

# Conservation archaeogenomics: ancient DNA and biodiversity in the Anthropocene

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**There is growing consensus that we have entered the Anthropocene, a geologic epoch characterized by human domination of the ecosystems of the Earth. With the future uncertain, we are faced with understanding how global biodiversity will respond to anthropogenic perturbations. The archaeological record provides perspective on human–environment relations through time and across space. Ancient DNA (aDNA) analyses of plant and animal remains from archaeological sites are particularly useful for understanding past human–environment interactions, which can help guide conservation decisions during the environmental changes of the Anthropocene. Here, we define the emerging field of conservation archaeogenomics, which integrates archaeological and genomic data to generate baselines or benchmarks for scientists, managers, and policy-makers by evaluating climatic and human impacts on past, present, and future biodiversity.**

## Ancient DNA, archaeology, and the Anthropocene

Throughout much of our history, humans have altered the biosphere, impacting plants, animals, and ecosystems through a variety of activities, and producing an archaeological record of human interactions with the natural world [1,2]. Although major anthropogenic impacts on biodiversity are linked to industrialization and the modern period, ancient peoples also interacted with, and influenced, the environment. Modern ecosystems are products of this deep history, and long-term perspectives on their evolution both with and without humans can provide important information on their capacity to withstand perturbations [3–5]. The pace and scale of modern anthropogenic environmental impacts and growing recognition of the importance of investigating ancient human–environmental interactions

have an important role in the Anthropocene debate (see [Glossary](#)), which centers around whether we have entered a new geologic epoch characterized by human domination of Earth's ecosystems [6–9]. While researchers debate if and when the Anthropocene began, one thing that is clear is that we need new data sets and approaches to help us understand and transcend the major environmental challenges of our time, including climate change, loss of biodiversity through extinction, emerging infectious diseases, and a host of other issues.

Here, we focus on one of these new approaches, which we call ‘conservation archaeogenomics’, or the genomic analysis of the archaeological remains of plants, animals, soils, and other materials to enhance present-day biological conservation and management. Archaeological sites contain evidence of important environmental and cultural changes that span millennia or more, and archaeological data sets can contribute much to conservation biology and management by allowing researchers to reconstruct past environments and the place of humans within those

## Glossary

**Ancient DNA (aDNA):** DNA extracted from nonliving sources, including teeth, bones, toe pads, desiccated tissue, seeds, plant remains, and paleofeces.

**Anthropocene:** the proposed recent geological epoch during which humans have dominated the earth's landscape.

**Archaeogenomics:** utilizing materials from archaeological sites to generate genomic information.

**Archaeology:** study of the human past using material remains.

**Environmental DNA (eDNA):** DNA obtained from environmental samples, including soil or water.

**Historical ecology:** the interdisciplinary study of ecosystem dynamics using historic and prehistoric data sets, often used to inform conservation.

**Metagenomics:** genomic analysis of DNA samples from mixed sources.

**Midden:** ancient trash deposits, often containing shells, bones, and plant materials.

**Paleofeces:** ancient feces from humans or animals. This differs from coprolites, which are fossilized feces.

**Paleogenomics:** the study of past genomes using aDNA methods.

**Provenience:** location of an object within a site and in relation to other artifacts and ecofacts.

**Shifting baselines:** the concept that what we view as natural changes through time.

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ecosystems, assess historical ecological variability, and identify past and present cultural practices impacting biodiversity [1–5]. Building on recent syntheses of the value of aDNA studies for directly addressing a variety of fundamental questions in ecology and evolution [10–13], we focus specifically on the power of aDNA data from archaeological materials to improve biological conservation and chart a course for future research on the topic.

Genomic approaches have become a promising tool for conservation practice, because using genome-wide data can offer a dramatic increase in the number of genetic markers that can be used to improve the precision of estimating adaptive and neutral diversity, and demographic parameters of relevance. This, in turn, results in better wildlife management recommendations, including the preservation of genetic diversity, identification of populations with unique evolutionary history and potential, and the mitigation of the effects of small population sizes on viability [14,15]. While there are challenges in undertaking effective conservation genomics projects [15], genomic analysis of archaeological samples (archaeogenomics) can extend patterns deep into the past and, along with complementary paleogenomic data from fossil and subfossil samples [12,16,17], can provide key information on long-term ecosystem responses to disease, human activities, and climate change [10,11,13,18–20]. Here, we focus on the following question: how can genomic analysis of archaeological materials enhance the conservation, management, and restoration of present-day (and future) biodiversity? To evaluate this question, we focus on five interrelated issues of broad significance: population and distribution changes, translocations, extinction, disease ecology, and environmental reconstruction.

### Conservation archaeogenomics: a transdisciplinary approach

While there is an abundance of new terminology associated with the ‘omics’ era, we treat archaeogenomics and paleogenomics as complementary (but distinct) approaches and much of our synthesis highlights the interrelationship between the two. Paleogenomics was first described as the study of ancestral regions of the genome and ancestral-state genome reconstruction using comparative approaches in extant taxa [21,22], but the field now also encompasses the reconstruction of past genomes through aDNA methods [12,16]. Archaeogenomics differs from paleogenomics because of the general cultural context of the archaeological samples being studied, which often provides a direct linkage to human–environmental interactions in a broad sense and can provide samples that may be rare or nonexistent in paleontological sites (Figure 1). Both archaeogenomics and paleogenomics have been transformed by recent advances in aDNA methods and high-throughput DNA sequencing (HTS) technology, expanding the types of question that can be addressed (Box 1). The case studies presented here reflect the infancy of the field of conservation archaeogenomics because most studies published to-date have focused on short mitochondrial DNA fragments (mtDNA) or a few nuclear markers. However, genome-level analyses are quickly becoming standard and we seek to demonstrate the value and future

### Box 1. Archaeogenomics methods: old and new

Similar to genomics, aDNA has changed rapidly with the advent of HTS technology. Due to the existence of relatively few samples and limitations on destructive analyses, early aDNA studies focused on evolutionary relationships and bottleneck detection, and utilized PCR to amplify short mitochondrial fragments or a few nuclear markers and Sanger sequencing methods [83]. However, with HTS technology, it is now possible to study ancient population dynamics and landscape genetics [11,19]. There are now many different ways of collecting genomic data from fresh tissues, including RAD, exome, intron and whole-genome sequencing, and SNP capture. However, when comparing modern and archaeological data, genomic markers must be selected for not only their informativeness and resolution power, but also their successful applicability to degraded samples. While mtDNA has been the marker of choice in aDNA studies due to its ease of recovery in old and degraded samples, high variability, matrilineal inheritance, and haplidity [84,85], SNPs offer higher power to detect bottlenecks, especially those with fast recoveries [32]. However, there is also a greater potential for ascertainment bias, especially when SNP arrays are designed from subsets of modern genetic diversity [86]. The feasibility of a particular project will depend on the goals, scale (i.e., number of taxa and samples), and budget. Furthermore, these new genomic approaches are best used in concert with other data that can improve the context and chronology of a particular sample and be guided by specific procedures and analysis of morphology, proteomics, accelerator mass spectrometry (AMS) radiocarbon dating, isotopes, and other techniques (Figure 2, main text). Together, these data sets can be integrated to explore human impacts on biodiversity and to inform conservation and management for the future.

impact that archaeogenomic research will have on conservation practice and policy.

Conservation biologists and managers rely on baseline data when evaluating potential actions for species management and preservation, and conservation archaeogenomics has a unique role in these reconstructions (Box 2). Conservation archaeogenomics involves collaboration between archaeologists, with intimate knowledge of local and regional sites, cultural histories, and faunal data sets (and their limitations); genomicists, with the capacity to execute methodological and analytic techniques; managers, who make policy and management decisions; and other relevant scientists. These teams can address the multiplying threats facing biodiversity by integrating novel technologies with unique data sets, including archaeological data (Figure 2), to study the evolution of ecosystems through space and time and evaluate their capacity to withstand human perturbations.

Archaeological sites provide subsamples of past environments, as ancient peoples interacted with, and used, the resources that were available to them. Past peoples intentionally created a record of their activities (by building structures, writing histories, and burying human and animal remains and associated artifacts) and unintentionally deposited materials as waste (including shellfish, bones, broken tools, plant remains, stone, and pottery into middens). Although selecting sites and materials associated with human activities for genomic analysis may seem limiting because it does not allow the survey of an entire ecosystem, it has the ability to provide a powerful perspective for understanding the cultural context of human–ecosystem interactions. Archaeological contexts can provide materials from sites that are tens of thousands or more years old all the way up to the past 50 years or so.

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