Destructive sampling natural science collections: An overview for museum professionals and researchers

Jan Freedman[1]*, Lucy van Dorp[2], and Selina Brace[3]

[1]*Plymouth City Museum and Art Gallery, Drake Circus, Plymouth, PL4 8AJ*

[2]*University College London Genetics Institute (UGI), Department of Genetics, Environment and Evolution, Darwin Building, Gower Street, London, WC1E 6BT*

[3]*Department of Earth Sciences, Natural History Museum, London, SW7 5BD*

**Corresponding author: jan.freedman@plymouth.gov.uk*

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Abstract

There are many reasons why museum collections may be used for destructive sampling, from DNA and isotope analysis to radiocarbon dating. The process is invasive and destroys a part, or all, of the specimen. This can result in reluctance by museum staff to allow specimens to be used in particular types of scientific research. We will present some of the motivations on both sides, but argue that the benefits of destructive sampling can outweigh the risks. Many analytical methods have improved dramatically in the last 30 years, requiring smaller sample sizes. With a focus on destructive sampling for genetic analysis, we will also present some examples from the literature where DNA from museum and archaeological specimens has greatly aided the reconstruction of a species' evolutionary history as well as enriching our understanding of the object sampled. In addition, we highlight the need for museum staff to understand exactly what researchers are asking for, and for researchers in turn to understand museum procedures. We include an example of a Destructive Sampling Policy and a Destructive Sampling Request Form, for institutions to adapt for their own use.

Keywords: DNA; Radiocarbon Dating; Destructive Sampling Policy; Destructive Sampling Request Form

Introduction

Museum natural science collections hold a wealth of information. From recording and portraying the incredible biodiversity of life on the planet to the historical distribution of local species, there is an enormous amount of knowledge to be gained. In addition, collections comprise an invaluable resource of hidden data that is often unexplored but that can be used for research purposes. This includes not only external data (such as morphometric information) but also information from within the specimen: DNA, proteins, radiocarbon, chemical isotopes, and mineral chemistry. Much of this information can only be unlocked by taking an invasive sample from the

specimen. This is known as 'destructive sampling', whereby a part or the whole of a specimen is destroyed to provide information. Museum professionals are keen for their collections to be used for research, but a misunderstanding of the full requirements of researchers and the impact on their collections can result in missed opportunities.

For the museum professional, there may be several concerns regarding destructive sampling. Much of the readily available literature relating to destructive sampling focuses on sampling for DNA extraction. Within this literature, the discussion is dominated by instructions on how to care for specimens to limit degradation. For example, one chapter in the *Care and Conservation of Natural History Collections* (Carter and Walker, 1999) is dedicated to 'Genetic Material' (Brown, 1999), yet this focuses solely on the preservation of DNA in a variety of specimens. Spooner and Russ (2014) also provide a whole chapter on 'Curating DNA Specimens', outlining useful information for the museum professional regarding the fragility of historic specimens and the importance of destructive sampling today. Although useful for collections care to enable future research, neither of these examples provide clear guidance for evaluating destructive sampling requests. Other publications outline more detailed methodologies for sampling specimens. For example, Junqueira et al. (2002) describe the removal and destruction of the wings of flies after washing museum specimens in distilled water. de Moraes-Barros and Morgante (2007) also describe destructive sampling of the skins of three-toed sloths (*Bradypus variegatus* Schinz, 1825 and *Bradypus tridactylus* Linnaeus, 1758), successfully extracting DNA from small, dried fragments (1.5cm x 0.3cm) (de Moraes-Barros and Morgante, 2007). It is also possible, in some cases, to sample museum osteological collections without externally damaging the specimens: Wisely et al. (2004) extracted small samples of bone (10-20mg) from inside the nasal cavity of 72 specimens of black-footed ferret (*Mustela nigripes* (Audobon & Bachman, 1851)). They achieved a high success rate of DNA sampling, whilst minimising visible damage to the specimens. These few examples illustrate different methods used to sample specimens, but also highlight that methods vary based on the specimen, research question, and researcher. Whilst it is helpful to know how specimens are sampled, there is still a lack of practical guidance that the museum professional may turn to when faced with destructive sampling requests.

Along with a lack of accessible, clear, published guidelines for museum professionals, there are other reasons why there may be apprehension about destructive sampling. A museum's main role is to preserve collections, not destroy them. It can sometimes be difficult for the museum professional to know how to assess requests for destructive sampling as it may not be clear exactly what the researcher is requesting or why. Often, research requests are written using detailed, highly specialist language, which can make them difficult for museum professionals with expertise in different areas to understand, let alone evaluate. Furthermore, for very rare or precious specimens, curators may receive requests from multiple research groups with similar objectives. At this point, it can be exceedingly difficult to select a proposal based on merit. Finally, requests may be treated with caution, especially if the museum holds specimens that have undergone previous sampling that has resulted in damage that may appear extreme by today's standards (Figures 1 and 2).

Figure 1: Incomplete femur of a human, Homo sapiens Linnaeus, 1758, from Bob's Cave, Kitley Estate (PCMAG:KBC162). Five large holes were drilled into the specimen for accelerated mass spectrometry (AMS) in the 1990s. Analysis dated this bone to approximately 5,035 years before present (Chamberlain, 1996). Image: Plymouth Museums, Galleries and Archives.

From the perspective of a researcher, museum and archival samples are an incredibly valuable resource for the study of diverse biological processes. Researchers often lack the opportunity to collect fresh material and rarely have access to distant species, both spatially and temporally. Museum specimens provide an exception, and natural science collections can often provide good insights into ecological and evolutionary change over time (Tin et al., 2014). Considering sampling for genetic information, many objects in museum collections retain DNA, primarily natural science specimens, but also material in archaeological, ethnographic, and even library collections (Fiddyment et al., 2015). Exploiting this genetic information can provide unusual insights into an object that would not be possible without destructive sampling.

The sometimes-differing objectives of museum professionals and researchers, coupled with the speed of technological advances, highlights that a framework for supporting meaningful dialogue between both is necessary. Even where research is actively part of a museum's agenda, it may sometimes be challenging for researchers to effectively convey the implications and aims behind their proposal to museum staff, highlighting a need for better communication. Additionally, researchers are often unaware of museum procedures or what collections are available to them. Coupled with this, the role of a museum is to preserve the long-term value of their collections (Wisely et al., 2004). As research improves, and in particularly the invasiveness of destructive sampling procedures changes, a legitimate concern for museum professionals is whether to allow sampling with existing technologies rather than to wait for the development of less destructive approaches. As a result, even the most active of collaborations can be challenged by the need to address the requirements of researcher and museum professional in parallel.

We suggest there is a strong need for (1) a better understanding of how specimens are sampled and the importance of museum collections in research, (2) clearer communication between researchers and museum professionals, and (3) good practice methods for submitting and handling destructive sampling requests.

The research process and aDNA

One way to support clear communication is through an understanding of the research process. As an example, it is important for all parties to acknowledge that one of the risks of destructive sampling is that it might cause damage to the specimen but produce no informative results.

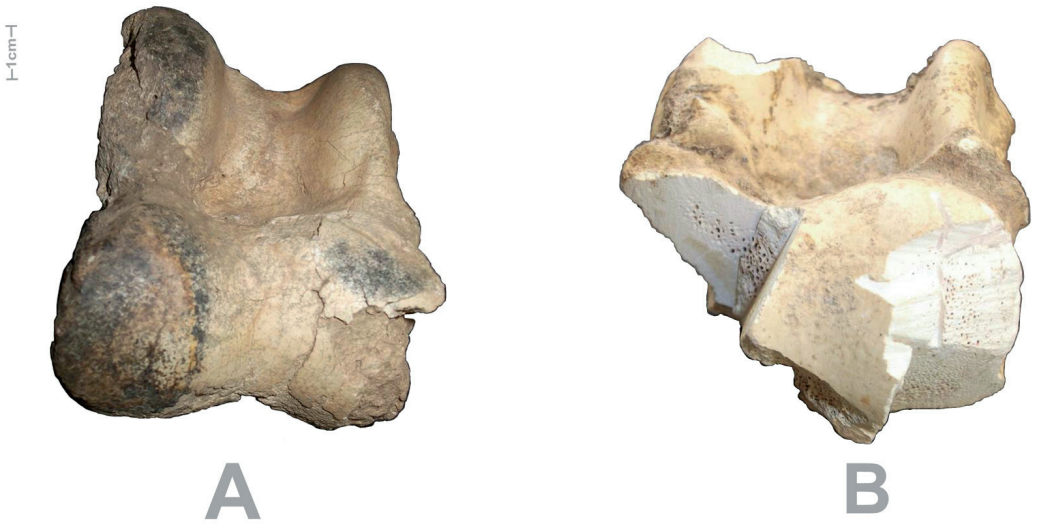

Figure 2: (A) A complete astragalus of an Aurochs, Bos primigenius (Bojanus, 1827) (PCMAG: KBC53) compared to (B) an Aurochs astragalus (PCMAG:KBC54) sampled for radio-carbon dating, both from Bob's Cave, Kitley Estate, Devon. Specimen B originally had cut marks on it showing evidence of human butchery however destructive sampling severely damaged the specimen. It was radiocarbon dated to 12,000 years old (Bailey et al., 1996). Image: Plymouth Museums, Galleries and Archives.

This is particularly pertinent for genetic analyses. DNA extracted from museum specimens is classified as ancient DNA (aDNA). aDNA research refers to the process of sampling, extracting, sequencing, and analysing the DNA from a biological, post-mortem sample, where the sample was not specifically preserved for DNA analyses. It is important to note, therefore, that the term 'ancient' does not specifically refer to the age of the DNA; the specimen can have died tens, hundreds, or hundreds of thousands of years ago. If the specimen was not immediately sampled or appropriately stored after death, the DNA will begin to fragment and decompose. This damage makes museum aDNA extremely difficult to work with, and aDNA research requires a dedicated laboratory, specialized protocols, and bioinformatics workflow. The number of bases of aDNA sequenced, for example, is typically extremely short and fragmented across the genome, and this makes them difficult to piece back together or align. In addition, post-mortem damage can alter the base sequence through deamination (the loss of an amino group), a common substitution being a cytosine (C) base erroneously read as thymine (T).

What is more, the dynamics of DNA degradation and the relationship between DNA fragmentation, time, and environment are not fully understood. Martínková and Searle (2006) explored the impact of the age of specimens and different storage conditions on the amount of genetic information obtained from museum specimens of stoats (*Mustela erminea* Linnaeus, 1758). They considered the success of DNA amplification through polymerase chain reaction (PCR) in stoats sampled across 18 museums in 11 countries. As a general rule, they found that DNA amplification was more successful in more recent specimens, and that specimens previously frozen or kept in airtight containers yielded more DNA than those kept in boxes or on shelves. However, across the 267 specimens tested, there was considerable variability. For example, some 100-year-old specimens yielded more DNA than more recent specimens did. They also noted differences in the amount of DNA obtained from skin, hair, and other tissues. A more recent study (Kistler et al., 2017) applied a meta-analysis approach, combining 185 paleogenomic datasets to compare DNA survival with sample age and environment. They found that cytosine deamination (C to T damage) increased over time, whilst the process of fragmentation increased with precipitation and temperature, but was not correlated to the age of the sample. They further suggested that tissues or microenvironments that create a closed system with reduced chemical exchange, such as in dense bone, may additionally aid the preservation of DNA in a post-mortem sample.

Another consideration is that DNA is essentially everywhere, meaning that modern DNA that is present in the environment or that has accumulated on the object, can be preferentially sequenced, rather than the very small amount of degraded aDNA present in a sample. The amount of DNA that genuinely comes from the object sampled is known as the endogenous content. Of the total DNA extracted from a sample, only a very small fraction is truly endogenous, commonly less than 1% for bone and teeth extracts (Carpenter et al., 2013). Most of this 'other' DNA will be environmental, including modern bacterial and plant DNA, but also foreign mammalian DNA including that from modern humans that have handled the sample. However, in a 'shotgun' sequencing approach, where all DNA fragments from an extract are sequenced, these contaminating sequences can be computationally removed post-sequencing.

Significantly, these aspects of aDNA research highlight that just because a researcher asks a curator to destructively sample a specimen for DNA sequencing, it doesn't mean that they will be successful or even that they will be able to do anything useful with it, with poor DNA preservation being a major limiting factor. It is important that this aspect of the research process is communicated well to the museum professional to avoid frustration over disappointing results following destructive sampling.

Minimal sampling for DNA

In the case of destructive sampling for aDNA, the conflicting interests of researcher and museum professional are lessening as sampling and sequencing technologies improve. The amount of material now required to extract and sequence DNA can be greatly reduced, from hundreds down to tens of milligrams of material. Where once whole specimens, or large parts of specimens, had to be destroyed, now most aDNA researchers can, if the sample is well preserved, extract large amounts of genetic information from material such as bone by drilling small holes to release bone powder in a process called micro-sampling. This process can use drill bits that are as small as 2-3mm in diameter, so the hole created in the sample is very small (Rowe et al., 2011).

Knowledge of the most appropriate sampling sites is also improving. A recent study by Sirak et al. (2017) reports on minimally-invasive sampling of the petrous bone in the human inner ear for DNA analyses. The petrous bone is a particularly interesting case: it represents one of the densest bones in the human body, and has recently been identified as an exceptional site for endogenous DNA preservation (Pinhasi et al., 2015). An understanding of which bones offer the best DNA preservation means researchers can now sample precious specimens more efficiently, and a welcome coincidence regarding the petrous bone is that it is well hidden from view, meaning that the external appearance of the skull remains almost entirely intact and visually undisturbed.

Over the last 30 years, improvements in sampling, laboratory methods, and DNA sequencing techniques have resulted in smaller samples being required from specimens. The average sample size needed for genetic analyses was previously in the region of 500mg (Rohland and Hofreiter 2007), but current methods mean that this can, in well-preserved material, be reduced to 50mg or less (Gansauge and Meyer 2013). The sequencing method that will be employed is a further important consideration, as methods have changed dramatically over recent years (Knapp and Hofreiter 2010). The most recent sequencing method to revolutionize the field is Next Generation Sequencing (NGS), initially described in 2005 (Margulies et al., 2005). Prior to this, most DNA sequencing would have applied polymerase chain reaction (PCR) amplification with Sanger sequencing, a targeted sequencing approach (Pääbo et al., 1989). PCR requires specific DNA fragments to be present in the sample, and for successful amplification and sequencing, the total length of those fragments must be at least 100 base pairs (bp) (Knapp and Hofreiter 2010). The NGS approach, in contrast, does not target any particular DNA fragment, as it permits all DNA fragments within the sample to be sequenced. This and other points are discussed further by Burrell et al. (2015), who specifically address the use of museum specimens in the context of advances in DNA sequencing technologies.

Micro-sampling of appropriate sites is an important development for minimising destruction to objects and maximising research output. An important point, however, is that the amount of material required is still absolute rather than proportional to the size of the specimen. A 2-3mm micro-sampling site in a mammoth tusk, for example, represents less overall damage than the same size sample from a small rodent limb bone. This has represented a problem for entomological collections, where entire specimens were often required for genetic analyses. However, improved extraction methods and Next Generation Sequencing (NGS) techniques no longer routinely require whole specimens to be destroyed. Heintzman et al. (2014), for example, successfully sequenced DNA from 134 museum beetle (Coleoptera) remains using only a single hind leg per beetle.

As well as improvements in sampling and sequencing approaches, computational tools to account for contamination and post-mortem damage in aDNA sequences are also continuing to develop. Additionally, meta-genomic approaches are becoming increasingly popular and allow for larger proportions of the raw sequence data to be evaluated. This means that DNA extracted from an object can be considered not only in terms of its endogenous content but also through evaluation of the accompanying bacterial, plant, and mammalian DNA. It is also, in most cases, a requirement for publication that researchers make DNA sequences publicly available using repositories such as GenBank (Benson et al., 2013). Some museums have also started their own DNA repositories, including the Natural History Museum of Oslo DNA Bank (Natural History Museum of Oslo, n.d.). Public repositories allow publication of a single sequence to potentially benefit a community of researchers, and also avoid the need for recurrent sampling of the same or similar specimens. For museum professionals, allowing destructive sampling of one or few specimens can thus contribute to a great volume of research. This demonstrates that what stands to be lost may be much less than what can be gained.

The DNA extracted from museum specimens can, for example, contribute significantly to our understanding of past populations and species. DNA can provide information on genetic diversity and population structure at key points in time, for example during colonisation events (Brace et al., 2015), as well as providing a genetic characterisation of species that are rare or extinct, such as the cave lion (*Panthera leo spelaea* Goldfuss, 1810) (Barnett et al., 2016). One of the most compelling examples is found in the iconic woolly mammoth (*Mammuthus primigenius* (Blumenbach, 1799)): a recent study utilised a dataset of 143 mammoth mitochondrial genomes to assess global population structure during the Late Pleistocene (Chang et al., 2017). Ancient DNA analyses have also allowed us to address our own

evolutionary past, including gene flow between anatomically modern humans and Neanderthals (*Homo neanderthanensis* King, 1864) (Kuhlwilm et al., 2016). However, it is not only DNA that can prove useful in these contexts. A novel approach to studying extinct species was taken by Welker et al. (2015), where analyses of ancient proteins were applied to resolve the evolutionary history of Darwin's South American ungulates, using collagen from museum specimens of *Toxodon* Owen, 1837 and *Macrauchenia* Owen, 1838.

A key advantage to researchers of using museum specimens is that they are often name- and date-bearing, allowing easy integration of specimens into known taxonomic frameworks. In addition, genetic data from museum specimens can be used to generate reference sequences from which further species identifications can be made, and can help to resolve taxonomic questions by placing species within phylogenies (Welker et al., 2015). Taxonomic inventories, for example, now commonly include DNA barcoding as a mechanism for identifying and characterising the diversity of a species. This facilitates rapid identification of a species, as well as allowing the opportunity for wide-scale screening of species diversity (Miller et al., 2016). Many of these inventories are also publicly accessible, a good example being the Barcode of Life Data System (http://www.boldsystems.org) (Ratnasingham and Hebert 2007). Analysis of DNA and ancient proteins can also be used to confirm when samples are closely related and, in some instances, provide information on the ancestry or geographic origins of a sample (Schroeder et al., 2015). This can facilitate research, and has the potential to add additional information to museum object displays and to communicate the research process to visitors.

As the ability to successfully sample museum specimens for research becomes easier and more cost effective, and as knowledge of specimens held in natural science collections becomes better and more openly documented, the value of natural science collections to research will continue to increase.

A changing world

Improving technology isn't just reducing the size of the sampling sites, but is also widening the possibilities with regards to which museum specimens can be successfully sampled. One example is formalin-fixed specimens, which were previously widely regarded as intractable for DNA analysis. However, in a recent study, researchers successfully extracted mitochondrial DNA from 10 snakes preserved in formalin and other fluids, using a modified DNA extraction protocol (Ruane and Austin, 2017). The specimens were up to 100 years old. Not only were the researchers able to extract sufficient genetic information to position these samples in an existing phylogeny, but this project also generated the first genetic sequence from the rare Indian snake *Xylophis stenorhynchus* (Günther, 1875).

Further examples of neglected study systems that are now being recognised as tractable include material from the tropics. Post-mortem DNA decay is highly correlated with temperature, and warm, tropical climates are known to result in increased DNA degradation (Smith et al., 2003). Research into aDNA has therefore typically focused on colder regions and samples sourced from permafrost. However, several studies in recent years have utilised tropical specimens in museum collections to look at rare and endangered Caribbean species such as the endangered Hispaniolan hutia, *Plagiodontia aedium* F. Cuvier, 1836, and the Hispaniolan solenodon, *Solenodon paradoxus* Brandt, 1833 (Brace et al., 2012; Turvey et al., 2016). Tropical specimens stored in museum collections have also been utilised to study extinct species such as the Bahamian giant tortoise (*Chelonoidis alburyorum* Franz & Franz, 2009) (Kehlmaier, 2017) and multiple species of extinct Lesser Antillean rice rats, (Cricetidae: Sigmodontinae) (Brace et al., 2015), while Schroeder et al. (2015) were able to trace the genetic ancestry of three enslaved Africans who died on the Caribbean island of Saint Martin in the late 1600s.

Previous studies have also looked at the potential to extract DNA without damaging the specimen, a process that is termed non-destructive sampling. Sampling specimens for DNA without destruction can be pertinent for small specimens such as insects, although Heintzman et al. (2014) have shown that minimally sampling beetles is a viable option. A non-destructive approach typically involves soaking all or part of the specimen in extraction buffer (Gilbert et al., 2007). This approach has been shown in PCR experiments to yield amplifiable DNA (Thomsen et al., 2009) from historic museum beetle specimens dating to 1820, and did not appear to impact on the integrity of the specimen. However, it is important to point out that the extraction efficiency is lower in non-destructive sampling, and only successful with more recent historical material (Ibid.). Assessing how

applicable this method could be with NGS techniques represents an interesting avenue for future research.

Destructive sampling procedures for museum professionals

The above examples of destructive sampling demonstrate the importance of this approach for modern research on collections. However, there is a need for greater communication between museum professionals and researchers in order to improve access to specimens and increase the understanding of the sampling required. To clarify what the researcher is asking, and for researchers to understand what the museum will allow, a 'Destructive Sampling Agreement' document and 'Destructive Sampling Request Form' should be created. Template examples are shown in Appendix 1 and 2, which have been developed by looking at examples from Leeds City Museum, Tully House Museum and Art Gallery, The Manchester Museum, the National Museum Wales, Cardiff, and the Natural History Museum. These forms can be used and adapted by readers.

The Destructive Sampling Agreement should outline the procedures for researchers, and state what information the researcher needs to submit to the museum. The agreement should state what the museum will do on receiving a request, and if the request is granted. The agreement should be clear that not all requests will be granted, and that the museum will assess each request on its own merit (see Appendix 2)

The Destructive Sampling Request Form is divided into two sections: the first section is to be completed by the researcher and sent to the museum, and the second section is to be completed by the museum professional. The first section requests details of the researcher, project, analytical laboratory, expected outcomes, and why the specimen is required. This information enables the member of museum staff to understand *exactly* what is being requested. If information is not clear, or too jargon-heavy, additional information can be requested. The second section allows the museum professional to assess the request in detail using a list of key questions. These questions are essential in not only ensuring the research proposal is understood fully, but also in assessing the risks to the collection and identifying the benefits of the research to the museum. Ultimately, the museum has the final decision on whether their specimens are used. A set of conditions to be met by the researcher is laid out at the end of Section 1 of the form. It is essential that, where a specimen is used for research that is written up in a publication, the specimen accession number and museum must be cited in the publication: this is made explicit in both the agreement and sampling form. One important condition is that the museum be acknowledged in any resultant publications, and that co-authorship is considered, based on intellectual involvement. This highlights to museum stakeholders that collections are being used in new research (Rouhan et al., 2017).

Destructive sampling best practice will involve using these forms together with a clear dialogue with researchers. Any samples taken from specimens should be extracted under the advice of the museum professional, be as minimally invasive as possible, and - where possible - in a discrete area where it will not affect any key diagnostic features of the specimen. Any unused material should be returned following sampling. It is essential to take photographs of the specimen(s) before sampling, and to attach the images to the database record. Any forms, associated documentation, or correspondence should be attached to the relevant database record and kept with the object history files. In addition, all publications resulting from research on an object should be attached to the relevant database record(s).

Conclusion

Natural science collections represent an amazing resource not only for museum staff and visitors, but also researchers. Harnessing the research potential of museum objects may require some form of destructive sampling, and this creates the need for a compromise between protecting the object and learning from the material. One common reason for requesting destructive sampling of bone and sub-fossil material is for genetic analyses, examples of which we present here. Notably, the amount of material required for aDNA research has decreased, and sequencing techniques are generating more data from a single sample. With improving techniques and a greater realisation of the importance of museum collections, the need for a successful dialogue between researchers and museum staff is becoming more important. One method for facilitating this dialogue is through the creation and implementation of appropriate destructive sampling procedures. These not only ensure that the museum can understand the research request, but also allow researchers to understand the correct museum procedures required to treat collections with appropriate care.

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Appendix I

An example of a Destructive Sampling Agreement, adapted looking at the policies from the Natural History Museum, London, National Museum Wales, The Manchester Museum, Tully House Museum and Gallery, and Leeds City Museum.

[MUSEUM NAME] Destructive Sampling Policy

One of [MUSEUM NAME]'s key missions is to enable collections to be used to enhance research. We encourage opportunities to use our collections, including destructive sampling.

Destructive sampling involves irreversible damage to an object, and, as such, decisions on sampling are taken with serious consideration.

To ensure that collections are used to their full potential, with minimal damage, the following guidelines have been laid out for researchers:

Researchers will complete the Destructive Sampling Request Form in full and send it to the curator in charge of that collection. This will include full details of the research proposal and why the specimens from [MUSEUM NAME] are required.

Researchers are encouraged to speak directly to the curator to find out more about the specimens needed for the research, i.e. suitable specimens, the best areas to sample a specimen, fragility of specimens, etc. The smallest possible sample from the least intrusive appropriate area will be taken.

Once the Destructive Sampling Request Form has been sent to the museum, the curator may ask questions to clarify information about the research project.

Where possible, and where this does not compromise the research effort, sampling should be undertaken on site under supervision and guidance of the curator and/or conservator.

If sampling is permitted, the applicant agrees to the following (which is also outlined on the Destructive Sampling Request Form):

- To provide full details of analysis techniques to the museum.
- To return all borrowed specimens and unused samples to [MUSEUM NAME] within 6 months after sampling has taken place.
- To make available all relevant results of the analysis to [MUSEUM NAME], which will be held in confidence until publication, or until a period of two years has elapsed (whichever is sooner).
- To provide a copy of all relevant publications relating to the samples listed on this form.
- To cite all specimens used in the publication with their unique museum number as supplied by the curator.
- To acknowledge [MUSEUM NAME] in any publications resulting from the sampling of the listed specimens.
- Where appropriate, to consider including the curator as a co-author on publications, if a significant intellectual contribution to a publication has been made.
- If DNA samples have been taken, to submit sequences extracted to a public repository and provide [MUSEUM NAME] with the reference numbers along with copies of sequenced data if the museum requests this. The museum will not share this data until after they have been published. Sampling muse be done in accordance with individual museum policy and in line with legal requirements and professional ethical guidelines.

Appendix 2

An example layout of a Destructive Sampling Request Form.

[MUSEUM NAME] DESTRUCTIVE SAMPLING REQUEST FORM			
Thank you for your interest in using our collections for your research. Please complete the form below with all the details of the proposed sampling and research outcomes. The curator in charge of the collection will assess the proposal and respond to you within X days. If clarification is required on any points, the curator will contact you directly.			
Section 1: To be completed by the researcher			
Name:		Position:	
Telephone:		Email:	
Address:		Date of request:	
Details of the project:			
Research outcomes (highlighting significance of destructive sampling requested):			

Analytical details:			
Type of sample required:		Amount of material required:	
Name of analyst:		Address of analytical lab:	
Sampling methods (please state the sampling methods and analysis):			
Details of specimens to be sampled (please add more rows if required):			
Accession number:		Specimen name:	
Accession number:		Specimen name:	
Accession number:		Specimen name:	
If this proposal is accepted, I will:			

- Return all borrowed specimens and unused samples to [MUSEUM NAME] within 6 months after sampling has taken place.
- Make available all relevant results of the analysis to [MUSEUM NAME], which will be held in confidence until publication.
- Provide a copy of all relevant publications relating to the samples listed on this form.
- Cite all specimens used in publications with their unique museum number as specified by the curator.
- Acknowledge [MUSEUM NAME] in any publications resulting from the sampling of the listed specimens.
- Where appropriate, consider including the curator as a co-author on publications, if a significant intellectual contribution to a publication has been made.
- If DNA samples have been taken, submit sequences extracted to a public repository and provide [MUSEUM NAME] with the reference numbers, along with sequenced data if requested. The museum will not share this data until after they have been published.
- Provide full details of analysis techniques to the museum.

Signed:		**Date:**	

Section 2: To be completed by museum curator		
Please assess the research proposal with the following considerations:		
About the project:	**YES**	**NO**
Is there a clear hypothesis being tested?		
Can this research be carried out without using destructive sampling on specimens?		
Could the research be done with freshly collected material?		
About the researcher:		
Does the researcher/research group have demonstrable experience of using this technique?		
Does the researcher/research group have a good record of meeting the conditions of sampling?		
About the specimen(s):		
Does the museum have full legal title to the specimen(s) requested?		
Could the method of preservation or storage of the specimen reduce the success of analysis (i.e. stored in formalin, stored in warm humid environment)?		
Has identification of the specimen(s) been independently verified?		
Is the specimen fully documented to allow any correspondence, results, etc. to be attached to records?		
Is the specimen subject to legislation that may restrict its use for the proposed work (Nagoya Protocol, CITES, etc.)?		

Proposal APPROVED / NOT APPROVED (delete as appropriate)			
Name:			
Position:			
Date:			
Specimen photographed before and after sampling (YES/NO)?		Database record updated (YES/NO)?	
Note to curator: Once completed, this form must be attached to the relevant database record and stored with the collection history files.			