplinary Perspectives*. Berlin: de Gruyter, pp. 9–22.
- Samida S (2020) Über mediale präsenz und prominenz DNA-gestützter vergangenheitsforschung [On the media presence and prominence of DNA-based research into the past]. *NTM* 28: 182–192.
- Samida S and Eggert MKH (2013) *Archäologie Als Naturwissenschaft? Eine Streitschrift [Archaeology as Science? A Polemic]*. Berlin: Vergangenheitsverlag.
- Shuttleworth R and Meekosha H (2017) Accommodating critical disability studies in bioarchaeology. In: Byrnes JF and Muller JL (eds) *Bioarchaeology of Impairment and Disability: Theoretical, Ethnohistorical, and Methodological Perspectives*. New York: Springer, pp. 19–38.
- Skoglund P, Malmström H, Raghavan M, et al. (2012) Origins and genetic legacy of Neolithic farmers and hunter-gatherers in Europe. *Science* 336(6080): 466–469.
- Smith AB (1995) Application for an ABI Research Grant. Natural Environment Research Council. Elizabeth Jones Personal Collection.
- Spigelman M and Lemma E (1993) The use of the polymerase chain reaction (PCR) to detect *Mycobacterium tuberculosis* in ancient skeletons. *International Journal of Osteoarchaeology* 3(2): 137–143.
- Stone A and Stoneking M (1993) Ancient DNA from a pre-Columbian Amerindian population. *American Journal of Physical Anthropology* 92(4): 463–471.
- Stoneking M and Krause J (2011) Learning about human population history from ancient and modern genomes. *Nature Reviews Genetics* 12(9): 603–614.
- Than K (2010) Neanderthals, humans interbred - First solid DNA evidence. *National Geographic*, 8 May. Available at: <http://news.nationalgeographic.com/news/2010/05/100506-science-neanderthals-humans-mated-interbred-dna-gene/> (accessed 18 January 2021).
- Tsing AL (2015) *The Mushroom at the End of the World: On the Possibility of Life in Capitalist Ruins*. Princeton, NJ: Princeton University Press.
- Vigilant L, Pennington R, Harpending H, et al. (1989) Mitochondrial DNA sequences in single hairs from a Southern African population. *Proceedings of the National Academy of Sciences of the United States of America* 86(23): 9350–9354.
- Warinner C, Hendy J, Speller C, et al. (2014) Direct evidence of milk consumption from ancient human dental calculus. *Scientific Reports* 4(7104): 1–6.
- Weaver TD and Roseman CC (2005) Ancient DNA, late Neandertal survival, and Modern-human-Neandertal genetic admixture. *Current Anthropology* 46(4): 677–685.
- Willerslev E, Davison J, Moora M, et al. (2014) Fifty thousand years of Arctic vegetation and megafaunal diet. *Nature* 506(7486): 47–51.

Author biographies

Elizabeth D Jones is a historian of science with degrees from North Carolina State University, Florida State University, and University College London. She specializes in the contemporary history, philosophy, and sociology of paleontology, ancient genetics, ancient genomics, and de-extinction. Her research also overlaps

with work in science communication studies, media studies, and celebrity studies. Throughout her career, Jones has had first-hand international experience working with paleontologists and geneticists in both the field and the lab. Currently, Jones is a Postdoctoral Research Scholar at North Carolina State University on a National Science Foundation research project for data ethics in citizen science.

Elsbeth Bösl is a historian of technology and science with an academic background in archaeology. She is assistant professor at the Chair of Social and Economic History and the History of Technology at the University of the German Armed Forces at Munich. Her areas of expertise include the history of archaeology, interdisciplinary research, and archaeogenomics.