Received: 31 July 2020 | Accepted: 13 August 2020

DOI: 10.1111/1755-0998.13245

MOLECULAR ECOLOGY RESOURCES WILEY

SPECIAL FEATURE: GENOMICS OF NATURAL HISTORY COLLECTIONS FOR UNDERSTANDING EVOLUTION IN THE WILD

INTRODUCTION

Genomics of natural history collections for understanding evolution in the wild

Abstract

A long-standing question in biology is how organisms change through time and space in response to their environment. This knowledge is of particular relevance to predicting how organisms might respond to future environmental changes caused by human-induced global change. Usually researchers make inferences about past events based on an understanding of current static genetic patterns, but these are limited in their capacity to inform on underlying past processes. Natural history collections (NHCs) represent a unique and critical source of information to provide temporally deep and spatially broad time-series of samples. By using NHC samples, researchers can directly observe genetic changes over time and space and link those changes with specific ecological/evolutionary events. Until recently, such genetic studies were hindered by the intrinsic challenges of NHC samples (i.e. low yield of highly fragmented DNA). However, recent methodological and technological developments have revolutionized the possibilities in the novel field of NHC genomics. In this Special Feature, we compile a range of studies spanning from methodological aspects to particular case studies which demonstrate the enormous potential of NHC samples for accessing large genomic data sets from the past to advance our knowledge on how populations and species respond to global change at multiple spatial–temporal scales. We also highlight possible limitations, recommendations and a few opportunities for future researchers aiming to study NHC genomics.

1 | INTRODUCTION

Biologists have long sought to understand how organisms change through time and space in response to their environment. A related goal is to predict how organisms might respond when faced with future environmental changes. In the current context of human-induced global change, understanding how and why species evolve in response to change may be key to maintaining ecosystem processes (Jump, Marchant, & Peñuelas, 2009).

Typically, biologists make inferences about past events based on static patterns in genetic and phenotypic data. Space-for-time substitutions are often used to make inferences or predictions about how organisms might respond to changes in the environment (Razgour et al., 2019) or along the course of a population expansion (Cwynar & MacDonald, 1987; Phillips, Brown, Webb, & Shine, 2006). Alternatively, population genetic models can be used to make inferences about past demographic or selective events using contemporary population genetic data (Li & Durbin, 2011). However, these population 'snapshots' are limited in their capacity to inform on underlying processes since multiple processes can generate the same static patterns, leading to incorrect inference (Jensen, Kim, DuMont, Aquadro, & Bustamante, 2005). 'Resurrection' studies have opened an important window into the past via revival of past propagules, though these are often possible over a limited timescale of propagule viability (Cousyn et al., 2001; Franks, Hamann, & Weis, 2018), although forward-looking effort will make this more accessible in the future (Etterson et al., 2016).

Ideally, tracking changes in genotype and phenotype through time could be done using long-term studies of organisms in the wild. However, such long-term studies are rare because of the intrinsic challenge of maintaining a natural, continuous, long-term experiment. And it is only in recent years that genotyping and evolutionary genetic understanding have advanced such that long-term and repeated archiving of genetic material is viewed as a productive strategy (Hansen, Olivieri, Waller, & Nielsen, 2012), with some recent systematic efforts to begin large-scale DNA archiving (Droege et al., 2016; The National Ecological Observatory Network (neon); The Royal Botanic Gardens, Kew).

Natural history collections (NHCs) represent a potentially powerful alternative to provide deep and broad time-series of samples. NHC samples have long represented an immense and critical resource for studies of morphology, taxonomy and biogeography (Lavoie, 2013; Page, MacFadden, Fortes, Soltis, & Riccardi, 2015;

Pergams & Lawler, 2009; Smith, Johnston, & Lücking, 2016). For longitudinal studies in evolution, spatiotemporal collections of historical and ancient samples stored in NHCs provide a critical source of information because they allow us to directly observe genetic changes over time and space and link those changes with specific ecological events (Holmes et al., 2016; Kitano et al., 2008; Martin et al., 2014). This ability to directly investigate evolutionary processes and their ecological causes is key to address pressing and long-standing questions. In addition, NHCs harbour an immense diversity of organisms. For example, global herbaria (NHCs for plant and fungi) store ~350 M specimens (Besnard et al., 2018). This diversity makes a large range of species accessible to studies of systematics, phylogenetics, domestication and evolutionary biology; this is especially useful for hard to locate species in the wild (including extinct or endangered species). As an added bonus, specimens available from NHCs are typically categorized, searchable and well documented, and with increasing digitization, may have many layers of specimen-associated data (Hedrick et al., 2020; Pearson et al., 2020). NHCs represent the accumulation of immense effort invested in fieldwork and curation, and often contain populations from difficult to reach or currently unsafe regions.

Despite its potential, over the last 20 years most genetic studies using museum specimens have relied on PCR-based methods to amplify short DNA fragments from NHC samples (Hofreiter et al., 2015). These methods have been preferred as a consequence of the particularly challenging nature of DNA retrieved from NHC samples, often referred to as 'historical' or 'ancient DNA' (aDNA) (Hofreiter et al., 2015). DNA obtained from NHC samples dramatically deviates from DNA extracted from fresh tissue, and characteristic aDNA damage patterns can be observed in historical samples (<200 years old) (Dabney, Meyer, & Pääbo, 2013). Recent methodological and technological developments, in tandem with the decreasing cost of sequencing, are revolutionizing the possibilities of this research field, allowing reduced-representation and whole genome sequencing, and expanding the focus to less-well supported, nonmodel species (Bi et al., 2019; Martin et al., 2013; Olofsson et al., 2019). In this Special Feature, we present studies spanning methodological aspects (wet laboratory protocols and bioinformatics methodologies specific to aDNA) to particular case studies which demonstrate the enormous potential of NHC genomics in phylogenetics, microbiology, epigenetics, conservation genetics and evolutionary ecology studies.

2 | SUMMARY OF THE SPECIAL FEATURE

2.1 | Novel techniques for overcoming challenges in NHC genomics

The main challenge of historical or ancient samples is to obtain enough DNA of quality high enough for sequencing. DNA obtained from NHC samples is typically highly fragmented and degraded (Allentoft et al., 2012; Dabney et al., 2013; Weiß et al., 2020). DNA fragmentation in NHC samples is mainly caused by spontaneous depurination and hydrolysis of the DNA backbone (Lindahl & Andersson, 1972; Lindahl & Nyberg, 1972). This translates into an excess of adenine (A) and guanine (G) before breaking points (Briggs et al., 2007). In addition, DNA degradation in NHC samples shows an increase in cytosine (C) to thymine (T) substitutions at the ends of aDNA fragments (Dabney et al., 2013). This excess of C to T substitutions correlates with the sample age, and it is used as a criterion of authenticity in ancient genetic studies (Allentoft et al., 2012; Weiß et al., 2020). Many NHC specimens are <100 years old, leading to more subtle patterns of deamination in comparison with samples that are thousands of years old. Finally, DNA retrieved from NHC samples often comes in small amounts and includes a combination of endogenous and microbial DNA. This microbial DNA can be due to premortem or postmortem colonization of the tissue (Eisenhofer et al., 2019). Altogether, standard protocols are often poorly suited to NHC samples and new flexible methodological approaches are needed.

In addition to the fragmentation and degradation naturally found in aDNA, extraction success is also dependent on a number of factors such as age, preservation method and amount of available tissue (Gamba et al., 2016; Lonsinger, Daniel, Adams, & Waits, 2019; Rohland, Glocke, Aximu-Petri, & Meyer, 2018; Särkinen, Staats, Richardson, Cowan, & Bakker, 2012). For example, the decay rate of plant tissue is known to be faster than animal tissue, meaning that recent plant samples can display damage patterns similar to much older animal samples (Weiß et al., 2020). The conditions in which samples were preserved have also a large impact on the success of the DNA extraction (Lindahl, 1993). In this regard, soft tissues are more prone to be colonized postmortem by microorganisms than hard tissues, leading to a decrease in endogenous DNA to be retrieved during extraction (Weiß et al., 2020). Another limitation is the restricted number and volume of samples that are available for sampling. NCH samples are invaluable and irreplaceable; destructive sampling for DNA extraction cannot be done recklessly (Tin, Economo, & Mikheyev, 2014), and ethical practices should be followed (Pálsdóttir, Bläuer, Rannamäe, Boessenkool, & Hallsson, 2020).

In most cases, only a very small amount of sample is available for DNA extraction. Since DNA quality and yield are known to have a large impact in downstream high-throughput next-generation sequencing (NGS) technologies, improvements to known extraction protocols have been extensively researched in the field of ancient genomics (Gamba et al., 2016; Lonsinger et al., 2019; Särkinen et al., 2012). Many researchers are eager to know which protocol is best for obtaining the maximum yield using the minimum amount of sample for a particular taxon, sample age and type of tissue.

In this Special Feature, Tsai and collaborators explore the effect that type of extraction protocol and type of tissue have on DNA yield in birds (Tsai, Schedl, Maley, & McCormack, 2019). They compared the two most common extraction methods, the classic phenol–chloroform and the widely used silica column-based Qiagen DNeasy Blood and Tissue kit, on three types of dried avian tissue (toe pads, skin, and bones) (Tsai et al., 2019). The modified phenol–chloroform protocol rendered larger amounts of DNA than the silica column across all tissues (Tsai et al., 2019). However, the silica column recovered larger

DNA fragments (Tsai et al., 2019). Regarding the effect of tissue, toe pads yielded larger amounts of DNA, followed closely by skin punches (Tsai et al., 2019). The relative success of skin punches for DNA extraction expands the types of tissue available for sampling in birds while at the same time, offers a less noticeable/damaging option on the specimen. Overall, when dealing with historical avian samples, the authors recommend using the phenol–chloroform protocol with toe pads and if those are not available to use skin punches (Tsai et al., 2019). Adding to the effort of Tsai and collaborators, Billerman and Walsh (2019) thoroughly reviewed the most popular tissues and methods for DNA extraction in avian samples together with, sequencing and bioinformatic protocols. As concluding remarks from the review, the authors recommend minimizing damage to the specimen to ensure that more researchers can have access to tissue for future genetic studies as well as access to the specimen for taxonomical purposes (Billerman & Walsh, 2019). Collecting blood samples when possible will have no physical damage on the specimen and blood is a good source for avian DNA (Billerman & Walsh, 2019). Another recommendation is data accessibility, DNA sequencing information collected from museum samples should be made publicly available to promote research and maximize the number of research questions that can be addressed (Billerman & Walsh, 2019).

When dealing with nonmodel species, particularly those with large genomes, modern genomic studies often rely on reduced-representation approaches such as restriction-enzyme-associated DNA sequencing (RADseq). Reduced-representation approaches offer a cost-effective alternative to shallowly sequenced genomes, which in the absence of a reference genome are difficult to analyse. Reduced-representation approaches offer higher quality and greater depth of sequencing for specific loci, and have specific, well-tested pipelines for its analysis (Andrews, Good, Miller, Luikart, & Hohenlohe, 2016; Catchen, Amores, Hohenlohe, Cresko, & Postlethwait, 2011; Peterson, Weber, Kay, Fisher, & Hoekstra, 2012). Thus, RADseq may be an ideal method to study genomics in NHC data sets. Unfortunately, the use of restriction enzymes will further shorten the already fragmented aDNA, ruling out the use of standard RADseq with NHC samples. However, recent alternatives have been developed to adapt these reduced-representation approaches to retrieve aDNA at population and genome-wide scales (Burrell, Disotell, & Bergey, 2015; Orlando, Gilbert, & Willerslev, 2015).

In studies using a hybridization-based capture approach, biotinylated baits are commonly used to enrich particular genomic regions. Baits ensure that the desired genomic regions are immobilized by streptavidin-coated beads and the remaining genetic fragments are washed away prior to sequencing. Baits are often commercially synthesized (Gnirke et al., 2009), and they must be designed in silico based on reference assemblies. These characteristics make hybridization-based approaches both time-consuming and expensive, particularly for large sample sizes and nonmodel organisms. In this Special Feature, Lang and collaborators propose several novel modifications to the hyRAD protocol (Suchan et al., 2016) that combines homemade baits produced from reduced-representation libraries of fresh samples that then can be used to efficiently enrich historical libraries (Lang et al., 2020). With this approach, both historical and contemporary genomic samples from nonmodel species can be jointly analysed. Their modifications include labelling and retaining bait adapters to enable the selective reamplification of the 'immortalized' bait library even after baits have been mixed with target DNA for capture. They also include a series of 'shift-bases' to avoid base calling errors caused by identical enzyme cut sites. To test the efficiency of this method capturing genetic variation information, the authors used two plant species in the Brassicaceae family, the model species *Arabidopsis thaliana* and the nonmodel *Cardamine bulbifera* (Lang et al., 2020). The results obtained from *A. thaliana* showed the efficacy of this method by recovering previously known genetic diversity and population structure patterns (Lang et al., 2020). The genomic data obtained from *C. bulbifera* produced de novo polymorphisms that were used to characterize populations' geographical and temporal gradients (Lang et al., 2020). Altogether, this joint analysis of contemporary samples using RADseq and historical samples using the modified hyRAD method offers a less biased, cost-effective and faster alternative to identify genome-wide trends over time (Lang et al., 2020).

Gauthier and collaborators offer further improvements to the analysis of reduced-representation data from historical specimens of nonmodel organisms (Gauthier et al., 2020). Besides demonstrating the efficacy of the hyRAD method to obtain sequencing data in NHC samples of two nonmodel butterfly species, the authors also developed and tested a new bioinformatic pipeline called POPHYRAD that (a) aligns each sequence read against the probe catalogue, (b) identifies and controls for deamination patterns, (c) eliminates putative paralogues, PCR duplicates, low-quality genotypes and indels, and (d) keeps only biallelic loci for downstream analysis of structure over time and space (Gauthier et al., 2020). Finally, with the genomic data analysed with the POPHYRAD pipeline, they investigated changes in genetics structure over time and space in these butterfly species (Gauthier et al., 2020).

In addition to genetic polymorphism within and among populations, advances in aDNA sequencing are also now enabling investigation of epigenetic variation over time (reviewed in (Gokhman, Malul, & Carmel, 2017)). One example is the study from Rubi and collaborators to characterize methylation patterns of deer mice (*Peromyscus* spp.) using skulls obtained from the Upper Peninsula of Michigan in three different time periods: 1940, 2003 and 2013–2016 (Rubi, Knowles, & Dantzer, 2019). They generated reduced-representation methylomes at base pair resolution using a combination of double digest restriction site-associated associated DNA sequencing (ddRAD) and bisulphite treatment (Rubi et al., 2019). Using this approach, the authors were able to characterize patterns of cytosine methylation in two species of deer mouse, demonstrating the use of historic samples for epigenomics (Rubi et al., 2019).

One final limiting factor when studying large numbers of samples is the costs associated with sequencing. In Illumina platforms, multiplexing offers a cost-effective method to increase the number of sequenced samples per lane (Craig et al., 2008; Meyer & Kircher, 2010; Smith et al., 2010). During multiplexing, samples are labelled individually with unique identifiers (barcodes) that are inserted in the

sequencing platform-specific adapters (Meyer & Kircher, 2010). Samples are then combined together into a single DNA library and sequenced on the same lane, decreasing the per-sample sequencing cost. After sequencing, the sequences corresponding to each sample are demultiplexed based on the sample-specific barcode. Despite the cost-associated benefits, recent studies have reported high rates of misassignment associated with multiplexing in Illumina platforms due to index hopping (Costello et al., 2018; Vodák et al., 2018). When misassignment occurs, reads carrying an unintended barcode will be assigned to the wrong sample causing false conclusions to be drawn from interpretation of downstream genomic analyses (Günther & Nettelblad, 2019). Van der Valk and collaborators explore this issue by directly quantifying the rate of index hopping in 100-year-old gorilla (*Gorilla berengei*) samples obtained from NHCs (van der Valk, Vezzi, Ormestad, Dalén, & Guschanski, 2019). On average, they estimated that 0.470% of the reads contained a hopped index (van der Valk et al., 2019). This low value of index hopping was attributed to using a library protocol particularly designed for degraded samples, which largely removes free-floating adapters through a series of size selection and cleaning steps. The authors cautioned that, despite their low index hopping rate, the number of wrongly assigned reads depends on the number of reads that any given sample contributes to the total pool (van der Valk et al., 2019). This is particularly relevant for sets of data containing historical and ancient samples as these can vary wildly in the amount of endogenous DNA present in each sample (van der Valk et al., 2019). Using simulations informed by their empirical estimates of endogenous content and rates of index hopping, van der Valk and colleagues demonstrate that even low rates of index hopping can lead to false signals of population admixture, biasing ancient genomic studies (van der Valk et al., 2019). To try to minimize this problem, the authors recommend minimizing variation in sample endogenous DNA content when sequencing a sample pool on the same lane (i.e. prepooling qPCR of sample DNA content) (van der Valk et al., 2019). Moreover, in those cases when multiplexed samples are sequenced across multiple lanes or flow cells, repooling after the first sequencing run could be done if high variation in (endogenous) read number is observed (van der Valk et al., 2019).

2.2 | Applications of NHC genomics

As sequencing technology advances and methods to recover DNA from ancient and historical tissues improve, the ability to leverage genetic data from spatiotemporal molecular data sets maintained in NHCs is changing the types of questions we can address. Over the past two decades, the way scientists utilize NHC samples has shifted from classical morphology, taxonomy and biogeography to a diversity of applications including molecular-based studies of evolution (Heberling, Prather, & Tonsor, 2019; Olofsson et al., 2019). To begin with, it helps for species of interest to be correctly identified. Although NHC specimens have long been used for taxonomic purposes, in certain cases morphology-based taxonomy can pose a challenge leading to the misidentification of species (Slippers et al., 2014). This is particularly true in those cases where only part of the specimen is available for identification, when dealing with sister species with similar morphologies (e.g. cryptic species) or an unknown species (Hua et al., 2019; Slippers et al., 2014). In these cases, molecular identification using aDNA can provide an unequivocal identification (Miller, 2007). Vershinina and collaborators provide an example of how aDNA from NHC specimens can help us correctly identify samples and avoid false biogeographic reconstructions (Vershinina, Kapp, Baryshnikov, & Shapiro, 2019). Using ancient DNA, they corrected a morphological misidentification made from a partial jaw of an Equid, initially described as *Equus hemionus*, the Asiatic wild ass (Cucchi et al., 2017; Vershinina et al., 2019). Molecular results showed that the partial jaw belonged to *E. caballus*, motivating a substantial reinterpretation of the evolutionary history of Equids, which in addition to wild asses includes horses, zebras, kiangs and donkeys (Cucchi et al., 2017; Vershinina et al., 2019). This study highlights the relevance of molecular identification in challenging cases and how it can clarify the evolutionary trajectories of species.

One of the main causes of human-induced global change is biodiversity loss due to the transformation of habitat (e.g. fragmentation) (Fahrig, 2003). Biodiversity collapse refers not only to the loss of species but also to population size and biomass reduction (Hallmann et al., 2017; Lister & Garcia, 2018). When population size dramatically decreases, genetic diversity will also decrease with potentially negative consequences for the mid- and long-term population survival (Agha, Gross, Rohrlack, & Wolinska, 2018; Booy, Hendriks, Smulders, Van Groenendael, & Vosman, 2000; Razgour et al., 2019). In this Special Feature, Gauthier and collaborators demonstrate how over the past 100 years, populations of two butterfly species (*Erebia embla* and *Lycaena helle*) have suffered from genetic erosion possibly due to habitat fragmentation. Genetic erosion was seen as an increase in fixed alleles and consequently a reduction of genetic diversity (Gauthier et al., 2020). In addition, one of the species (*Erebia embla*) exhibited increased isolation by distance (IBD) through time possibly caused by habitat fragmentation (Gauthier et al., 2020). This study demonstrates the value of genetic information from historical specimens: if the authors had focused only on current populations, they would have inferred low levels of genetic variation and IBD, perhaps attributable to natural causes (e.g. life history traits like low dispersal ability). In that scenario, the decreasing diversity and increasing isolation trend possibly associated with anthropogenic habitat fragmentation would remain unidentified. This distinction between a declining trend and naturally low levels of genetic diversity is pivotal when designing management and restoration practices and could be the difference between being able to preserve the population or failing to prevent its extinction. Thus, the study from Gauthier and collaborators exemplifies how using temporal historical enhances researchers' ability to infer which evolutionary process led to the current population structure, potentially informing future conservation practices and outcomes.

When the surrounding environment changes, mobile organisms have the chance to migrate to a more suitable location (Nogués-Bravo et al., 2018). Plants with lower dispersal capabilities or highly

selfing mating systems might experience intensified, detrimental consequences of environmental change if they fail to adapt or migrate in a timely manner in response to such changes (Aitken, Yeaman, Holliday, Wang, & Curtis-McLane, 2008). In this section, Lang and collaborators show the potential of herbaria collections to document genetic changes in plant populations over time and space. By combining current populations and historical samples of *C. bulbifera*, they observed that geographically distant population were genetically diverged both among historical and modern samples (Lang et al., 2020). One hypothesis is that anthropogenic habitat fragmentation has limited gene flow between populations. Alternatively, rapid and intense environmental changes can lead to bottlenecks, increasing genetic drift and augmenting genetic differences among populations (Lopez, Retuerto, Roiloa, Santiso, & Barreiro, 2015).

In addition to heritable changes in the genetic code, modifications of DNA that do not involve changes in DNA sequence also contribute to organism responses to environmental change (Burggren, 2016; Lind & Spagopoulou, 2018). Epigenetic changes can influence gene expression that may be targeted by selection, and epigenetic changes can influence many aspects of evolution (Banta & Richards, 2018). Heritable transgenerational epigenetic changes may be particularly relevant in populations with low levels of genetic diversity where epigenetic change may preface genetic adaptations (Burggren, 2016). NHC samples open a new avenue to document how these epigenetic changes have influenced phenotypic change over time. In this Special Feature, Rubi et al. reported reduced cytosine methylation, potentially due to postmortem DNA damage, and greater individual variation in older NHC specimens of deer mouse (Rubi et al., 2019). With respect to methylation in gene bodies and promoters, patterns were consistent with those observed in mammalian somatic cells (Rubi et al., 2019). These results highlight the promise but also the challenges for the use of temporal data sets derived from NHCs in epigenetic studies (Rubi et al., 2019).

Another field of study that has been rapidly growing because of new technical advances in sequencing and bioinformatics is metagenomics. Microbial communities have critical roles in the environment, and it is only now that we are starting to unravel the extent and complexity of microbial interactions with other elements in the ecosystem (Quince, Walker, Simpson, Loman, & Segata, 2017). Microorganisms perform important roles in the organism's health and growth, and act as a link between an individual's genotype/phenotype and its environment, and thus may be part of the 'extended phenotype' (Hunter, 2018; Rodriguez et al., 2019). Human-induced environmental change has not only influenced plants and animals, but it also has impacted microbial populations (Cavicchioli et al., 2019). For example, fertilizers, fungicides and herbicides also affect microbial communities of crop fields (Benitez, Osborne, & Lehman, 2017; Caradonia et al., 2019). NHCs can potentially help us understand how these anthropogenic environmental changes have affected the microbiome over time, and by extension, communities of larger organisms.

One limitation of using NHC samples in metagenomic studies is postmortem contamination (Gutaker, Reiter, Furtwängler, Schuenemann, & Burbano, 2017; Warinner et al., 2017). Specifically, microbial communities that colonize the samples after the specimen was collected can confound results from microbiome composition studies. In a study using samples collected over 180 years of *Ambrosia artemisifolia* and *Arabidopsis thaliana*, Bieker and collaborators showed that some microbial species are exclusive to postmortem herbarium specimens and are not found in contemporary plant collections. These microbial species may compromise up to 7% of the historic samples' microbial DNA content (Bieker et al., 2020). In the particular case of the invasive species *Ambrosia artemisifolia*, only after removing these contaminants, did researchers observe a shift in the microbial community over time (Bieker et al., 2020). Altogether, this study demonstrated that it is possible to obtain metagenomic profiles from herbarium samples and perform temporal studies to identify changes in the community, but incorporation of additional analysis specific to NHC metagenomics data may be necessary (Bieker et al., 2020). Studies such as this could be further complemented by looking at environmental changes in association with shifts in the microbial community.

3 | CONCLUDING REMARKS

The studies compiled in this Special Feature illustrate how, with the development of new sequencing technologies and bioinformatic approaches, temporal and spatial data sets maintained in NHCs can now be increasingly utilized for genomic studies. Utilizing this precious resource opens a number of new possibilities in the fields of evolutionary ecology, genetics, taxonomy, microbial ecology and epigenetics. Using NHC samples, we can reconstruct species history and understand how anthropogenic pressures impact the evolutionary trajectory of species and populations. We can now directly investigate the pressing question of how populations have adapted to changing environmental conditions over time by combining genetic data from NHC samples and environmental data (e.g. historical climate records). If we unravel the genetic mechanisms for adaptation to environmental change, we can apply this information to predict how species might respond to environmental change and design conservation practices to better manage natural resources (e.g. assisted migration and genetic rescue). By identifying the genetic mechanisms behind rapid adaptation, we may better manage whether species succeed (the goal of conservation, or agriculture in response to climate change) or fail (the goal of invasive species management) in the face of novel environments. Altogether, natural history collection genomics allows us to understand how anthropogenic pressures impact the evolutionary trajectory of species and populations and make informed decisions for the future.

AUTHOR CONTRIBUTIONS

L.L., K.G.T., E.S.B. and J.R.L. conceived the study. L.L. wrote the paper with input from K.G.T., E.S.B. and J.R.L.

KEYWORDS

aDNA, environmental change, evolution, natural history collections

FUNDING INFORMATION

ESB was supported by an NSF Postdoctoral Research Fellowship in Biology under Grant 1711950. The views and opinions of authors expressed herein do not necessarily state or reflect those of the US government or any agency thereof. KGT was supported by A Pennsylvania State University Eberly Postdoctoral Fellowship and National Science Foundation grants and NSF Idaho EPSCoR Program award OIA-1757324.

Lua Lopez[1,2]
Kathryn G. Turner[2,3]
Emily S. Bellis[2,4]
Jesse R. Lasky[2]

[1]*Department of Biology, California State University San Bernardino, San Bernardino, California*
[2]*Department of Biology, Pennsylvania State University, University Park, Pennsylvania*
[3]*Department of Biological Sciences, Idaho State University, Pocatello, Idaho*
[4]*Arkansas Biosciences Institute & Department of Computer Science, Arkansas State University, Jonesboro, Arkansas*

Correspondence
Lua Lopez, Department of Biological Sciences, California State University San Bernardino, San Bernardino, CA 92407.
Email: lopezperez.lua@gmail.com

ORCID

Lua Lopez https://orcid.org/0000-0002-3619-763X
Kathryn G. Turner https://orcid.org/0000-0001-8982-0301
Emily S. Bellis https://orcid.org/0000-0001-6066-1466

REFERENCES

Agha, R., Gross, A., Rohrlack, T., & Wolinska, J. (2018). Adaptation of a Chytrid parasite to its Cyanobacterial host is hampered by host intraspecific diversity. *Frontiers in Microbiology*, *9*, 921. Retrieved from https://www.frontiersin.org/article/10.3389/fmicb.2018.00921. https://doi.org/10.3389/fmicb.2018.00921

Aitken, S. N., Yeaman, S., Holliday, J. A., Wang, T., & Curtis-McLane, S. (2008). Adaptation, migration or extirpation: Climate change outcomes for tree populations. *Evolutionary Applications*, *1*(1), 95–111. https://doi.org/10.1111/j.1752-4571.2007.00013.x

Allentoft, M. E., Collins, M., Harker, D., Haile, J., Oskam, C. L., Hale, M. L., … Bunce, M. (2012). The half-life of DNA in bone: Measuring decay kinetics in 158 dated fossils. *Proceedings of the Royal Society B: Biological Sciences*, *279*(1748), 4724–4733. https://doi.org/10.1098/rspb.2012.1745

Andrews, K. R., Good, J. M., Miller, M. R., Luikart, G., & Hohenlohe, P. A. (2016). Harnessing the power of RADseq for ecological and evolutionary genomics. *Nature Reviews Genetics*, *17*(2), 81–92. https://doi.org/10.1038/nrg.2015.28

Banta, J. A., & Richards, C. L. (2018). Quantitative epigenetics and evolution. *Heredity*, *121*(3), 210–224. https://doi.org/10.1038/s41437-018-0114-x

Besnard, G., Gaudeul, M., Lavergne, S., Muller, S., Rouhan, G., Sukhorukov, A. P., … Jabbour, F. (2018). Herbarium-based science in the twenty-first century. *Botany Letters*, *165*(3–4), 323–327. https://doi.org/10.1080/23818107.2018.1482783

Bi, K., Linderoth, T., Singhal, S., Vanderpool, D., Patton, J. L., Nielsen, R., Good, J. M. (2019). Temporal genomic contrasts reveal rapid evolutionary responses in an alpine mammal during recent climate change. *PLOS Genetics*, *15*(5), e1008119. https://doi.org/10.1371/journal.pgen.1008119

Bieker, V. C., Sánchez Barreiro, F., Rasmussen, J. A., Brunier, M., Wales, N., & Martin, M. D. (2020). Metagenomic analysis of historical herbarium specimens reveals a postmortem microbial community. *Molecular Ecology Resources*, *20*(5), 1206–1209. https://doi.org/10.1111/1755-0998.13174

Billerman, S. M., & Walsh, J. (2019). Historical DNA as a tool to address key questions in avian biology and evolution: A review of methods, challenges, applications, and future directions. *Molecular Ecology Resources*, *19*(5), 1115–1130. https://doi.org/10.1111/1755-0998.13066

Booy, G., Hendriks, R. J. J., Smulders, M. J. M., Van Groenendael, J. M., & Vosman, B. (2000). Genetic diversity and the survival of populations. *Plant Biology*, *2*(4), 379–395. https://doi.org/10.1055/s-2000-5958

Briggs, A. W., Stenzel, U., Johnson, P. L. F., Green, R. E., Kelso, J., Prüfer, K., Pääbo, S. (2007). Patterns of damage in genomic DNA sequences from a Neandertal. *Proceedings of the National Academy of Sciences*, *104*(37), 14616–14621. https://doi.org/10.1073/pnas.0704665104

Burggren, W. (2016). Epigenetic inheritance and its role in evolutionary biology: Re-evaluation and new perspectives. *Biology*, *5*(2), 24. https://doi.org/10.3390/biology5020024

Burrell, A. S., Disotell, T. R., & Bergey, C. M. (2015). The use of museum specimens with high-throughput DNA sequencers. *Journal of Human Evolution*, *79*, 35–44. https://doi.org/10.1016/j.jhevol.2014.10.015

Catchen, J. M., Amores, A., Hohenlohe, P., Cresko, W., & Postlethwait, J. H. (2011). Stacks: Building and genotyping loci de novo from short-read sequences. *G3: Genes|genomes|genetics*, *1*(3), 171–182. https://doi.org/10.1534/g3.111.000240

Cavicchioli, R., Ripple, W. J., Timmis, K. N., Azam, F., Bakken, L. R., Baylis, M., … Webster, N. S. (2019). Scientists' warning to humanity: Microorganisms and climate change. *Nature Reviews Microbiology*, *17*(9), 569–586. https://doi.org/10.1038/s41579-019-0222-5

Costello, M., Fleharty, M., Abreu, J., Farjoun, Y., Ferriera, S., Holmes, L., … Gabriel, S. (2018). Characterization and remediation of sample index swaps by non-redundant dual indexing on massively parallel sequencing platforms. *BMC Genomics*, *19*(1), 332. https://doi.org/10.1186/s12864-018-4703-0

Cousyn, C., De Meester, L., Colbourne, J. K., Brendonck, L., Verschuren, D., & Volckaert, F. (2001). Rapid, local adaptation of zooplankton behavior to changes in predation pressure in the absence of neutral genetic changes. *Proceedings of the National Academy of Sciences of the United States of America*, *98*(11), 6256–6260. https://doi.org/10.1073/pnas.111606798

Craig, D. W., Pearson, J. V., Szelinger, S., Sekar, A., Redman, M., Corneveaux, J. J., … Huentelman, M. J. (2008). Identification of genetic variants using bar-coded multiplexed sequencing. *Nature Methods*, *5*(10), 887–893. https://doi.org/10.1038/nmeth.1251

Cucchi, T., Mohaseb, A., Peigné, S., Debue, K., Orlando, L., & Mashkour, M. (2017). Detecting taxonomic and phylogenetic signals in equid cheek teeth: Towards new palaeontological and archaeological proxies. *Royal Society Open Science*, *4*(4), 160997. https://doi.org/10.1098/rsos.160997

Cwynar, L. C., & MacDonald, G. M. (1987). Geographical variation of lodgepole pine in relation to population history. *The American Naturalist*, *129*(3), 463–469. Retrieved from http://www.jstor.org/stable/2461695. https://doi.org/10.1086/284651

Dabney, J., Meyer, M., & Pääbo, S. (2013). Ancient DNA damage. *Cold Spring Harbor Perspectives in Biology*, *5*(7), a012567. https://doi.org/10.1101/cshperspect.a012567

Droege, G., Barker, K., Seberg, O., Coddington, J., Benson, E., Berendsohn, W. G., Zhou, X. (2016). The Global Genome Biodiversity Network (GGBN) data standard specification. *Database: the Journal of Biological Databases and Curation*, *2016*, baw125. https://doi.org/10.1093/database/baw125

Eisenhofer, R., Minich, J. J., Marotz, C., Cooper, A., Knight, R., & Weyrich, L. S. (2019). Contamination in low microbial biomass microbiome studies: Issues and recommendations. *Trends in Microbiology*, *27*(2), 105–117. https://doi.org/10.1016/j.tim.2018.11.003

Etterson, J. R., Franks, S. J., Mazer, S. J., Shaw, R. G., Gorden, N. L. S., Schneider, H. E., … Weis, A. E. (2016). Project Baseline: An unprecedented resource to study plant evolution across space and time. *American Journal of Botany*, *103*(1), 164–173. https://doi.org/10.3732/ajb.1500313

Fahrig, L. (2003). Effects of habitat fragmentation on biodiversity. *Annual Review of Ecology, Evolution, and Systematics*, *34*(1), 487–515. https://doi.org/10.1146/annurev.ecolsys.34.011802.132419

Franks, S. J., Hamann, E., & Weis, A. E. (2018). Using the resurrection approach to understand contemporary evolution in changing environments. *Evolutionary Applications*, *11*(1), 17–28. https://doi.org/10.1111/eva.12528

Gamba, C., Hanghøj, K., Gaunitz, C., Alfarhan, A. H., Alquraishi, S. A., Al-Rasheid, K. A. S., … Orlando, L. (2016). Comparing the performance of three ancient DNA extraction methods for high-throughput sequencing. *Molecular Ecology Resources*, *16*(2), 459–469. https://doi.org/10.1111/1755-0998.12470

Gauthier, J., Pajkovic, M., Neuenschwander, S., Kaila, L., Schmid, S., Orlando, L., & Alvarez, N. (2020). Museomics identifies genetic erosion in two butterfly species across the 20th century in Finland. *Molecular Ecology Resources*, *20*(5), 1191–1205. https://doi.org/10.1111/1755-0998.13167

Gnirke, A., Melnikov, A., Maguire, J., Rogov, P., LeProust, E. M., Brockman, W., … Nusbaum, C. (2009). Solution hybrid selection with ultra-long oligonucleotides for massively parallel targeted sequencing. *Nature Biotechnology*, *27*(2), 182–189. https://doi.org/10.1038/nbt.1523

Gokhman, D., Malul, A., & Carmel, L. (2017). Inferring past environments from ancient epigenomes. *Molecular Biology and Evolution*, *34*(10), 2429–2438. https://doi.org/10.1093/molbev/msx211

Günther, T., & Nettelblad, C. (2019). The presence and impact of reference bias on population genomic studies of prehistoric human populations. *PLOS Genetics*, *15*(7), e1008302. https://doi.org/10.1371/journal.pgen.1008302

Gutaker, R. M., Reiter, E., Furtwängler, A., Schuenemann, V. J., & Burbano, H. A. (2017). Extraction of ultrashort DNA molecules from herbarium specimens. *BioTechniques*, *62*(2), 76–79. https://doi.org/10.2144/000114517

Hallmann, C. A., Sorg, M., Jongejans, E., Siepel, H., Hofland, N., Schwan, H., & de Kroon, H. (2017). More than 75 percent decline over 27 years in total flying insect biomass in protected areas. *PLoS One*, *12*(10), e0185809. https://doi.org/10.1371/journal.pone.0185809

Hansen, M. M., Olivieri, I., Waller, D. M., Nielsen, E. E., & Group, T. G. W (2012). Monitoring adaptive genetic responses to environmental change. *Molecular Ecology*, *21*(6), 1311–1329. https://doi.org/10.1111/j.1365-294X.2011.05463.x

Heberling, J. M., Prather, L. A., & Tonsor, S. J. (2019). The changing uses of herbarium data in an era of global change: An overview using automated content analysis. *BioScience*, *69*(10), 812–822. https://doi.org/10.1093/biosci/biz094

Hedrick, B. P., Heberling, J. M., Meineke, E. K., Turner, K. G., Grassa, C. J., Park, D. S., … Davis, C. C. (2020). Digitization and the future of natural history collections. *BioScience*, *70*(3), 243–251. https://doi.org/10.1093/biosci/biz163

Hofreiter, M., Paijmans, J. L. A., Goodchild, H., Speller, C. F., Barlow, A., Fortes, G. G., … Collins, M. J. (2015). The future of ancient DNA: Technical advances and conceptual shifts. *BioEssays*, *37*(3), 284–293. https://doi.org/10.1002/bies.201400160

Holmes, M. W., Hammond, T. T., Wogan, G. O. U., Walsh, R. E., LaBarbera, K., Wommack, E. A., … Nachman, M. W. (2016). Natural history collections as windows on evolutionary processes. *Molecular Ecology*, *25*(4), 864–881. https://doi.org/10.1111/mec.13529

Hua, C. J., Zhang, D., Zou, H., Li, M., Jakovlić, I., Wu, S. G., … Li, W. X. (2019). Morphology is not a reliable taxonomic tool for the genus Lernaea: Molecular data and experimental infection reveal that *L. cyprinacea* and *L. cruciata* are conspecific. *Parasites & Vectors*, *12*(1), 579. https://doi.org/10.1186/s13071-019-3831-y

Hunter, P. (2018). The revival of the extended phenotype. *EMBO Reports*, *19*(7), e46477. https://doi.org/10.15252/embr.201846477

Jensen, J. D., Kim, Y., DuMont, V. B., Aquadro, C. F., & Bustamante, C. D. (2005). Distinguishing Between Selective Sweeps and Demography Using DNA Polymorphism Data. *Genetics*, *170*(3), 1401–1410. https://doi.org/10.1534/genetics.104.038224.

Jump, A. S., Marchant, R., & Peñuelas, J. (2009). Environmental change and the option value of genetic diversity. *Trends in Plant Science*, *14*(1), 51–58. https://doi.org/10.1016/j.tplants.2008.10.002

Kitano, J., Bolnick, D. I., Beauchamp, D. A., Mazur, M. M., Mori, S., Nakano, T., & Peichel, C. L. (2008). Reverse evolution of Armor plates in the Threespine stickleback. *Current Biology*, *18*(10), 769–774. https://doi.org/10.1016/j.cub.2008.04.027

Lang, P. L. M., Weiß, C. L., Kersten, S., Latorre, S. M., Nagel, S., Nickel, B., & Burbano, H. A. (2020). Hybridization ddRAD-sequencing for population genomics of nonmodel plants using highly degraded historical specimen DNA. *Molecular Ecology Resources*, *20*(5), 1228–1247. https://doi.org/10.1111/1755-0998.13168

Lavoie, C. (2013). Biological collections in an ever changing world: Herbaria as tools for biogeographical and environmental studies. *Perspectives in Plant Ecology, Evolution and Systematics*, *15*(1), 68–76. https://doi.org/10.1016/j.ppees.2012.10.002

Li, H., & Durbin, R. (2011). Inference of human population history from individual whole-genome sequences. *Nature*, *475*(7357), 493–496. https://doi.org/10.1038/nature10231

Lind, M. I., & Spagopoulou, F. (2018). Evolutionary consequences of epigenetic inheritance. *Heredity*, *121*(3), 205–209. https://doi.org/10.1038/s41437-018-0113-y

Lindahl, T. (1993). Instability and decay of the primary structure of DNA. *Nature*, *362*(6422), 709–715. https://doi.org/10.1038/362709a0

Lindahl, T., & Andersson, A. (1972). Rate of chain breakage at apurinic sites in double-stranded deoxyribonucleic acid. *Biochemistry*, *11*(19), 3618–3623. https://doi.org/10.1021/bi00769a019

Lindahl, T., & Nyberg, B. (1972). Rate of depurination of native deoxyribonucleic acid. *Biochemistry*, *11*(19), 3610–3618. https://doi.org/10.1021/bi00769a018

Lister, B. C., & Garcia, A. (2018). Climate-driven declines in arthropod abundance restructure a rainforest food web. *Proceedings of the National Academy of Sciences*, *115*(44), E10397–E10406. https://doi.org/10.1073/pnas.1722477115

Lonsinger, R. C., Daniel, D., Adams, J. R., & Waits, L. P. (2019). Consideration of sample source for establishing reliable genetic microsatellite data from mammalian carnivore specimens held in natural history collections. *Journal of Mammalogy*, *100*(5), 1678–1689. https://doi.org/10.1093/jmammal/gyz112

Lopez, L., Retuerto, R., Roiloa, S., Santiso, X., & Barreiro, R. (2015). A multi-faceted approach for assessing evolutionary significant conservation units in the endangered Omphalodes littoralis subsp. gallaecica (Boraginaceae). *Perspectives in Plant Ecology, Evolution and Systematics*, *17*(1), 54–65. https://doi.org/10.1016/j.ppees.2014.09.003

Martin, M. D., Cappellini, E., Samaniego, J. A., Zepeda, M. L., Campos, P. F., Seguin-Orlando, A., … Gilbert, M. T. P. (2013). Reconstructing genome evolution in historic samples of the Irish potato famine pathogen. *Nature Communications*, *4*(1), 2172. https://doi.org/10.1038/ncomms3172

Martin, M. D., Zimmer, E. A., Olsen, M. T., Foote, A. D., Gilbert, M. T. P., & Brush, G. S. (2014). Herbarium specimens reveal a historical shift in phylogeographic structure of common ragweed during native range disturbance. *Molecular Ecology*, *23*(7), 1701–1716. https://doi.org/10.1111/mec.12675

Meyer, M., & Kircher, M. (2010). Illumina sequencing library preparation for highly multiplexed target capture and sequencing. *Cold Spring Harbor Protocols*, *2010*(6), pdb.prot5448. https://doi.org/10.1101/pdb.prot5448 Format

Miller, S. E. (2007). DNA barcoding and the renaissance of taxonomy. *Proceedings of the National Academy of Sciences*, *104*(12), 4775–4776. https://doi.org/10.1073/pnas.0700466104

Olofsson, J. K., Cantera, I., Van de Paer, C., Hong-Wa, C., Zedane, L., Dunning, L. T., … Besnard, G. (2019). Phylogenomics using low-depth whole genome sequencing: A case study with the olive tribe. *Molecular Ecology Resources*, *19*(4), 877–892. https://doi.org/10.1111/1755-0998.13016

Orlando, L., Gilbert, M. T. P., & Willerslev, E. (2015). Reconstructing ancient genomes and epigenomes. *Nature Reviews Genetics*, *16*(7), 395–408. https://doi.org/10.1038/nrg3935

Page, L. M., MacFadden, B. J., Fortes, J. A., Soltis, P. S., & Riccardi, G. (2015). Digitization of biodiversity collections reveals biggest data on biodiversity. *BioScience*, *65*(9), 841–842. https://doi.org/10.1093/biosci/biv104

Pálsdóttir, A. H., Bläuer, A., Rannamäe, E., Boessenkool, S., & Hallsson, J. H. (2020). Not a limitless resource: Ethics and guidelines for destructive sampling of archaeofaunal remains. *Royal Society Open Science*, *6*(10), 191059. https://doi.org/10.1098/rsos.191059

Pearson, K. D., Nelson, G., Aronson, M. F. J., Bonnet, P., Brenskelle, L., Davis, C. C., … Soltis, P. S. (2020). Machine learning using digitized herbarium specimens to advance phenological research. *BioScience*, *70*(7), 610–620. https://doi.org/10.1093/biosci/biaa044

Pergams, O. R. W., & Lawler, J. J. (2009). Recent and widespread rapid morphological change in rodents. *PLoS One*, *4*(7), e6452. https://doi.org/10.1371/journal.pone.0006452

Peterson, B. K., Weber, J. N., Kay, E. H., Fisher, H. S., & Hoekstra, H. E. (2012). Double digest RADseq: An inexpensive method for De Novo SNP discovery and genotyping in model and non-model species. *PLoS One*, *7*(5), e37135. https://doi.org/10.1371/journal.pone.0037135

Phillips, B. L., Brown, G. P., Webb, J. K., & Shine, R. (2006). Invasion and the evolution of speed in toads. *Nature*, *439*(7078), 803. https://doi.org/10.1038/439803a

Quince, C., Walker, A. W., Simpson, J. T., Loman, N. J., & Segata, N. (2017). Correction: Corrigendum: Shotgun metagenomics, from sampling to analysis. *Nature Biotechnology*, *35*(12), 1211. https://doi.org/10.1038/nbt1217-1211b

Razgour, O., Forester, B., Taggart, J. B., Bekaert, M., Juste, J., Ibáñez, C., Manel, S. (2019). Considering adaptive genetic variation in climate change vulnerability assessment reduces species range loss projections. *Proceedings of the National Academy of Sciences*, *116*(21), 10418–10423. https://doi.org/10.1073/pnas.1820663116

Rodriguez, P. A., Rothballer, M., Chowdhury, S. P., Nussbaumer, T., Gutjahr, C., & Falter-Braun, P. (2019). Systems biology of plant-microbiome interactions. *Molecular Plant*, *12*(6), 804–821. https://doi.org/10.1016/j.molp.2019.05.006

Rohland, N., Glocke, I., Aximu-Petri, A., & Meyer, M. (2018). Extraction of highly degraded DNA from ancient bones, teeth and sediments for high-throughput sequencing. *Nature Protocols*, *13*(11), 2447–2461. https://doi.org/10.1038/s41596-018-0050-5

Rubi, T. L., Knowles, L. L., & Dantzer, B. (2019). Museum epigenomics: Characterizing cytosine methylation in historic museum specimens. *Molecular Ecology Resources*, *20*(5), 1161–1170. https://doi.org/10.1111/1755-0998.13115

Särkinen, T., Staats, M., Richardson, J. E., Cowan, R. S., & Bakker, F. T. (2012). How to open the treasure chest? Optimising DNA extraction from herbarium specimens. *PLoS One*, *7*(8), e43808. https://doi.org/10.1371/journal.pone.0043808

Slippers, B., Roux, J., Wingfield, M. J., van der Walt, F. J. J., Jami, F., Mehl, J. W. M., & Marais, G. J. (2014). Confronting the constraints of morphological taxonomy in the Botryosphaeriales. *Persoonia*, *33*, 155–168. https://doi.org/10.3767/003158514X684780

Smith, A. M., Heisler, L. E., St.Onge, R. P., Farias-Hesson, E., Wallace, I. M., Bodeau, J., … Nislow, C. (2010). Highly-multiplexed barcode sequencing: An efficient method for parallel analysis of pooled samples. *Nucleic Acids Research*, *38*(13), e142. https://doi.org/10.1093/nar/gkq368

Smith, B. E., Johnston, M. K., & Lücking, R. (2016). From GenBank to GBIF: Phylogeny-based predictive niche modeling tests accuracy of taxonomic identifications in large occurrence data repositories. *PLoS One*, *11*(3), e0151232. https://doi.org/10.1371/journal.pone.0151232

Suchan, T., Pitteloud, C., Gerasimova, N. S., Kostikova, A., Schmid, S., Arrigo, N., & Alvarez, N. (2016). Hybridization capture using RAD Probes (hyRAD), a new tool for performing genomic analyses on collection specimens. *PLoS One*, *11*(3), e0151651. https://doi.org/10.1371/journal.pone.0151651.

The National Ecological Observatory Network (neon). *DNA sequences* [website]. Retrieved from https://www.neonscience.org/data-collection/dna-sequences

The Royal Botanic Gardens, Kew. *The DNA and Tissue Bank at Kew* [website]. Retrieved from https://dnabank.science.kew.org/homepage.html.

Tin, M.-M.-Y., Economo, E. P., & Mikheyev, A. S. (2014). Sequencing degraded DNA from non-destructively sampled museum specimens for RAD-tagging and low-coverage shotgun phylogenetics. *PLoS One*, *9*(5), e96793. https://doi.org/10.1371/journal.pone.0096793

Tsai, W. L. E., Schedl, M. E., Maley, J. M., & McCormack, J. E. (2019). More than skin and bones: Comparing extraction methods and alternative sources of DNA from avian museum specimens. *Molecular Ecology Resources*, *20*(5), 1220–1227. https://doi.org/10.1111/1755-0998.13077

van der Valk, T., Vezzi, F., Ormestad, M., Dalén, L., & Guschanski, K. (2019). Index hopping on the Illumina HiseqX platform and its consequences for ancient DNA studies. *Molecular Ecology Resources*, *20*(5), 1171–1181.https://doi.org/10.1111/1755-0998.13009

Vershinina, A. O., Kapp, J. D., Baryshnikov, G. F., & Shapiro, B. (2019). The case of an arctic wild ass highlights the utility of ancient DNA for validating problematic identifications in museum collections. *Molecular Ecology Resources*, *20*(5), 1182–1190. https://doi.org/10.1111/1755-0998.13130

Vodák, D., Lorenz, S., Nakken, S., Aasheim, L. B., Holte, H., Bai, B., … Hovig, E. (2018). Sample-Index Misassignment Impacts Tumour Exome Sequencing. *Scientific Reports*, *8*(1), 5307. https://doi.org/10.1038/s41598-018-23563-4

Warinner, C., Herbig, A., Mann, A., Fellows Yates, J. A., Weiß, C. L., Burbano, H. A., … Krause, J. (2017). A robust framework for microbial archaeology. *Annual Review of Genomics and Human Genetics*, *18*(1), 321–356. https://doi.org/10.1146/annurev-genom-091416-035526

Weiß, C. L., Schuenemann, V. J., Devos, J., Shirsekar, G., Reiter, E., Gould, B. A., … Burbano, H. A. (2020). Temporal patterns of damage and decay kinetics of DNA retrieved from plant herbarium specimens. *Royal Society Open Science*, *3*(6), 160239. https://doi.org/10.1098/rsos.160239

How to cite this article: Lopez L, Turner KG, Bellis ES, Lasky JR. Genomics of natural history collections for understanding evolution in the wild. *Mol Ecol Resour.* 2020;20:1153–1160. https://doi.org/10.1111/1755-0998.13245