COMMENT

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An archaeologist works on the osteological collection at the Anthropology National Museum in Mexico City.

Use ancient remains more wisely

Researchers rushing to apply powerful sequencing techniques to ancient-human remains must think harder about safeguarding, urge **Keolu Fox** and **John Hawks**.

The study of ancient-human populations and our now-extinct close relatives has thrived over the past decade, as genetic material is examined with cheaper and more sophisticated sequencing technologies. Only nine years ago, the partial sequencing of a Neanderthal genome was a major scientific achievement[1]. Today, researchers are pursuing what many have termed a factory-like approach to analysing ancient DNA[2], with the processing of hundreds of samples.

As a result, we have a much better understanding of (among other things) which human populations interbred with Neanderthals, and which didn't[3]; how people dispersed across Europe during the Bronze Age[4]; and how pastoralism developed in Africa[5].

But such progress comes at a price.

Extracting the best-quality DNA from ancient remains requires the partial destruction of those specimens. And once bones, teeth, hair and so on are ground ▶

into dust, future opportunities for using them to understand our past are lost.

We recognize the enormous potential of ancient DNA to help reveal human history. In fact, as long as interested parties give their consent, we are hoping to apply genomics to the remains of Hawaiian men and women who lived hundreds to thousands of years ago. (Our aim is to understand how the introduction of leprosy, smallpox, syphilis and other diseases from European colonialists in the eighteenth century have shaped the genomes of Native Hawaiians today.) We also recognize that some leading labs are taking steps to reduce the destructiveness of sampling, for instance by developing techniques that allow ancient-DNA sequences and radiocarbon dates to be obtained from the same sample instead of from multiple ones[6].

Yet we are becoming increasingly concerned. To our knowledge, no one currently has a full list of all the samples from ancient humans and closely related species examined so far (meaning samples ranging from hundreds to tens of thousands of years old). No one is tracking the success rate of data recovery across laboratories and samples. And no one knows how many specimens are left.

With such a rapid scale up in analytical capacity, the diverse stakeholders involved (archaeologists, molecular biologists and bioinformaticians; editors and journalists; museum curators; and the descendants of the populations being studied) must talk. They need to establish how to balance discovery now with the need to safeguard cultural remains in the long term.

Unless some ground rules are established, future scientists, armed with better, potentially less-invasive methods for extracting DNA from ancient samples[7] could well look back on this era as a time of heedless destruction, fuelled by the relentless pressure to publish — or what one anthropologist has described as an "impetuous anxiety for discovery"[8].

HOW BAD IS IT?

Over the past ten years, there have been tremendous successes in education and engagement efforts that aim to bring a broader range of people (including those with interests and responsibilities as descendants of particular ancient communities) into consultations about genetic research. For instance, since 2011, a growing consortium of genomicists, now in North America, Hawaii, Finland, New Zealand and Australia, have helped to guide summer training programmes for Indigenous people. These educate students about the potential uses and misuses of genomics, including ancient genomics, as well as how to sequence DNA.

Yet irrevocable decisions continue to be made about the sampling of ancient specimens, guided by the immediate research interests of a few.

As an example, many researchers focus their sampling effort on the petrous bone, the hard portion of the temporal bone at the base of the skull, which houses the intricate structures of the inner ear. This dense bone contains a high concentration of endogenous DNA.

Last year, a team looking at the morphology of the inner ear noted that researchers were breaking open bony labyrinths and drilling into hundreds of petrous bones for DNA without first taking photographs, or using scanning techniques such as micro computed tomography (microCT) to make morphological records[9].

Petrous bone could contain uniquely high concentrations of other potentially informative biomolecules, such as protein or lipid biomarkers[10]. Also, because it contains the structures of the inner ear, including the semicircular canals and cochlea, intact bone could reveal insights about an individual's balance or hearing.

> ***"Genomic research on ancient-human populations could hit a ceiling within decades."***

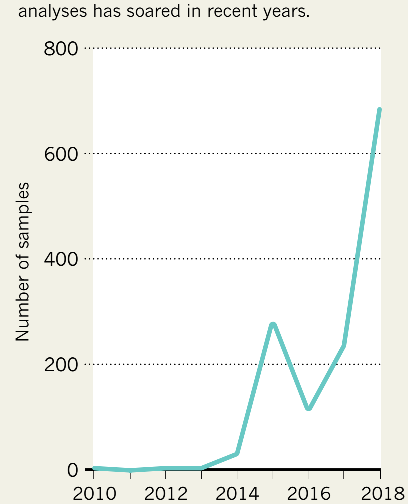
Some laboratories have used microCT scanning, both to preserve data from petrous bone, and to guide their drilling to minimize destruction of the specimen[11]. Unfortunately, such methods have not been adopted as a standard, partly because individual groups tend to focus on their own research agenda rather than on the bigger picture.

Destruction of fragments of ancient bones or teeth is key to many techniques used in palaeoanthropology — including ancient proteomics, radiocarbon analysis, electron-spin resonance dating, stable-isotope sampling, dental-calculus sampling to assess what food people ate, and the sectioning of teeth for studies of growth. But so far, investigators and commentators have begun to routinely apply the terms 'DNA factory' or 'industrial-scale' only to ancient genomics (whether in publications, at conferences or on social media).

Most of these other techniques are applied to tens of samples in any one study, occasionally to a single sample. Ancient genomics stands apart because the decreased cost of sequencing and the rapid acceleration of technologies have enabled some laboratories to pursue projects involving hundreds of samples. The publication of such large-scale studies has put pressure on others to use similarly impressive sample sizes. What's more, analysing the movement and evolution of ancient populations requires researchers to compare the genome of any one sample with those of as many of the individual's ancient contemporaries as possible. Thus, studies involving bigger sample sizes provide more reference data for other investigators to draw on, creating a feedback loop.

BONE BONANZA

The number of ancient samples used in DNA analyses has soared in recent years.



SOURCES: E CALLAWAY NATURE 555, 573–576 (2018); DAVID REICH

RETHINK PERSPECTIVE

In our view, two changes need to be implemented in ancient genomics research.

Give diverse stakeholders a say. Currently, a patchwork of regulations and institutions determines whether destructive research on ancient human remains can proceed. In some jurisdictions, Indigenous communities are formally involved in decision-making for research that involves the bones of their ancestors. In others, the decision could rest in the hands of a single curator.

But on its current trajectory (see 'Bone bonanza'), genomic research on ancient-human populations, or on close extinct relatives, could hit a ceiling within decades because of the scarcity of ancient remains. It is therefore urgent that, rather than sequencing an ancient genome in the hope that something interesting will emerge, researchers state up front what question they are seeking to answer — and that people with diverse perspectives evaluate their goals. Because human remains have intrinsic value and a role in the beliefs and cultures of many peoples of the world, as well as scientific value, decisions about whether or how to use them for research should be governed by a broad group, from researchers to the descendants of the populations being studied. For instance, if only three samples of a given ancient human population exist in the world, how many is it reasonable to destroy to answer a specific question about human migration?

JAMES KING-HOLMES/SPL

The petrous part of the temporal bone is used for radiocarbon dating.

This 'question-led' approach would enable people to consider the trade-off between collecting ancient DNA data today and waiting for future sequencing methods, which could potentially yield more information less expensively and less destructively[7]. (Sequencing DNA from ancient samples was much more hit and miss before the emergence in the mid- to late 2000s of targeted-capture next-generation sequencing, which enables researchers to separate endogenous from contaminant DNA, and then amplify it.) Also, greater engagement from more diverse stakeholders on how to handle scarce ancient remains as new technologies emerge will inspire conversations that bridge disciplines, lead to more accurate models and hypotheses and help form lasting partnerships. In our view, such an approach is crucial for fostering trust in a field in which, historically, the decisions of archaeologists and geneticists have led to deep distrust in many communities[12].

Create accountability. Just as timber and minerals are meticulously tracked at truck weighing stations and other venues to discourage the illegal acquisition of resources, curators, researchers and others must openly document the passage of ancient remains from one institution to another — and everything that happens to those remains along the way. With such a record, all ancient remains would be audited and people would know which specimens were ground into dust, but did not generate useful data, and which efforts generated data but did not result in a publication, and so on[13].

In the United States, the National Science Foundation (NSF) could take the lead on establishing such a database. Or grass-roots initiatives at museums, such as the Smithsonian Museum of Natural History in Washington DC or the Bernice Pauahi Bishop Museum in Honolulu, Hawaii, could help to shift practice. Buy-in from the research community could easily be obtained if referees and grantors required declaration of all sampling information. Importantly, such a decentralized approach would help to ensure that knowledge about ancient samples is not limited to a few groups[13].

WASTED RESOURCES

Many of the great archaeological sites of prehistory are now empty thanks to early archaeologists — sometimes little more than treasure-hunters — commanding armies of unskilled workers to scoop up the contents of caves, tombs and burial grounds. When so little was known, the bar was low; any discovery was interesting, and little or nothing was left for future generations. In fact, even as late as the 1990s, large sections of ancient human skeletons were destroyed for radiocarbon and other analyses that can now be accomplished using much smaller portions of bone.

Rather than repeat the mistakes of the past, future generations of scientists — from all countries of the world and from all sectors of society — must be given the opportunity to interpret our shared history. ■

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