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The Role of Ancient DNA Research in Archaeology

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Abstract

In this paper I briefly introduce work on ancient-DNA (aDNA) and give some examples of the impact this work has had on responses to questions in archaeology. Next, I spell out David Reich's reasons for his optimism about the contribution aDNA research makes to archaeology. I then use Robert Chapman and Alison Wylie's framework to offer an alternative to Reich's view of relations between aDNA research and archaeology. Finally, I develop Steven Mithen's point about the different questions archaeologists and geneticists ask, arguing that different disciplinary perspectives color researchers' perceptions of "the most important questions" or the "central topics" in a field. I conclude that evidence from aDNA research cannot solve archaeological disputes without closer, mutually respectful collaboration between aDNA researchers and archaeologists.

Ancient DNA data, like radiocarbon data, is not a silver bullet for problems in archaeology.

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1. Introduction

Since the first nuclear genome sequencing of ancient human DNA (Rasmussen et al. 2010), geneticists have been championing the importance of ancient-DNA work for archaeology. David Reich (2018) claims that the contribution of ancient-DNA work will be “far more revolutionary” for archaeology than the contribution of radiocarbon dating. Reich, among others, claims that ancient-DNA work has already resolved long standing disputes in archaeology and that it is only a matter of time before all archaeologists rely on ancient-DNA in their work. Some archaeologists are on board and share Reich’s optimism but others call for a careful, case by case approach to integrating ancient-DNA data into archaeology (see Callaway 2018 for an overview of this debate). ~~were correct~~ Other archaeologists see the value in ancient-DNA evidence but doubt it has applicability to all archaeological questions (Callaway 2018). Steven Mithen, for example, says that Reich and others’ work does a good job of answering the question of how we got here but that “there remains a place after all for archaeology, anthropology and history in telling us who we are, and who we would like to be” (2018).

Archaeologists are interested in who the ancient peoples they study were and what they were like. Given this, for many researchers non-aDNA archaeology continues to serve as an inferential window into past peoples. Further, archaeologists are also interested in how the peoples they study thought, which is not obviously accessed via aDNA techniques (see e.g. Currie and Killin 2019).

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There is always a rhetoric of optimism associated with the introduction of new technological resources into an existing established scientific practice. Archaeology is no stranger to this phenomenon, the introduction of radiocarbon dating was accompanied by both much fanfare and as well as vigorous dissent (see e.g. Renfrew 1999). Radiocarbon dating is a way of assessing the time of death of an

organism by measuring the amount of Carbon-14 still present in the organism's remains. Carbon-14, which is constantly being created in the Earth's atmosphere, is incorporated into plants via photosynthesis and then into other organisms, either by them ingesting those plants or by them eating other organisms who have ingested those plants. Carbon-14 is radioactive and has a natural rate of decay and so the amount of Carbon-14 in an organism decreases from the time the organism stops ingesting plant matter containing Carbon-14. For some researchers, radiocarbon dating was going to solve all of archaeology's problems and put archaeological claims on an objective base once and for all. Various dating techniques are now commonplace in archaeology ~~but~~ and the history of the acceptance and development of these various techniques is one of the different types of collaboration between archaeologists and the scientists developing the relevant technologies. Chapman and Wylie (2016) present a detailed history of some of this collaborative work surrounding radiocarbon dating but, perhaps more importantly for our purposes, they also propose a sophisticated epistemological analysis of the ways in which evidence from radiocarbon dating came to be incorporated as evidence for archaeological hypotheses. Here I argue that we have no reason to believe that ancient-DNA evidence simply overturns or undercuts archaeological hypotheses nor that such evidence comes with automatic warrant, borrowed from genetics. In other words, I argue that Reich's optimism, is misplaced.

In what follows I briefly lay out the state of play in work on ancient-DNA and give some examples of the impact this work has had on archaeological inquiry. Next, I articulate Reich's reasons for his optimism about the contribution of genetics to archaeology. I then use Chapman and Wylie's framework to offer an alternative to Reich's view of relations between genetics and archaeology. Finally, I develop Mithen's point about the different questions archaeologists and geneticists ask, arguing that different disciplinary perspectives color researchers' perceptions of "the most important questions" or the "central topics" in a field.

Before I begin, a quick note on terminology is in order. Throughout this paper I will refer to work on ancient-DNA and the impact that evidence from ancient-DNA work has on hypotheses in archaeology. Various terms have been introduced to characterize this work, for example Johannes Krause calls it "archaeogenetics"¹ (Callaway 2018), and others call it geneticarchaeology. The key to understanding this work for our purposes is not so much that it is work in genetics but rather that the genetic material of interest is derived from the remains of ancient peoples. Once the genetic material has been extracted, the work carried out on it relies on techniques commonly used in molecular population genetics.

2. Ancient-DNA

Ancient-DNA is extracted from human remains, from the remains of animals found in close proximity to these humans and from pathogens found in the human and animal remains. Prior to the technological advances that allowed for the extraction of ancient-DNA, population geneticists were already working on understanding the human lineage. For example, Allan Wilson and his colleagues (Cann et al. 1987) used a small sequenced segment of mitochondrial DNA (mDNA) taken from people from different groups around the world and, using statistical inference techniques from genetics, established a tree whose trunk derived from a woman in Africa around 200,000 years ago, dubbed “mitochondrial Eve”. When we talk of an organism’s genome, we refer to all of the DNA passed on from one generation to the next via reproduction. In humans, and organisms like us, mDNA is passed on via cytoplasmic inheritance from mothers. mDNA makes up a very small part of our total cellular DNA complement but its mode of transmission allows for very useful inferences about descent. This type of work derived from Luca CavalliSforza’s (see e.g. Cavalli-Sforza et al. 1997) idea that we could reconstruct the history of human migration by inferring from genetic differences among our contemporaries across the world. Cavalli-Sforza and his colleagues’ work focused on contemporary DNA and also on a very small proportion of our genome. More recent ancient DNA (aDNA) research, in contrast, uses genetic material from ancient peoples and samples from a much greater proportion of their genomes.

Early aDNA work had similar limitations to Cavalli-Sforza’s work, as the DNA sequenced from ancient humans was also only from a small part of the genome. Ancient mDNA was sequenced as well as DNA from specific genes, for example the FOXP2 gene (see e.g. Enard et al. 2002). Researchers focused on variations between a segment of the genome found in ancient hominins, for example Neanderthals, and that same segment in contemporary humans. The relevant variations are known as single nucleotide polymorphisms (SNPs). In highly conserved genes, genes that occur in very similar form deep into the evolutionary tree, SNPs attract a lot of attention. For example, the gene FOXP2 is found in mice² and on up to humans but there are a few points at which one of the bases (adenine, cytosine, guanine and thymine) is different in the human and mouse version of the gene. These are SNPs. Much aDNA work at this time—early 2000’s—was focused on differences between Neanderthal and contemporary human DNA and while Neanderthal’s shared the SNPs that distinguished the human FOXP2 gene from the mouse FOXP2 gene, there is one SNP that distinguishes Neanderthal FOXP2 from

more recent human FOXP2. All contemporary humans have a variant that is lacking in Neanderthal DNA (Maricic et al. 2013).

When the difference between Neanderthal and human FOXP2 genes was first discovered, there were many who thought that this difference could be the genetic key to understanding human evolution (see e.g. Pääbo 2014). This is not the main point of aDNA research now. Reich (2018), among others, is skeptical that we can uncover any biological or behavioral differences between us and our ancestors via the comparative study of ancient and contemporary DNA.³ What aDNA work is best suited for is answering questions about human origins. Ancient DNA evidence can help fill in, and at many points correct, Cavalli-Sforza's picture of human migration across the globe. Several developments were required to produce the aDNA evidence that Reich promotes as revolutionary for archaeology. I briefly characterize three: methods of extraction, amount of genome sequenced and methods of genetic analysis.

How aDNA is extracted from ancient remains, what part of the skeleton DNA is extracted from and how the samples are handled prior to genetic analysis are all crucial to the quality of aDNA data. DNA is extracted from bones but such DNA can be severely degraded, making it hard to discover any useful sequences of nucleotides. DNA is better preserved in skeletons in colder climates and in some rare cases, such as "Iceman," most of whose entire body was preserved in glacial ice (Reich 2018, pp. 99–100), DNA can be extracted from material other than bone. Skeletons from the Near East and Africa have much less useable DNA than those from Northern Europe. The discovery that bone extracted from the inner ear region of the skull has a much higher concentration of useable DNA opened up aDNA extraction from skeletons from warmer parts of the world (Reich 2018, p. 94). Not only the method of extraction but also the handling of the extracted samples has been refined considerably. This part of the process was improved after the first part of the Neanderthal genome sequence published (Green et al. 2006) was demonstrated to contain SNPs that were evidence of contamination with contemporary human DNA (Wall and Kim 2007). When our key comparisons are being made at the level of SNPs, individual base pair differences, researchers cannot afford to have any other DNA mix with the sampled aDNA.⁴ Protocols introduced by Green et al. (2010) for both extraction and sample preparation helped resolve this issue. It is now standard to indicate that protocols are in place to avoid contamination of aDNA samples. For example, in Sheena Fraser and her collaborators' work on Neolithic cattle (2017; discussed below), both their aDNA extraction techniques and the protocols followed to avoid contamination of their

sample—making sure that all aDNA is analyzed in a lab in which no modern animals have been analyzed—are carefully noted. Noting that such protocols have been followed is as much a part of archaeology using aDNA evidence as providing the specifics of the radiocarbon dating process used is a part of archaeology in general.

Next, the amount of genetic material sequenced is far greater in recent aDNA work than it was in Allan Wilson and his colleagues' (Cann et al. 1987) and others' work. Reich's group, and others working on aDNA sequencing, aim to sequence a significant proportion of the relevant aDNA genome. Both nuclear DNA and mitochondrial DNA are sequenced allowing for comparisons between larger areas of the genome. Our earlier example of comparing FOXP2 sequences revealed one SNP distinguishing contemporary humans from Neanderthals, comparing sequences of hundreds of thousands of base pairs reveals much more variation. Also, just as mDNA sequences can be used to infer conclusions about matrilineal descent, Y chromosome sequences can be used to infer conclusions about patrilineal descent.⁵ There is an increase in sequence data now available from each individual but there is also a huge increase in the number of individuals whose aDNA has been sampled. aDNA sequences have been published from around 1300 individuals (Callaway 2018) and Reich claims that far more individuals have had their aDNA sequenced than have had their sequences published. Reich's aspiration is to produce aDNA sequences from 2000 individuals per year.

Finally, more methods of genetic analysis are used in aDNA work than were used by (or available to) Cavalli-Sforza et al. Inferring descent from contemporary genetic data involves statistical inferences. Statistical inferences are part and parcel of population genetics, whether classical or molecular (see Lynch 1998 for classical population genetics; and Graur 2016 for molecular evolution). Mutation rates—rates of occurrence of a new base at a location on the genome—and patterns in the genome that are anticipated to result from natural selection are combined with an understanding of the impact of recombination, via sexual reproduction, into an account of how patterns in the genome are transmitted and change over time. The amount of Neanderthal DNA in modern humans, whose distant ancestors interbred with Neanderthals, is a very small fraction of their total DNA complement as a result of thousands of generations of reproduction and hence recombination. On the other hand, ancient humans who lived only 8000 to 10,000 years after the disappearance of Neanderthals will have a larger amount of DNA from Neanderthals if their ancestors interbred with Neanderthals. Reich argues that comparison between different aDNA samples provides much better evidence of

relations of descent and migration patterns than comparison between ancient and contemporary DNA samples. This also greatly increases the strength of conclusions that we can draw. For example, we can infer the existence of certain ancestral human populations from contemporary DNA data from people from various parts of the world (Reich calls these “Ghost populations” if they are established as a result of statistical inference alone). If aDNA is extracted from an individual that is close to the predicted pattern and the individual is established, via archaeological techniques, to have lived at the relevant time, then Reich concludes that the relevant population existed and that the aDNA results establish the place of this population in the human lineage (see 2018, chapter 4). I conclude this section with a few examples of the impact of aDNA evidence on archaeological questions.

Archaeologists make inferences about human activity at a particular time and in a particular place by analyzing the “material culture” left behind. Human remains, human artifacts, remains of buildings, remains of animals and crops are all examples of material culture. Archaeologists often settle for a detailed, inferred account of the lifeways of a small group of people at a place and time over broad generalizations about patterns of behavior of large groups of people over long periods of time. These latter issues are certainly discussed and alternate explanations of such larger patterns are sources of controversy in archaeology. aDNA is by no means the first source of new evidence that has fueled dispute in archaeology (see e.g. Renfrew 1999). One such broader pattern, distribution of a particular type of pottery (or stone axes or burial mounds), could result from migration of a group of people bringing their cultural product with them or from the passing of ideas or techniques between different groups of people. The Bell Beaker style of pottery was widely distributed in Europe from around 2750 BC and had disappeared by 2200 to 1800 BC. There was something of a consensus in archaeology that the Bell Beaker pottery style was not spread by migration of one group of people. Olalde et al. (2018) (in a collaboration including Reich’s team) argued on the basis of aDNA data that, specifically in Britain, Bell Beaker pottery was introduced by a large migration of people who ended up replacing 90% of Britain’s gene pool within a few 100 years. Olalde et al. presented their findings as definitive and as closing the debate over the spread of Bell Beaker ware. Not all archaeologists agreed with this conclusion (see Callaway 2018). The result is touted by Reich, and others, as an example of a definitive application of aDNA work to archaeology.

An example of the use of aDNA to focus on a more local issue than Bell Beaker ware spread is Fraser et al.’s (2017) work on Orkney cattle.⁶ There are several

hypotheses about the introduction of cattle to the Orkney Islands during the development of farming there, starting around 3500 BC. Aurochs are an extinct species of wild cattle that lived in Asia, Europe and North Africa and were domesticated in various places. Migrants could have brought aurochs with them to Orkney during initial settlement or the same migrants could have brought aurochs skulls with them. Alternately, wild aurochs could have colonized Orkney. Finally, there could have been breeding between wild female aurochs and male domestic cattle before the introduction of the cattle to Orkney. Fraser et al. extracted ancient mtDNA from remains of large cattle in Orkney from the Neolithic period. They also used isotope data to establish the grazing location of the cattle. They conclude that the ancient mtDNA evidence, along with isotope evidence and geological evidence about available land bridges (which could have facilitated aurochs migration) points to aurochs/domestic cattle hybrids, who were produced by interbreeding before their introduction to Orkney, living in Orkney. I now turn to the claims Reich makes about the impact of aDNA on archaeology in general.

3. Has aDNA Ushered in the Most Significant Revolution in Archaeology?

Reich makes a number of claims about the importance of aDNA for archaeology and offers aDNA research as a key to answering archaeological questions. Here are some examples: “The question that the archaeological record cannot answer—but the DNA record can—is how [Neanderthals] were related to us” (Reich 2018, p. 26). Discussing the origin of Indo-European languages, he says that ancient DNA helps pinpoint the origin of Indo-European languages but “DNA cannot of course reveal what languages people spoke. But what geneticists can do is to establish that migrations occurred. If people moved, it means that cultural contact occurred too—in other words, genetic tracing of migration makes it possible also to trace potential spreads of culture and language” (Reich 2018, pp. 120–121). Reich catalogues many sequences of aDNA extracted from ancient human populations, such as the Denisovans (Krause et al. 2010; Reich 2018, pp. 53–54), and each are presented as breakthroughs in archaeology. Each of these cases result from the sequencing of aDNA taken from remains of ancient humans found at specific places, dated by archaeologists. He also claims that Y chromosome work on aDNA reveals the massive social inequities at the beginning of the Bronze Age (Reich 2018, p. 237).⁷

Reich chronicles many such specific contributions of aDNA to archaeology but he also articulates a view about the general impact of aDNA research on archaeology. He compares the impact of radiocarbon dating and aDNA on archaeology,

concluding that aDNA is having a far more revolutionary impact on archaeology than radiocarbon dating has had.⁸ He provides two arguments for this conclusion. First, he says “It is tempting to view ancient DNA as just one more new scientific technology that became available to archaeologists after the radiocarbon revolution, but that would be underestimating it. Prior to ancient DNA, archaeologists had hints of population movement based on the changes in the shapes of ancient skeletons and the types of artifacts people made, but these were hard to interpret. But by sequencing whole genomes from ancient people, it is now possible to understand in exquisite detail how everyone is related” (Reich 2018, p. 276). I respond in more detail to this argument in Sect. 5 below. For now, I note that if the sole aim of archaeology is to discover how people are related, then aDNA is a better resource for archaeology than radiocarbon dating. His second argument starts with the following premise: “The measure of a revolutionary technology is the rate at which it reveals surprises” and continues “in this sense, ancient DNA is more revolutionary than any previous scientific technology for studying the past, including carbon dating” (Reich 2018, p. 276). Reich supports this argument by drawing an analogy between the introduction of aDNA and the introduction of the light microscope in the seventeenth century. The light microscope opened up a whole range of objects for us to characterize and introduced many surprises about our world. He goes on to say “When a new instrument opens up vistas into a world that has not previously been explored, everything it shows is new, and everything is a surprise. This is what is happening now with ancient DNA. It is providing definitive answers to questions about whether changes in the archaeological record reflect movements of people or cultural communication. Again and again, it is revealing findings that almost no one expected” (Reich 2018, p. 276). Reich’s premise about the history of science is an empirically testable claim and, while it would take a considerable amount of work, the respective track records of radiocarbon dating and aDNA in archaeology could be compared. Here, empirical information drawn from science studies would be helpful. As things stand, there are vastly more publications in archaeology that rely on evidence from radiocarbon dating than aDNA. This situation may change, as new aDNA work is published at a rapid rate, but assessing the significance of the contribution of either technology to archaeology will take more careful work in history and philosophy of science and will require more sophisticated metrics than mere number of publications invoking each alternate technology. In the next section I turn to an analysis of the role of radiocarbon dating in archaeology and argue that we can apply elements of this framework to assessing the role of aDNA in archaeology. This approach draws different conclusions to Reich’s about the relations between aDNA and archaeology.

4. External Sources of Archaeological Evidence

So far I have taken aDNA research to be a source of evidence for archaeological hypotheses. I have taken this approach, because it is key to the way that Wylie views archaeology (see e.g. Wylie 1989, 2000): archaeology fuses alternate lines of evidence. Chapman and Wylie (2016) provide a detailed examination of the introduction, use and impact of radiocarbon evidence to archaeology. Their analysis draws on Wylie's earlier work but also on work in philosophy and history of science by Hasok Chang, Lorraine Daston, Peter Galison and Helen Longino (e.g. Chang 2004; Daston 2007; Galison 2010; Longino 2002), therefore extending a significant and influential line of thinking about science and scientific practice. Here I briefly lay out Chapman and Wylie's approach to archaeologists' use of radiocarbon dating and then argue that this approach is also well suited to appraising relations between archaeology and aDNA evidence.

Chapman and Wylie understand that archaeologists "recruit material postulates from fields as diverse as nuclear physics and physical chemistry, paleoecology and geology, material science and human physiology, social geography, cultural anthropology and ethno-history" (2016, p. 143) and, as we have seen here, aDNA research and genetics. However, they warn that "No matter how scientifically or technically sophisticated it may be, the scaffolding drawn from neighbouring fields rarely establishes archaeologically relevant evidential claims without extensive reinforcement and calibration that depends on a great many internal (archaeological) and external resources" (2016, p. 9). The scaffolding they refer to here is technological and theoretical input from the relevant fields. Their overall project is guided by the following: "considerable wisdom is embodied in the creativity and skilled practice of archaeologists that is only made explicit when trouble arises, typically in the context of close-to-the-ground debate about specific cases" (2016, p. 6). So, rather than taking a contribution from aDNA research as a definitive knockdown of a specific archaeological hypothesis, Chapman and Wylie would consider such a contribution as more evidence to fuel further discussion. Chapman and Wylie's overarching project is to "identify a number of epistemic norms that we believe will serve archaeologists better than the all-or-nothing ideals of truth and objectivity that tend to dominate programmatic debate about the scientific status of evidential reasoning and of archaeology itself" (2016, p. 10; see also Currie 2018 who takes a similar approach to historical sciences in general.). Chapman and Wylie capture the integration of external sources of evidence into archaeology by viewing archaeology as a "trading zone," Galison's term for a

discipline whose “boundaries [are] permeable and its practitioners conversant enough in the languages and practices of dozens of other fields to bring radically diverse resources to bear on archaeological problems” (Chapman and Wylie 2016, p. 11).⁹ Viewing archaeology as a trading zone, is to view the field as consisting of practitioners with wide ranges of expertise and who are conversant in methods and approaches from neighboring fields from where they draw their alternate lines of evidence. Applied to the case of radiocarbon dating, this approach reveals that radiocarbon dating, rather than being a gold standard, “secure in its own terms,” required a series of calibrations via various archaeological techniques. According to Chapman and Wylie, the pattern of relations between archaeology and radiocarbon dating is one of “enthusiastic uptake, disillusionment and then painstaking refinement—a life history of technical imports to archaeology—that has been repeated many times over” (2016, p. 144).

There is a normative component to Chapman and Wylie’s trading zone notion: trading zones are hard earned and can only be established through good epistemic practice, specifically requiring mutual epistemic respect between participants. For example, when radiocarbon dating was originally appealed to by archaeologists, it was deemed secure because it was part of nuclear physics and so any radiocarbon dating claim took external epistemic warrant from nuclear physics. Work in both physics and archaeology revealed that there are many confounds to what radiocarbon dating measures—“the point at which organic material [stops] exchanging carbon with the atmosphere”—and there can be gaps between this measurement and the cultural events that archaeologists are interested in. Until a state of mutual input and respect between all parties is achieved, the relevant situation does not count as a successful trading zone. Chapman and Wylie map the stages of the integration of progressively more sophisticated types of radiocarbon dating into archaeology onto the stages that go into producing a successful trading zone. One key part of this process is the assessment of radiocarbon dating evidence, not on its own terms, but on archaeologists’ terms. Ways of using radiocarbon dating were gradually brought into archaeology and the way in which radio-carbon data lent support to archaeological hypotheses was made sense of against the background of understanding the way in which other sources of evidence lent support to those same hypotheses.

We have only a sketch of Chapman and Wylie’s project here but we have enough to present an alternative account to Reich’s of the state of play between aDNA and archaeology. In the case of the Bell Beaker debate, aDNA researchers presented their sequencing data of aDNA extracted from a number of individuals from the

relevant time period. The sequencing data was not up for negotiation, its epistemic warrant comes from genetics and also from the improvements to the process of securing aDNA discussed in Sect. 2 above.¹⁰ One point that aDNA researchers do not make as explicit as they perhaps could, is that there is already a great deal of archaeological work implicit in the aDNA work. Researchers such as Reich are dependent on archaeologists for the dating work on the bones and associated materials and this information helps frame the claims that aDNA workers make. Keeping this point implicit does not encourage the kind of mutual epistemic respect required of a trading zone. If aDNA work is introduced into discussions in archaeology along with explicit acknowledgement that the work was made possible not only by advances in genetics but by painstaking archaeological work, the aDNA project would appear more collaborative. Generating more and more aDNA sequence analyses does not resolve this issue. Reich's promise to deliver the aDNA sequences of 2000 individuals a year is a promise to deliver more data but does not appear to be an opening move in a mutually epistemically respectful interdisciplinary practice. If this increasing volume of aDNA evidence were to be presented as providing potential for resolving archaeological discussions, rather than as definitively closing them, this would constitute a move towards such an epistemically respectful interdisciplinary practice.

Perhaps focusing on Reich's approach misleads about the overall picture of aDNA and archaeology. One of my examples above is the role aDNA plays in a large-scale dispute in archaeology, the Bell Beaker case, but the other is an example of the kind of practice on the ground that Chapman and Wylie point to as revealing the "skilled practice" of archaeologists. Fraser et al.'s (2017) work makes use of aDNA evidence, along with many other considerations to address a contested issue in the understanding of animal domestication. Zeder et al. (2006), in their review of aDNA work on domestication, explicitly call for "archaeologists and geneticists [...] to recognize that not all data pertaining to the domestication process resides within the boundaries of their own discipline" (2006, p. 150). This is a call for an interdisciplinary approach that is conducive to developing a trading zone. It could be that the trading zones for aDNA researchers will start small, developing around areas of local dispute, such as the specifics of cattle domestication in Orkney. Perhaps headline grabbing disputes about general archaeological issues are not the place to look for the subtle interdisciplinary work that fosters trading zones.

Chapman and Wylie's account of the gradual integration of radiocarbon dating and archaeology is a useful template for predictions about the integration of aDNA research and archaeology. For much aDNA research, we are currently in a pre-

trading zone phase. The results of genetic analysis of aDNA are presented in the form of answers to archaeological questions or ways in which to definitively resolve disputes. If the trajectory of the collaboration between aDNA research and archaeology follows that of radiocarbon dating and archaeology, I predict many more rounds of “enthusiastic uptake, disillusionment and then painstaking refinement.” Eventual productive collaboration will be secured largely by the work of archaeologists on the ground adapting aDNA results to confront archaeological questions and educating themselves further in the best uses and pitfalls of genetic analysis. Future success in archaeology will not come just from the mountains of data Reich and his colleagues intend to supply them with. I now turn to another reason to question Reich’s optimism about the influence of aDNA research on archaeology: Reich’s underestimation of the range of questions archaeologists confront.

5. The Wide Range of Archaeological Questions

We saw in Sect. 3 that Reich argues that aDNA research will revolutionize archaeology, because it provides a way of definitively answering archaeological questions and resolving archaeological disputes. Here I return to this claim and assess it from a different perspective. As I briefly mentioned in Sect. 3, Reich generally assumes that the most important questions facing archaeologists are questions of how peoples are related to one another and the migration patterns of ancient peoples. Further, he proposes that aDNA tells us where we are from. He says that one of the upshots of aDNA research is that “We now know that nearly every group living today is the product of repeated population mixtures that have occurred over thousands and tens of thousands of years. Mixing is in human nature, and no population is—or could be—‘pure’” (2018, p. 268). When discussing the relative paucity of aDNA data from sub-Saharan Africa, he looks forward to the time when we have much more data and “we will be able to comprehend the range of human variation in Africa in the last tens of thousands of years and make meaningful reconstructions of population structure” (2018, p. 225). Finally, he says “A great lesson of the ancient DNA revolution is that its findings almost always provide accounts of human migrations that are very different from preexisting models, showing how little we really knew about human migrations and population formation prior to the invention of this new technology” (2018, p. 121). Reich and his collaborators are right when they argue that their aDNA data (Olalde et al. 2018) made an important contribution to the Bell Beaker dispersal question and Mithen agrees with them (Mithen 2018). However, I have already noted that not all archaeologists agree that the aDNA data has ended discussion about this issue (for a

review see Callaway 2018). Further, Mithen says that while aDNA research can do a good job of telling us how we got here, it does not tell us who we are. In this section I expand on Mithen's point.

Archaeology frequently involves re-appraisal of previous work via the introduction of new evidence as well as new sources of evidence. In this respect the introduction of aDNA data into the Bell Beaker dispute is not at all unusual for archaeological practice. Remains from digs performed earlier in the twentieth century are stored and carefully catalogued (or catalogued as carefully as techniques at the time allowed). In work on remains found in Neolithic tombs the questions archaeologists confront in their reappraisals are many and varied and include: How did the people die? Were the people simply interred or were their remains prepared for burial? What can be inferred about the burial practices of the relevant people? Can any hypotheses about social structure be inferred from the way people were buried, who was buried or from objects and/or other animals found close to their remains? What was the diet of the people? Did members of the population suffer from pathologies (or trauma) that impacted their lives prior to death? Lawrence (2006), Walsh et al. (2011) and Hutchison et al. (2015) all present reappraisal's of remains from previous digs at burial chambers in Orkney. Lawrence, Walsh, Hutchison and their colleagues all use radiocarbon dating, isotope analysis and extensive and careful analysis of bones to discover evidence of pathologies. Earlier archaeologists often attributed bone damage to trauma during life or damage inflicted during excarnation (removal of flesh) after death. As Lawrence, Walsh, Hutchison and their colleagues point out, not only are they responding to the paucity of sources of evidence presented in the original reports of the respective digs, they are also responding to the theory-laden observations of the earlier archaeologists. Lawrence, for example, seeks to rebut claims that are a result of a tendency of earlier archaeologists to get carried away with myths about burial practices, letting such myths color even their recording of observations of bone damage (or the lack thereof) (2006, p. 57). All these archaeologists note that seemingly quite straightforward observations—noting the presence of articulated as opposed to disarticulated skeletons in the tomb—can be skewed by theoretical pre-suppositions. This problem reinforces the need for careful re-examination of the remains assisted by up to date techniques of evidence gathering.

What does all this have to do with aDNA data and its relevance to archaeology? None of Lawrence, Walsh, Hutchison and their colleagues reject the use of aDNA data. Most of them either have already had aDNA data prepared from the remains they focus on (or they plan to) for use in future published work. The issue is the

questions that these archaeologists attempt to answer and the appropriateness of particular types of data for answering each type of question. The questions I presented above asked of Neolithic peoples who buried (some of) their dead in chambered tombs is a very small subset of the important questions that drive archaeological research. None of these questions is an obvious candidate to be addressed by using aDNA data, although aDNA data may help address some. Also, none of these questions is a question about migration or who these people are descended from. All are questions about the life, death and practices of these Neolithic folk. This is what I take it Mithen is pointing to when saying that archaeology tells us who we are (or who these Neolithic people were). Perhaps what is happening is that aDNA researchers such as Reich view their results from the theoretical perspective of their own discipline. Human population geneticists are primarily concerned with mapping human variation and using that variation (among other signatures in genomes) to trace human lineages. aDNA researchers have produced lots of data that supports this enterprise and have introduced new and surprising findings in that context. However, successful work in population genetics does not necessarily make a contribution to all of archaeology (and where it does contribute, it need not do so revolutionarily). Reich's theoretical perspective frames the questions he takes to be most important (and which seem, on the face of it, to be definitively answerable with genetic data) but this perspective does not encompass the wide range of questions that archaeologists address.

6. Conclusion

The rise of aDNA research has been accompanied by somewhat hyperbolic claims about its transforming impact on archaeology. Here I have argued, following Chapman and Wylie, that aDNA research should be successfully integrated into archaeology in somewhat the same way that radiocarbon dating has been integrated. The process of integration will result in a trading zone, in which evidence from different sources is appraised in a thoroughly interdisciplinary manner by archaeologists, geneticists and all other parties to the discussion. In the short run, the most successful use of aDNA data by archaeologists will come from its introduction by archaeologists into focused work on local, well-formed archaeological questions, rather than from the wholesale importing of results bearing their own pre-established epistemic warrant from aDNA researchers. Finally, I have argued that this latter approach is better suited to answer questions in human population genetics than the majority of questions in archaeology.

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¹ There is now a Wikipedia entry entitled "Archaeogenetics". See <https://en.wikipedia.org/wiki/Archaeogenetics>. Accessed 2 June 2019.

² FoxP2 is also present in birds (see Bolhuis and Everaert 2013 for contributions to this area of research).

³ He does not have this skepticism about contemporary work on the genetic basis of human behavioral traits, citing Genome Wide Association Studies on human behavioral traits as exemplary work in genetics (see e.g. Reich 2018, p. 256). This position is not uniformly shared by his colleagues in human population genetics (see e.g. Martin et al. 2017).

⁴ Contamination of a sample by human DNA is not the only problem; bacterial DNA could contaminate a sample and greatly affect the interpretation of the sequence extracted.

⁵ In typical cases men carry an X and a Y chromosome while women carry two X chromosomes.

⁶ This work draws on aDNA work on domestication. Zeder et al. (2006) provide a review of some of this work in both plants and animals.

⁷ The Y chromosome work reveals many ancient humans in a particular time period with the same male parent. This lends support to the idea that powerful individual men ruled in the relevant time period.

⁸ Reich's arguments are not in defense of the claim that aDNA research is revolutionary in and of itself, rather, he defends the claim that aDNA research makes a revolutionary contribution to archaeology. Assessing the status of contributions made by aDNA research to population genetics, for example, requires an independent line of argument.

⁹ Some philosophers of science have proposed the notion of "scientific imperialism" as a contrasting notion to trading zones for characterizing interdisciplinary interactions in science (see e.g. Dupre 1994). Scientific imperialism picks out cases in which one group of scientists push their ideas and methods onto other scientists on the presumption that their approach will do a better job. The scientific imperialist assumes that their methods and theories carry a kind of epistemic warrant lacking in the methods and theories of fields they aim to take over (see contributions to Maki et al. 2018 for examples of putative scientific imperialism).

¹⁰ As mentioned in foot note 3 above, Reich champions GWAS work on human behavioral traits as exemplary work in genetics. This highly disputed area of human genetics research is by no means an unassailable source of epistemic warrant for claims made by aDNA researchers.