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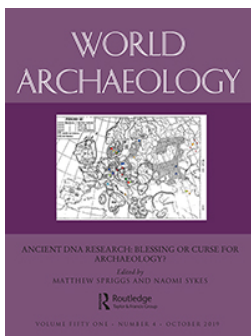
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Beyond curse or blessing: the opportunities and challenges of aDNA analysis

The papers in this volume all have different perspectives but, together, they suggest that the discipline of archaeology continues to struggle with the multi-directional and multi-scalar tensions that have come with the rapidly evolving methods of aDNA analysis. In many ways, the development of aDNA analysis would seem to mirror that of the early development of radiocarbon dating, when new ^{14}C determinations could be grumpily dismissed as ‘archaeologically unacceptable’ (Piggott 1959, 289) rather than engaged with. It is a welcome development that we have got past this stage in aDNA studies in a much-shortened timespan, and effective interdisciplinary collaborations are now developing that involve aDNA analyses as but one powerful technique in the archaeological armoury. However, more than any other scientific technique that has emerged, and been applied to archaeological materials, over the last few decades (including isotope analysis, lipid analysis or proteomics) genetic analysis appears to have opened up deep anxieties about ways of working, as well as the value, role and impact of our field.

In introducing the volume, we wish to explore some of the themes and contradictions evident in the contributions, whilst also giving space to consider issues that have not been examined at all. For instance, we received no submissions to the volume concerning non-human animal and plant aDNA. It is true that the call for submissions did not explicitly highlight aDNA on anything but humans, but it may be too that those working on non-human aDNA had already moved beyond the blessing or curse trope and found it off-putting. It remains the case, however, that when aDNA comes up in casual conversation among archaeologists there is often an assumption that it very largely concerns the aDNA of humans and closely related hominid species, one of them even now only known from genetic rather than morphologically distinctive remains: the famous Denisovan ‘pinkie’ digit (Reich et al. 2010; Reich 2018, Chapter 3). This is despite blockbuster sci-fi movies such as *Jurassic Park* where dinosaur aDNA could be recovered from the meal of a mosquito encased in amber, or well-publicized (albeit somewhat premature) claims that mammoths and Tasmanian tigers could soon be with us again thanks to cloning using aDNA (https://en.wikipedia.org/wiki/Mammoth_cloning; <https://cosmosmagazine.com/biology/return-of-the-living-thylacine>. Both sites consulted 22/2/2020).

To begin with some commonalities among the papers in this volume, migration is a running theme, as aDNA research has undoubtedly transformed our understanding of ancient human movements. The new data do not always sit comfortably with archaeological theories, however. Past diffusionist master narratives that sought to explain any and all cultural changes as a result of migration and population replacement largely fell into disrepute by the 1960s, in part under the withering attack of American ‘new archaeology’, with its mantra of local adaptation as the explanation of culture change (Trigger 1989, 222–7, 244, 326). Now we are back at having to explain mass migration in the past, but without assuming the fact of migration is in itself explanatory of anything.

In the absence of clear interpretations, the data can be read, and used, in many different ways. It is, therefore, unsurprising that nearly all of the contributions in this volume make reference to Gustaf Kossina’s culture-historical models, and how they were used to justify Nazi ideologies of racial

supremacy (cf. Arnold 2006). There is a perception that aDNA analysis of human remains could become the twenty-first-century version of such culture-history, with potential to be similarly damaging. The papers by Hakenbeck (2019) and Frieman and Hofmann (2019), this volume, sound clear and well-evidenced warnings about how archaeological studies that incorporate aDNA data, or rather interpretations of these data, are again being used to fuel Alt-right narratives. These concerns should not be dismissed, especially in the light of a recent speech by the German President, Frank-Walter Steinmeier, who stated at the Fifth World Holocaust Forum 'I wish I could say that we Germans have learnt from history once and for all. But I cannot say that when hatred is spreading' (23/01/2020 <https://icds.ee/speech-by-frank-walter-steinmeier-german-president-in-jerusalem/>)

Nationalist and racist ideologies are undoubtedly on the rise, not just within Germany but across Europe and around the world. Given the current political climate, and given the long history of archaeological evidence being used to legitimize extremist beliefs (e.g. Hakenbeck 2019 and Booth's 2020 timely example here of ancient data being co-opted by both pro and anti-Brexit campaigners) there has never been a greater need for archaeologists and palaeogeneticists to be mindful of the narratives that their work is being used to generate. When often wilfully inaccurate reporting of aDNA results is being promulgated by journalists and others, scholars have a duty to intervene to correct misconceptions about what their results can actually tell us about the past.

From a positive perspective, archaeologists do have the knowledge and skills both to contextualize and challenge naïve migration narratives. They have done so in the past and can certainly do so again. There is also a clear desire to see palaeogeneticists play an important role in this effort. However, because the majority of aDNA specialists do not come from humanities or social sciences backgrounds, they are often perceived as being far less intimate with the cultural dimensions of their datasets.

Hakenbeck (2019) has highlighted that when geneticists take a bottom-up approach to sampling and undertake fine-grained analyses of populations (rather than assuming one individual is representative of that population) the results allow for more sophisticated interpretations whereby consistencies and differences between lines of evidence – e.g. material culture, human remains, morphology and genetic traits – can start to be explained. This kind of approach has already been widely adopted in studies of Chinese prehistory, with aDNA now revealing important insights into social organization and kinship structures (e.g. Dong et al. 2015). Frieman and Hofmann (2019) and Charlton, Booth, and Barnes (2019) call for similar approaches to be adopted as standard. The latter's argument is particularly compelling, coming as it does from a group of researchers who are trained in both genetics and archaeology and thus have a deep understanding of the problems and opportunities inherent within both disciplines.

Two papers in this volume (Booth 2019 and Spriggs and Reich 2020) have stressed that many perceptions that archaeologists have of genetic research are not so much a reality but rather a product of misunderstanding; that genetic models are not reductive but are kept simple deliberately in order that they can be tested reliably using the available data. These explanations highlight two important issues. The first relates to whose hypotheses are being tested – is it fair that palaeogeneticists, who have traditionally been the researchers in receipt of large-scale funding, be criticized for answering their own questions, rather than those that archaeologists wish to see answered? The second pertains to whether aDNA is, in its current state of the art, even capable of answering the kinds of cultural questions that archaeologists wish to see addressed. For instance, from the titles of some recent aDNA papers (Xu et al. 2012; Haak et al. 2015; Posth et al. 2018), one might be excused for thinking that genetics now gives us a unique window on what languages people spoke in the past. It does not. Such inferences can only come from a very explicitly argued interweaving and understanding of linguistic, archaeological, genetic and other data (palaeobotanical, zoological,

etc.). Even then, as with the very divergent arguments regarding when and where proto-Indo-European and its later-developed subgroups were originally spoken, no easy consensus is likely to be arrived at any time soon, however loud the publicity surrounding the latest *Nature* or *Science* aDNA blockbuster paper.

Millar and Lambert have argued (Millar and Lambert 2019, this volume) that palaeogenetics is still in the 'descriptive phase' of the field's evolution, whereby the emphasis is on gathering large amounts of aDNA and then determining the questions *post hoc*. They suggest that the discipline is some way off maturation, which they predict will see future palaeogeneticists test a range of evolutionary hypotheses. As the field matures, perhaps we may also see the archaeological models become more complex because, rather than relying solely on aDNA data, they are integrating evidence from a range of bioarchaeological and biomolecular techniques. Collard et al. 2019, this volume) have made precisely this point, suggesting that not only should multiple independent lines of evidence be sought from the same archaeological materials but that the questions asked of that material should be co-created. In Collard et al.'s case, this co-creation extends beyond interdisciplinary collaboration to transdisciplinary investigation whereby non-academic stakeholders, here Indigenous Australian communities, are fully engaged with the research from the start. Such approaches have the benefit of mitigating many of the criticisms that have been levelled at aDNA research and, indeed, at archaeological research in general: less than ethical treatment and sampling of remains, unproductive and unintegrated destructive analysis and lack of communication with researchers of different disciplines with an interest in the same remains to be sampled and failure to disseminate results in appropriate form to diverse audiences.

Regardless of how projects are designed, the fact cannot be ignored that genetic analysis is a destructive process. In the earliest years of aDNA analysis, sample acquisition was largely unproblematic, since the method was new and high profile, studies were infrequent and the potential for high-quality data was sufficient for archaeologists and curators to grant permissions analysis. As the method has become well established and widespread over the last decade, the number of requests for destructive analysis has increased dramatically, with competing labs requesting the same materials but with less concern for justification as aDNA is promoted as part of the standard toolkit. Within this volume, several papers (notably Sirak and Sedig 2019 and Charlton, Booth, and Barnes 2019) have highlighted the petrous bone (part of the temporal bone, which is itself part of the endocranium and contains the component of the inner ear) as being the sample of choice. This anatomical element is a useful case-study to highlight how the field of ancient DNA has changed and needs to change further as it matures into the future.

The petrous bone

Spriggs and Reich's contribution to the volume explains how the archaeologists involved in their Vanuatu research made several attempts, using three different labs, to extract aDNA from human remains recovered from the Teouma cemetery on Efate Island in Vanuatu. It was not until the petrous bone was identified as a potential source of well-preserved DNA (Gamba et al. 2014; Pinhasi et al. 2015) that they achieved successful results. This example shows how knowledge about the petrous bone has reduced hit-and-miss sampling, allowing for more targeted protocols that are likely to yield results (Sirak and Sedig 2019, this volume). However, as the desire for high-quality aDNA data is coincident with palaeogenomics arguably still being in its 'descriptive phase' (Millar and Lambert 2019, this volume) the situation has given rise to something of a petrous obsession amongst sample collectors. This is starting to raise ethical concerns amongst archaeologists and curators alike as Sirak and Sedig note. Even some

aDNA researchers (notably those coming from archaeological backgrounds such as Charlton, Booth, and Barnes 2019) are beginning to question the wisdom of the widespread emphasis on the petrous bone. For although the petrous bone is a good choice in terms of taphonomic processes (e.g. high bone density facilitating good collagen preservation even in poor burial conditions) less consideration has been given to the cultural processes inherent in the creation of the archaeological record. As Charlton et al. make clear, it is likely that aDNA datasets are problematically skewed because variations (be they sociocultural and/or gender based) in funerary traditions have not been taken into account.

Charlton, Booth, and Barnes (2019) have also pointed out that privileging aDNA analysis on the petrous bone is to the detriment of other sources of equally important data, such as isotope or morphological analysis. The inner ear is responsible for sound detection and balance in vertebrates and therefore carries unique information that has been studied extensively in palaeontology and biology (e.g. Ekdale and Soares 2013; Mourlam and Orliac 2017). It is useful not only in studies of human evolution (Spoor et al. 2003; Ponce de León et al. 2018) but in studies of evolution more generally. For example, Schweizer et al.'s (2017) study on wolves, dingoes, and domesticated dogs explored the use of the inner ear shape as a marker of domestication, a subject of direct interest for the archaeozoological community. However, because of the small size of the petrous, it is frequently completely destroyed during aDNA analysis. The scale of information loss has recently been articulated by Evin et al. (in press) who have made the case that if all petrous bones used for aDNA (and other biomolecular) studies over the last years had been CT-scanned before destruction, it would have been possible to perform invaluable comparative studies of hearing evolution and inner ear morphology alongside the DNA analyses.

Pálsdóttir et al. (2019) have recently brought the zooarchaeology community's attention to the importance of achieving reasoned destructive sampling strategies when performing analyses requesting destruction of bio-archaeological remains for, e.g. C14 dating, aDNA, palaeoproteomics, collagen fingerprinting or isotope analyses. Though Pálsdóttir et al. (2019) focus on animal remains, the same is true for plants with cereal grains, chaff, seeds, charcoal, and wood that can be submitted to the same variety of bioarchaeological analyses.

Many of the issues that are discussed within this volume are equally applicable to other categories of archaeological evidence, including soils (e.g. Anderson-Carpenter et al. 2011; Briggs 2020; Smith et al. 2015), plants (e.g. Brown et al. 2015; Kistler et al. 2018) and animals (e.g. Larson and Fuller 2014). In an attempt to balance the content of the volume, we now move to discuss aDNA in animal studies.

There are good reasons for doing so. First, it is widely accepted that the ways in which people perceive and treat animals are reflections of broader attitudes to human–human relationships (e.g. Mullin 1999). As such, many of the concerns raised in this volume such as those about studies of migration (Hakenbeck 2019), the reconstruction of phenotypes (Frieman and Hofmann 2019) and sampling protocols (Sirak and Sedig 2019) can be explored in a safer space, since animal-based data are less likely to be co-opted for political ends. Second, to ignore non-human animals is surprising given the animal-centric origins of the method of aDNA analysis noted below.

Non-human animals

As explained in this volume by Millar and Lambert (2019) and Sirak and Sedig (2019), the field of ancient DNA was born in 1984 with the publication of genetic sequences extracted from the skin of an extinct species of horse, the Quagga (*Equus quagga quagga*), that was curated in the Mainz natural history collection, Germany (Higuchi et al. 1984). Since then, DNA has been sequenced from numerous other extinct species such as the thylacine (Krajewski, Buckley, and Westerman 1997),

dodo (Shapiro et al. 2002) and mammoths (Poinar et al. 2006) whose remains are housed in museum collections around the world.

Though the fascination with, and attention to, extinct animals remain high, there is increasing recognition that collections of extant animals have potential to shed light on the dynamics of genetic change through time and space. Understanding how geographically diverse populations of a single species have been shaped by natural and anthropogenic forces over the last few centuries has important ramifications for modern conservation efforts in order to prevent additional extinctions.

Conservation policies purport to be purely scientific (the subtext being that decisions are therefore not culturally biased) but they are laden with stereotypical value judgements. The labels 'wild' and 'native' are equated with pristine and natural, and therefore perceived as inherently good. In stark opposition are the 'feral' and 'introduced' or, worse, the 'alien' and 'invasive', all presented in negative terms. It has not gone unnoticed that the language employed in biodiversity and wildlife management discourse is startlingly similar to that found in right-wing nationalistic rhetoric, both seemingly preoccupied with native versus alien status, and emphasizing the need for 'genetic purity' of populations. This similarity has generated heated debate and division within conservation biology, with those who wish to eradicate introduced species being labelled as xenophobic, whilst those opposing eradication are seen as promoting biological homogenization (e.g. Coates 2006; Frawley and McCalman 2014; Preston 2009; Skandrani, Lepetz, and Prévot-Julliard 2014; Shackelford et al. 2013; Warren 2007). However, much of this contention is based on modern DNA datasets, with little deep-time empirical evidence concerning the actual native/alien status of the species under consideration. Integrated archaeological and palaeogenomic studies have the potential to remedy this, and they are increasingly showing how little we know about modern biodiversity.

For instance, in Britain, the brown hare (*Lepus europaeus*) is widely considered both wild and native and, as such, is the subject of a variety of conservation efforts (e.g. Game and Wildlife Conservation Trust, Hare Preservation Trust). Yet archaeological studies have demonstrated that it is the mountain hare (*Lepus timidus*) that is native to (some) areas of Britain, whereas the brown hare is neither native nor truly wild. Combined zooarchaeological, morphological and aDNA analyses make clear that the brown hare was first introduced to the island around 2,500 years ago, was farmed for approximately 500 years during the Roman period and only subsequently escaped to form feral populations (Lauritsen et al. 2018). Similarly, the Przewalski horse (*Equus ferus przewalskii*) as its Latin name implies, has long been considered the wild progenitor of modern-day domestic horses. It is listed as Endangered on the International Union for the Conservation of Nature (IUCN) Red List with a detailed conservation plan in place that includes captive breeding programmes at many international zoos (King et al. 2015). However, recent genetic studies comparing modern and ancient DNA of global horse populations have revealed that, far from being a pristine wild population, the Przewalski horse is the feral descendant of an ancient domesticate (Gaunitz et al. 2018).

Do these findings render the conservation of the brown hare or Przewalski horse less urgent or important? The answer must surely be no, as both are important keystone species from a cultural perspective. In which case, it is perhaps time for us to re-think our values and consider if, rather than judging species based on modern genomic data that have been modelled according to perceived native/wild/feral/introduced status, they be considered on the basis of ecological function (as argued by Davis et al. 2011; Schlaepfer, Sax, and Olden 2011) and cultural significance (e.g. Fortwangler 2009, 2013; Sykes in press).

What these case-studies demonstrate is that, in the absence of the empirical aDNA data, it would be impossible to challenge the received wisdom within animal conservation. However, it is also clear

that, in the absence of the humanities' researchers (and indeed the humanities funding that supported both the brown hare and Przewalski horse studies), the fundamental questions would never have been asked.

These examples demonstrate the value of interdisciplinary collaboration but, as Collard et al. (2019) highlight here, such interdisciplinary studies often result in tensions which need to be mitigated. In fact, it is possible to minimize the emergence of disagreements, but this requires careful project design that emphasizes co-production and does not privilege any one form of analysis, scholarship or audience. There is a tendency for these kinds of projects to be funded by the humanities, such as the HERA-funded CitiGen project which has resulted in *The Ancient Genome Atlas* (www.ancientgenomes.com). CitiGen brought together academic and non-academic partners from the fields of DNA ancestry testing, family history research, and public engagement to facilitate dialogue between the humanities and the natural sciences over the uses of genomic data in the study of human population histories. But there are an increasing number of projects that are undertaking similar approaches focused on animal history, including the following example which is led by one of this volume's editors (N.S.).

The Easter Project

With funding from the Arts and Humanities Research Council, the Easter Project is exploring the origins of the Christian festival and the animals (rabbits, hares and chickens) associated with it (see Lauritsen et al. 2018). Beyond biocultural history, the project sets out to highlight the impact of shifting baseline syndrome (the phenomenon whereby people consider the socio-environmental circumstances of their childhood to be 'natural' and morally absolute) on human attitudes to cultural and biological 'aliens' – be they humans, animals or religious beliefs. In the absence of deeper historical and archaeological understanding, nostalgic ideals are frequently adopted blindly, and often erroneously, as the foundation for decision-making both at a personal level and more broadly in science and policy, as has been shown above in the case of animal conservation policy. The religion, traditions and animals of Easter are themselves the product of shifting baselines: although all 'alien' to Britain, they are viewed positively because they arrived in the long-forgotten past. Easter is therefore an excellent high-profile example to highlight the impact of shifting baselines and challenge negative attitudes to cultural and biological 'aliens'

To address such complex issues requires involvement of researchers from a variety of disciplines and backgrounds. Whilst the project is fundamentally a collaboration between zooarchaeologists, geneticist and linguists, it was recognized early that these three fields were inadequate to achieve the project's goals. As a result, from the inception of the project, a diverse range of stakeholders were consulted to co-create the questions and shape the direction of the research. This transdisciplinary team has met regularly, face-to-face, for extended periods and have conducted the research and dissemination collaboratively.

Figure 1 evidences this approach in relation to the work undertaken at Fishbourne Roman Palace, Sussex. This Roman period collection was targeted because it was known to contain large numbers of brown hare bones that the project sought to sample for zooarchaeological, genetic and isotope analysis as well as radiocarbon dating. The whole team visited the Palace to learn more from the curator, Dr Rob Symmons, about the challenges he faces, and receive guidance on best practice in terms of archive analysis and data deposition. The diverse team received basic training in zooarchaeological identification and worked under supervision to extract hare bones from the collection (Figure 1(a)). During this process, one of the professional zooarchaeologists



Figure 1. Co-production of research at Fishbourne Roman Palace, Sussex. (a) Transdisciplinary team composed of archaeologists, geneticists, morphologists, linguists, heritage managers, museum curators and creative writers receive introductory zooarchaeological training so they might work in the museum archives to extract brown hare bone fragments for full-suite analysis. (b) Unexpected identification of a rabbit bone fragment by Fay Worley, Historic England – left is a reference hare tibia, central the archaeological rabbit bone fragment, right a reference rabbit tibia. (c) 3-D modelling and reconstruction of the rabbit bone fragment prior to destructive sampling. (d) Adrian Bott, author of the Roman rabbit story (illustrated by Judith Dobie, Historic England). (e) Geneticists, Joel Alves and Greger Larson, playing an active role in the 2018 *Being Human Festival*, a national festival of the humanities.

identified a possible Roman rabbit bone (Figure 1(b)) that was later confirmed by genetic analysis and radiocarbon dating. Aware that obtaining proof of the rabbit's status would require destructive analysis of a unique specimen, the bone was 3-D scanned in advance of any destruction (Figure 1(c)). This is now the Easter Project's standard policy (see Evin et al. *in press*). A 3D print of the bone is now on display at Fishbourne museum and the Roman rabbit was central to the museum's and broader project's 2018–2019 public engagement programme. Critically, all team members were involved in the public engagement – from the project's author, Adrian Bott, who is writing a novel inspired by the Easter Project's research (Figure 1(d)) to the geneticists (Figure 1(e)) who have been active participants in various humanities' festivals, such as Britain's national Being Human Festival.

This close collaboration at every stage of the project helped to generate a culture of knowledge exchange that has opened up new avenues for investigation. For instance, the geneticists on the Easter E.g. Project have traditionally focussed on issues of animal domestication with an emphasis on the 'main event', that which accompanied the transition to farming in the Neolithic (e.g. Dobney

and Larson 2006; Larson et al. 2005, 2007; MacHugh, Larson, and Orlando 2017). This is despite their acceptance that aDNA analysis is, in isolation, a poor tool for examining what is, in effect, a change in human-animal relationships. They are now coming to realize that undertaking genetic analysis of Historic period material may offer more opportunities to test aDNA models of domestication by integrating the data not only with zooarchaeological studies of morphology but also evidence from historical texts and artistic representations. The power of such multi-proxy approaches has been highlighted by Irving-Pease et al.'s (2018) study of rabbit domestication, which showed a complete lack on consilience between genetic, zooarchaeological and historical strands of evidence, demonstrating that no single discipline holds the key to knowledge.

In another example of Historic period aDNA research, consilience was the order of the day. Loog et al. (2017) brought together zooarchaeological, historical and genetic data to show that, for chickens, the thyroid-stimulating hormone receptor (*TSHR*) came under selective pressure in Europe ~1,000 AD, coincident with a shift towards intensive chicken keeping observed within both the zooarchaeological and documentary records. This is all the more important as *TSHR* has been proposed as an early-stage 'domestication gene' (Flink et al. 2014). In this case, the genetic data were highly valuable for demonstrating the timing of the selective pressure but the drivers of that pressure (increased consumption of chickens and eggs as acceptable 'fast-day' foods, instigated by high-status Christians following the Benedictine reform of the late tenth century AD) could not have been determined without wider collaboration (Loog et al. 2017).

Other fascinating studies showing coincidence in artistic and scientific dataset include Wutke et al.'s (2016) study of horse coat colour, which indicate shifts towards chestnut-coloured horses in both the genetic and art historical records of medieval Europe. It is this kind of integrated approach that the Easter Project will adopt as the genetic data for hares, rabbits and chickens begin to emerge.

The prospect of integrating the aDNA datasets with the broader evidence collated by the project is exciting but it can already be predicted that tensions in this to-date harmonious project will begin to arise around issues of authorship and publication strategy.

Publications

Another running theme throughout this volume is publication and, in particular, concern over whose voices are loudest. Broadly speaking, the accusation levelled at geneticists is that they care more about getting articles into *Nature* and *Science* as quickly as possible (and before competing teams) than they do about ethical treatment of material or being mindful of how their narratives may be received politically. One defence presented in several of the papers within this volume is that geneticists are 'compelled' to publish in high-profile scientific journals, even though it is accepted that such journals lack the space or inclination to present the arguably more sophisticated narratives that are more familiar within the humanities (see Booth 2019 and Spriggs and Reich 2020, this volume).

A question that arises from this observation is: who is ultimately 'compelling' this publication strategy? As Frieman and Hofmann (2019) query in this volume, surely the drivers are the directors of laboratories and projects for whom it would be possible simply to change strategy? The issue here is that the majority of high-profile lab directors have been the beneficiaries of publishing in prestigious journals. For pioneers and early adopters of aDNA analysis, careers have been made with some of the most influential figures in the field emerging as celebrity scientists (see Jones 2017). These senior scientists now have a duty of care to help junior scientists achieve a similar level of success, most easily achieved through emulation. Given that study after study have shown the career benefits of publishing in high-impact journals (Symonds 2004; Laurance et al. 2013), it would be a

difficult (and even hypocritical) move for a lab director to encourage junior colleagues to follow a path that is less likely to lead to success. This does not mean that the system is not in need of change; even the editor-in-chief of *Proceedings of the National Academy of Sciences (PNAS)* is wrestling with the situation (Berenbaum 2019). In her editorial, Berenbaum highlighted that there are moves by funding agencies, institutions, publishers and individual researchers to sign up to the San Francisco Declaration of Research Assessment (DORA <https://sfdora.org/>). DORA is attempting to change the publication culture by encouraging hiring and promotion policies to be based on the intrinsic merit of the work, not the title of the journal or its impact factor. Although this culture change is unlikely to be quick, it is a step in the right direction.

This issue of *World Archaeology* is an opportunity to reflect and think about what the future of publication might look like. As editors, we found this volume particularly hard work. The initial call for papers resulted in several offers from archaeologists but the response from our geneticist colleagues was decidedly lukewarm. The reason for this is not difficult to ascertain: it is that *World Archaeology* is below the significance threshold for the majority of aDNA researchers. It is, therefore, with great appreciation that we acknowledge those geneticists who did offer thoughtful contributions which have enriched the discussion in these pages. But there is perhaps more that we can do. To return to the suggestions of Frieman and Hofmann (2019), the directors of labs and research projects do have the option of changing their publication and hiring strategies. In response to their suggestions, one of us (N.S.) is changing the policy of her lab and the research projects that she directs. Sykes's projects are overwhelmingly supported by humanities and social sciences funders, and yet the best of the research tends to be sent to higher impact scientific journals, the argument being that humanities journals are less well regarded. However, humanities journals are not going to improve in prestige if the research that is funded, often by Humanities Councils, is sent elsewhere. At a time when governments around the world are cutting humanities funding in favour of STEM subjects (Belfiore 2015; Costa 2019), there is a pressing need to demonstrate – not just claim – the importance of our disciplines. Publishing our highest-quality papers in humanities-oriented journals, backed up by well-thought-out press releases, is one way to achieve this.

Conclusion

Ancient DNA analysis has undoubtedly been revolutionary within archaeology, as part of a general scientific 'turn' within the discipline. Questions that could never have been asked even a decade ago are now being answered, bringing extraordinary insights about past societies, cultural change, population movements and their associated impacts on the environment. Such information is of direct relevance to the present, be it in terms of challenging received wisdom concerning concepts of 'native' or 'alien' species (plant, animal or human) or overturning naïve migration narratives that are becoming endemic with the rise of nationalistic politics. In this way, culturally informed aDNA analysis has the potential to showcase the importance of humanities-led research, at precisely the point that the humanities are being eroded internationally (a phenomenon itself seemingly correlated with a widespread political shift to the right).

To achieve this, there is a need to reconsider the way in which aDNA data are conceptualized, collected, interpreted and the data reported (academically and to broader multiple publics). As Jones (2017) has argued, while high-profile publications and associated media helped give rise to the field of aDNA, they are now having a destabilizing effect. Especially as aDNA results (particularly those concerning human populations) are co-opted at both ends of the political spectrum, as in the case of pro- and anti-Brexit campaigners (Booth 2019; Frieman and Hofmann 2019; Hakenbeck 2019).

Fortunately, it is very clear from this volume that the necessary changes are already happening, the different authors essentially charting the progress of the relationship between archaeologists and geneticists in the way outlined by Millar and Lambert (2019).

For instance, Spriggs and Reich's paper reflects on the some of the problems and benefits they encountered as researchers from two distinct disciplines set out initially to answer their own discrete questions, albeit in collaboration. They then took the next step towards a more transdisciplinary approach. Collard et al.'s (2019) paper describes just such a project where questions were co-created from the start and answered with multiple lines of evidence, even if not without some interdisciplinary tension. Booth (2019) provides a perspective from a new generation of researchers, who have been trained as archaeologists but now work closely alongside geneticists, selecting appropriate samples for analysis. Perhaps the best and most positive insight into the future of archaeological genetics is provided by Charlton, Booth, and Barnes (2019). The first author of this paper began her career as archaeologist but is now working as a full-fledged and well-regarded palaeogeneticist in her own right. Charlton, Booth, and Barnes (2019) reflective and critical perspective on current approaches to petrous bone analysis highlights the folly of embarking upon 'scientific' aDNA analysis without understanding the cultural drivers responsible for the formation of the archaeological record.

If Charlton, Booth, and Barnes (2019) can be seen as an example of the next generation of aDNA research, many of the concerns raised by Frieman and Hofmann (2019), Hakenbeck (2019) and Sirak and Sedig (2019) can be alleviated because the next generation of aDNA researchers will be archaeologists, not population geneticists or evolutionary biologists. As archaeologists, we might envisage a future where all aDNA researchers are fully aware not only of the cultural contexts of their investigations, the responsibility they have over the narratives they write but also the samples they use to write them.

Ancient remains are cultural and biological heritage (and not always the heritage of those storing the remains – see Collard et al. 2019; Sirak and Sedig 2019). As such, they have to be managed with great care and deep respect. Isolating DNA from archaeological or natural history specimens is a destructive process and it must be remembered that whilst collections may be tremendous stores of genomic information, they are also finite resources. Every sampling exercise diminishes the future potential to reveal novel information. While modern DNA and other biomolecular techniques require increasingly smaller quantities of skin or bone or hair to generate robust results, they still cause irrevocable damage – be it from the act of sampling or simply from the handling of specimens.

If we ensure that specimens are well-recorded (ideally as 3D models) prior to destruction, or better still not sampled at all until a robust case for destructive analysis has been made in consultation with appropriate archaeologists and curators, there is every potential that new insights from key material will continue to be obtained for generations to come.

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