Museum specimens: An overlooked and valuable material for conservation genetics

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Abstract
Museum specimens include genetic information from when they were collected. This historical information, which is very difficult to ascertain from samples collected currently, could be a valuable material for use in conservation genetics. However, the genetic analysis of museum specimens is technically difficult because of DNA fragmentation and the deamination of cytosine to uracil. In recent years, various methods have been developed for the genetic analysis of museum specimens, such as data analysis techniques including next-generation sequencing. The development of approaches that extract historical genetic information from museum specimens is expected to provide a new perspective on conservation genetics. This review focuses on the availability of museum specimens as genetic resources for conservation genetics. Some case studies are introduced, and perspectives on the future utility of conservation genetic studies using museum specimens are discussed. Moreover, recommended genetic analysis methods and important points for the usage of museum specimens are presented. This review provides a strong case for increasing the usage of museum specimens in conservation genetics studies in the future.

KEYWORDS
conservation genetics, genetic diversity, museum, next-generation sequencing, specimen DNA

1 INTRODUCTION

Global biodiversity has declined rapidly since the Industrial Revolution because of human-induced environmental changes (Butchart et al., 2010; IUCN, 2016; Pimm et al., 2014; Sala et al., 2000). It is widely predicted that this decline in biodiversity will continue in the future (Pereira et al., 2010; Sala et al., 2000). Conservation studies of endangered species help to elucidate the mechanisms involved in population declines. Therefore, they must be undertaken before conservation strategies can be developed for the target species (Frankham, 2009). Genetic information is essential for conservation studies of endangered species to prevent inbreeding depression and genetic disturbance (Frankham, 2009). The effects of inbreeding depression, such as a decline in fitness, are generally caused by decreased genetic diversity (Leimu, Mutikainen, Koricheva, & Fischer, 2006; Mattila et al., 2012; Saccheri et al., 1998). Using the Glanville fritillary butterfly, Melitaea cinxia (Nymphalidae), Mattila et al. (2012) demonstrated that populations with low genetic diversity were likely to experience inbreeding depression.
control genetic diversity exhibited reduced fitness-related traits, including reductions in adult weight, flight metabolic rate, and egg viability. Genetic disturbance, in turn, causes the loss of the original spatial genetic structure of a species (Frankham, 2009; Mellink, Arntzen, van Delft, & Wielstra, 2015; Pierpaoli et al., 2003). Genetic disturbance might also carry a risk of outbreeding depression, which is a decline in fitness caused by hybridization between genetically divergent individuals (Frankham, 2009; Tallmon, Luikart, & Waples, 2004). Therefore, considering genetic information in the construction of conservation units is essential to prevent inbreeding and outbreeding depression caused by genetic disturbance. The estimation of genetic diversity and structure contributes to our understanding of the mechanisms underlying the decline or extinction of endangered species. For example, habitat fragmentation or a reduction in habitat area has adverse effects on the genetic diversity and structure of target species (Honnay, Adriaens, Coart, Jacquemyn, & Roldan-Ruiz, 2007; McDermid, Nienhuis, Al-Shamliah, Haxton, & Wilson, 2014; Nakahama, Uchida, Ushimaru, & Isagi, 2018; Smitz et al., 2014; Vandergast, Bohonak, Weissman, & Fisher, 2007). Furthermore, changes in habitat quality caused by management methods and natural disturbances also affect genetic diversity and structure (Dacasa Rüdinger, Glaeser, Hebel, & Dounavi, 2008; Marchi et al., 2013; Nakahama, Uchida, Ushimaru, & Isagi, 2016).

In attempting to conserve an endangered species that has experienced a rapid decline in recent years, genetic analysis using only extant individuals might not be sufficient to elucidate recent shifts in genetic characteristics. Genetic analysis using extant individuals cannot estimate the original genetic structure of a species before a reduction in population size because severe bottlenecks often change the allele frequencies of endangered populations (Harper, Maclean, & Goulson, 2006; Kekkonen, Hanski, Jensen, Väisänen, & Brommer, 2011; Nakahama & Isagi, 2018). Moreover, identifying the mechanisms of decline through genetic analysis of remnant individuals may be very difficult if both the area and quality of the habitat, as well as genetic diversity, are already diminished in all remnant populations of a critically endangered species.

To address this problem, historic genetic analysis, which is the analysis of specimens collected in the past, can be a valuable tool for the study and application of conservation genetics in endangered species (Wandeler, Hoeck, & Keller, 2007). Historic genetic information can reveal the genetic diversity and structure of a species before the reduction of population numbers through human activities. Harper et al. (2006) showed that the allele frequencies of the Adonis blue butterfly, Polyommatus bellargus (Lycaenidae), populations in the United Kingdom changed from 1896 to 1998–1999 because of genetic drift, local extinction, and recolonization. Cousseau, Husemann, Foppen, Vangestel, and Lens (2016) and Kekkonen et al. (2011) also demonstrated that the genetic differentiation of the house sparrow in Europe increased because of a decline in its population size. If all remnant populations of a target species have experienced a severe bottleneck, the genetic information of the populations before human disturbance, in addition to that of extant populations, could be used to construct more accurate and suitable conservation strategies. Even if a species’ habitat is diminished and genetic diversity has declined in all extant populations, historic information about habitat and genetic characteristics could enable us to identify the factors and mechanisms responsible for the decline. By comparing pre- and post-decline populations, we can estimate the effects of changes in environmental factors on temporal changes in genetic diversity and structure (Nakahama et al., 2018). However, genetic analysis of specimens collected in the past is generally much more difficult than is the analysis of fresh samples (Wandeler et al., 2007; Weiß et al., 2016). This is because DNA molecules fragment over time, which reduces the rate of successful genetic analysis of older specimen samples (Strange, Knoblett, & Griswold, 2009; Tin, Economo, & Mikheyev, 2014; Wandeler et al., 2007; Watts, Thompson, Allen, & Kemp, 2007). Furthermore, in the case of ancient DNA, including specimen samples, the frequency of substitutions from cytosine (C) to thymine (T) is increased in the terminal regions of the DNA fragments (Briggs et al., 2007; Pääbo et al., 2004; Sawyer, Krause, Guschanski, Savolainen, & Pääbo, 2012; Weiß et al., 2016). Moreover, the collection of a sufficient number of specimen samples is more difficult for historic samples than it is for current samples because 10–20 samples are needed to conduct population genetic analysis.

Another challenge to using museum specimens for genetic studies is obtaining permission from museum curators because some museums do not permit the destruction of material (Freedman, van Dorp, & Brace, 2018). Recently, various techniques have been established to conduct genetic analysis using museum specimens, and the number of conservation genetic studies using such specimens has been increasing (Nakahama et al., 2018; Suchan et al., 2016; Tin et al., 2014; Wandeler et al., 2007). For the purpose of this review, museum specimens are defined as specimens deposited in museums, universities, botanical gardens, insectariums, and personal homes. This review focuses on the potential use of museum specimens for conservation genetics, specifically addressing these three points: (a) contributions of museum specimens to conservation genetic studies, (b) genetic analysis methods and important points for the
usage of museum specimens, and (c) perspectives on future conservation genetic studies using museum specimens.

2 | CONTRIBUTIONS OF MUSEUM SPECIMENS TO CONSERVATION GENETICS

The advantage of using museum specimens is that we can access information from when the specimens were collected. This historical information has four main uses (Figure 1). First, we can establish the genetic relationships of extinct species or populations (Mikheyev et al., 2017; Waku et al., 2016). These phylogenetic studies would inform the development of a conservation strategy, such as the construction of conservation units, because they provide information about past genetic relationships when the influence of human activity was low. Using museum specimens, Waku et al. (2016) evaluated the genetic relationships between the extinct Japanese otter (*Lutra lutra nippon*) and other related species based on the mitochondrial genome. Such studies could contribute to assessing the genetic validity of reintroducing extinct species and populations, as well as the construction of phylogenetic trees including extinct species. They would also aid molecular identification when a species thought to be extinct is rediscovered. Mikheyev et al. (2017) rediscovered the Lord Howe Island stick insect (*Dryococelus australis*) using molecular analyses to compare the mitogenomes of museum specimens and fresh samples collected on Ball’s Pyramid. Other genetic studies, such as phylogenetics, have often used museum specimens as a ready means to sample target taxa (Ohshima & Yoshizawa, 2006; Waku et al., 2016).

Second, estimation of the temporal transition of genetic diversity in relation to effective population sizes would contribute to assessing the extinction risk of a species and indicate the mechanism of decline (Fountain et al., 2016; Nakahama et al., 2018). Species that show few changes can be considered to have a low conservation priority because their genetic diversity resembles that of historical populations. However, we should prioritize the conservation of species whose genetic diversity and effective population sizes have extensively decreased in recent years. It is possible to estimate the environmental factors that affect genetic diversity and effective population size using information about the temporal changes in the spatial distribution of genetic diversity. Nakahama et al. (2018) showed that recent declines in the grassland

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**FIGURE 1** Advantages of obtaining historical genetic information from museum specimens. We can estimate the following four points; (a) the phylogenetic status of extinct species, (b) temporal transition of genetic diversity of endangered species, (c) conservation units of endangered species, and (d) decrease or adaptation mechanisms to environmental changes based on genomic information [Color figure can be viewed at wileyonlinelibrary.com]
area have adverse effects on genetic diversity and effective population sizes in the endangered grassland butterfly, *Melataea ambigua*. These approaches would be useful to identify the factors that lead to reductions in genetic diversity and effective population sizes for critically endangered species, which do not currently have healthy populations. The number of insect museum specimens is much higher than that of other taxa, making insects more suitable for population genetic analysis using museum specimens.

Third, the use of museum specimens can contribute to the construction of conservation units based on spatial genetic structure (Kekkonen et al., 2011; Nakahama & Isagi, 2018). The spatial genetic structure of some endangered species has been shown to change rapidly because of genetic drift, which increases genetic differentiation, or decreased numbers of migrating individuals because of human disturbances (Kekkonen et al., 2011; Nakahama & Isagi, 2018). Following convention, conservation units have often been constructed using only the genetic information of the current sample (e.g., Carlson et al., 2016). However, the genetic diversity, allele frequency, and spatial genetic structure of critically endangered species, which have experienced extreme bottlenecks in recent decades, might have changed (Fountain et al., 2016; Kekkonen et al., 2011; Nakahama & Isagi, 2018). Estimation of target species genetic information before severe reductions in population sizes, using museum specimens, would enable the construction of more accurate conservation units.

Last, museum specimens are also useful for conservation genomics, including genomic and epi-genomic analyses. In general, inbreeding depression of in-situ or ex-situ conservation individuals should be avoided (Frankham, 2009). In the case of individuals that are reared in ex-situ conservation facilities, adaptation to the rearing environment should also be prevented because it could lead to reduced fitness in the wild (Frankham, 2009). Genomic and epi-genomic analyses using museum specimens could be used to elucidate the mechanisms behind these problems, as temporal difference can be detected using present and past samples. Gelabert et al. (2020) and Irestedt et al. (2019) determined the whole genomes of extinct species and discussed their processes of extinction on the basis of whole genome data. Moreover, Rubi, Knowles, and Dantzer (2020) demonstrated the utility of museum specimens for conducting epi-genomic analyses. Although these previous studies did not focus on conservation genomics, genomic and epi-genomic analyses have the potential to contribute to breakthroughs in conservation genomics.

### 3 Genetic Analysis Methods Using Museum Specimens

The methods suggested for the genetic analysis of museum specimens using conventional sequencing are Sanger sequencing and microsatellite analysis of short-length sequences (Table 1). The target of these analyses is usually short-length sequences of approximately 50–400 bp in length. Thus, Sanger sequences from specimen samples have less information than do those from fresh samples. Although universal primers for Sanger sequencing are used for specimen samples (Meusnier et al., 2008), unique primers are often designed for the analysis of short specimen sequences when using both methods (Hausmann et al., 2016; Ohshima & Yoshizawa, 2006). For microsatellite analysis, the genetic information obtained does not change regardless of the length of the DNA sequence used. Therefore, it is recommended that markers with shorter amplification lengths are developed because they tend to increase the success rate of analysis (Nakahama & Isagi, 2017; Nakahama, Izuno, Arima, & Isagi, 2015).

Through the recent development of next-generation sequencing technology, the number of genetic analyses has increased dramatically. In the case of determining genomic information of target or related species, sequencing or skimming of the whole, mitochondrial, or chloroplast genome could be performed using museum specimens (Cridland et al., 2018; Mikheyev et al., 2017; Waku et al., 2016; Zeng et al., 2018). Although the per-sample cost of analysis using this approach is high, these analyses are useful to determine the phylogenetic position of extinct species or populations. For population genetics with tens to hundreds of samples, more economical and efficient methods for detecting genome-wide single-nucleotide polymorphisms (SNPs), including the multiplexed ISSR genotyping by sequence (MIG-seq) and the restriction site-associated DNA sequencing (RAD-seq), have been developed (Miller, Dunham, Amores, Cresko, & Johnson, 2007; Suyama & Matsuki, 2015). Iwasaki et al. (2019) showed that MIG-seq could produce efficient reads for collecting SNPs from plant specimen samples collected at least 30–40 years earlier. Normal RAD-seq is an unsuitable method for sequencing museum specimen DNA because this method requires fresh and undegraded DNA (Miller et al., 2007). Tin et al. (2014) developed improved RAD-seq based methods, which were successful at genotyping insect specimen samples collected 30–100 years earlier. Moreover, these methods do not require genome information about the target species. Therefore, these methods are suitable for the study and application of conservation genomics.
genetics in endangered species, which are mostly non-model species.

Target capture is a mainstream analysis tool that uses specimen DNA (Bailey et al., 2015; Bi et al., 2013; Jones & Good, 2016; McCormack et al., 2016; Van Dam et al., 2017). To date, study species using this approach have been limited to organisms whose related species' genome or probe markers have been determined because this method requires the availability of probe sequences to conduct analysis (Bailey et al., 2015; Perry, Marioni, Melsted, & Gilad, 2010; Wang et al., 2010). Recently, ultra-conserved elements (UCEs), which are highly conserved and abundant nuclear sequences distributed throughout the genomes of most organisms, have been highlighted as potential universal probes for target capture (McCormack et al., 2016; Van Dam et al., 2017). Moreover, cost-effective, new target capture methods, which do not require probe sequences, have also been developed (Knyshov et al., 2019; Linck et al., 2017; Peñalba et al., 2014; Suchan et al., 2016). Although these techniques are mainly used in evolutionary biology and the study of molecular phylogenies (Bailey et al., 2015; Jones & Good, 2016; Van Dam et al., 2017), they could also contribute to conservation genetics.

**4 | POINTS OF ATTENTION FOR MUSEUM SPECIMEN ANALYSIS**

Conducting genetic analyses using specimen samples is more complicated than using fresh samples because of specimen-specific issues related to DNA degradation. Below, we outline some factors that will help to achieve successful sequencing and genetic analyses of museum samples.

Collection bias of museum samples should be avoided for genetic analysis. For some organisms, such as butterfly species, collectors may have selected individuals or

| Analysis methods                  | Sequencer               | Genome information | Specific marker       | References                                                                 |
|-----------------------------------|-------------------------|--------------------|-----------------------|---------------------------------------------------------------------------|
| Sanger sequencing                 | Sanger sequencer        | Unnecessary        | Necessary/unnecessary  | Frey et al. (2017); Janecka et al. (2014); Ohshima and Yoshizawa (2006); Satoh, Shutoh, Kurosa, Hayasaka, and Kaneko (2018); Xenikoudakis et al. (2015) |
| Microsatellite                     |                         | Unnecessary        | Necessary             | Habel et al. (2014); Harper et al. (2006); Hoeck, Bollmer, Parker, and Keller (2010); Janecka et al. (2014); Kekkonen et al. (2011); Mizuki, Yamasaki, Kakutani, and Isagi (2010); Nakahama et al. (2018); Nakahama and Isagi (2018); Xenikoudakis et al. (2015) |
| Hybridization capture using RAD probes | Next-generation sequencer | Unnecessary        | Unnecessary           | Linck, Hanna, Sellas, and Dumbacher (2017); Suchan et al. (2016) |
| RAD-tag analysis                   |                         | Unnecessary        | Unnecessary           | Tin et al. (2014)                                                      |
| MIG-seq                            |                         | Unnecessary        | Unnecessary           | Iwasaki et al. (2019)                                                   |
| Target capture                     |                         | Unnecessary        | Necessary/unnecessary  | Bailey et al. (2015); Blaimer, Lloyd, Guillory, and Brady (2016); Knyshov, Gordon, and Weirauch (2019); McCormack, Tsai, and Faircloth (2016); Van Dam et al. (2017) |
| Genome skimming                    |                         | Necessary          | Unnecessary           | Hughey, Boo, and Boo (2016); Mikheyev et al. (2017); Waku et al. (2016); Zeng et al. (2018) |
| Amplicon sequencing                 |                         | Unnecessary        | Necessary/unnecessary  | Forin et al. (2018); Haran et al. (2018)                                   |
| Genome resequencing                 |                         | Necessary          | Unnecessary           | Cridland, Ramirez, Dean, Sciligo, and Tsutsui (2018); Gelabert et al. (2020); Hykin, Bi, and McGuire (2015) |
taxa without the full range of morphological characteristics (e.g., aberrant forms) because of their rarity (Yago, 2017). Therefore, there is the risk that a collection may not fully reflect the actual population. Although collection bias may not be a serious problem for genetic analysis using neutral loci, samples for genetic analysis should be preferentially selected from those collections with little morphological bias.

Another important consideration for using museum specimens in genetic studies is to ensure that specimen transport, preservation, and handling before and after museum deposition is performed in such a way as to avoid or minimize the risk of DNA fragmentation. This is important because DNA fragmentation makes genetic analyses more difficult. Numerous actions can increase the degradation of DNA. First, exposure to steam or water, which is used to soften museum specimens, promotes DNA degradation in dried and pinned insect specimens (Nasu, Hirowatari, & Yoshiyasum, 2016). For successful genetic analysis, insect specimens that have not undergone a softening treatment should be used for analyses. Second, thermal drying treatments, higher than 60°C, which are used to soften museum specimens, promotes DNA degradation in dried and pinned insect specimens (Nasu, Hirowatari, & Yoshiyasum, 2016). For successful genetic analysis, insect specimens that have not undergone a softening treatment should be used for analyses. Second, thermal drying treatments, higher than 60°C, which are used to dry specimens also present risks for DNA degradation in dried plant specimens (Särkinen, Staats, Richardson, Cowan, & Bakker, 2012). Therefore, it is important to moderate temperature when drying specimens. Third, formalin fixation of immersed specimens leads to a high frequency of sequence alteration (Williams et al., 1999). It is difficult to achieve fixation without formalin, and it is a standard method. Therefore, small amounts of tissues should be cut before fixation and preserved in 99% ethanol to use for DNA extraction and conducting genetic analyses. Some fumigants pose risks of further DNA fragmentation in museum specimens. For example, fumigation using dichlorvos, methyl bromide, ethylene oxide, and propylene oxide impedes the extraction and amplification of DNA from museum collections (Espeland et al., 2010; Kigawa, Nochide, Kimura, & Miura, 2003). However, 60% carbon dioxide treatment, thermal treatments with low temperatures (−20°C), and fumigation using methyl iodide, naphthalene, paradichlorobenzene, and sulfuryl fluoride do not negatively affect DNA molecules (Espeland et al., 2010; Kigawa et al., 2003). Hence, these treatments or fumigants can be used to control pests and molds. For dried insect specimens, a method has been developed for preparing samples with well-preserved DNA (Nakahama, Isagi, & Ito, 2019). Moreover, for other taxonomic groups, methods for the preparation of specimens with well-preserved DNA over a long period are expected in the future.

It is important to use specimens stored under conditions ideal for DNA preservation. Nakahama and Isagi (2017) reported that DNA extracted from moldy, dry specimens was severely degraded. Specimens that are degraded in appearance because of mold or putrefaction may also have degraded DNA, so this is an important factor in specimen selection. It may even be warranted to interview the curator about specimen preservation conditions in the museum as part of the selection process. Further, specimens that have undergone fumigation using dichlorvos, methyl bromide, ethylene oxide, and propylene oxide or have been exposed to steam or water as part of their processing should be avoided for genetic studies as these treatments degrade DNA.

Large amounts of DNA should be extracted to increase the chances of success in genetic analyses of museum specimens. For DNA extraction, proteinase K treatments, which remain active for two or three nights, and extended centrifugation for ethanol precipitation (30 min) can increase the amount of DNA extracted (Nakahama & Isagi, 2017). Cota-Sánchez, Remarchuk, and Ubayasena (2006) and Gütaker, Reiter, Furtwängler, Schuenemann, and Burbano (2017) also developed a DNA extraction protocol for plant specimens. For PCR, increasing the cycle number or decreasing the melting temperature may assist in the amplification of DNA from museum specimens (Nakahama & Isagi, 2017; Ohshima & Yoshizawa, 2006). However, increasing the number of cycles and decreasing the melting temperature might also increase the frequency of non-specific amplification (Wandel et al., 2007).

The most serious problem for genetic analysis using museum specimens is the risk of genotyping error. DNA fragmentations of museum specimen samples often leads to allelic dropout (Wandel et al., 2007). These problems are particularly noticeable in PCR-based analysis, such as microsatellite analysis and Sanger sequencing. This is because conducting PCR on fragmented DNA samples poses a risk of stochastic non-amplification of one of the two alleles, which is known as allelic dropout. Moreover, substitutions from cytosine to thymine (i.e., deamination) accumulate at the end of DNA fragments as time passes after specimen preparation (Sawyer et al., 2012; Weiß et al., 2016). Several approaches have been proposed to achieve higher reliability of genotyping. First, the use of NEBNext FFPE DNA Repair Mix (New England Bio Labs) is recommended after DNA extraction (Sproul & Maddison, 2017). This kit repairs degraded DNA fragments and deamination. Second, in PCR-based analysis, repeated and independent PCR amplifications are useful for determining the presence or absence of genotyping errors (Nakahama et al., 2018; Wandel et al., 2007). Third, the ends of DNA fragments should be removed because these regions have a risk of deamination (Sawyer et al., 2012; Wandel et al., 2007; Weiß et al., 2016).
Together, these approaches could improve the reliability of genetic analyses and make them more robust.

Non-destructive use is recommended for genetic analysis because specimens are very valuable. Non-destructive DNA sampling methods from museum specimens have been developed for many taxonomic groups, including vertebrates (Mundy, Unitt, & Woodruff, 1997; Rohland, Siedel, & Hofreiter, 2004), insects (Andersen & Mills, 2012; Gilbert, Moore, Melchior, & Worobey, 2007; Porco, Rougerie, Deharveng, & Hebert, 2010; Tin et al., 2014), freshwater invertebrates (Carew, Coleman, & Hoffmann, 2018), and plants (Sugita et al., 2020) (Table 2). However, it may be necessary to use specimens destructively, depending on the taxonomic group and the amount of DNA required for analysis. In that case, it may be necessary to consider reducing the amount of the specimen that is destroyed or carefully consulting with a curator (Shiga, 2013).

5 | CONCLUSION AND PERSPECTIVES FOR FUTURE USE

In this paper, I reviewed the methods, potential, and notable points regarding conducting conservation genetic studies using museum specimens. Museum curators and scientists will be able to highlight the value of museum specimens by increasing the application of genetic analysis research using museum specimens in the future. However, unfortunately and understandably, the number of studies using museum specimen samples is much lower than those using only fresh samples (Wandeler et al., 2007). Here, I propose several future directions to utilize specimen DNA samples for conservation genetics. First, it is important to reduce the start-up hurdles by generalizing the use of low-cost analysis methods. Although many analysis methods have been recently developed that use next-generation sequencing, most of these methods are expensive and require a substantial amount of work. Moreover, some methods can only process a few organisms that are determined by their whole or organelle genomes because these methods require genomic information (Cridland et al., 2018; Mikheyev et al., 2017). However, MIG-seq, which rapidly produces genome-wide single-nucleotide polymorphism genotyping data at a low cost, could be used to analyze non-model organisms (Suyama & Matsuki, 2015). Iwasaki et al. (2019) reported that successful analyses using plant specimen samples collected at least 30 years before. It is essential to clarify the age of museum specimens that can be analyzed in each taxonomic group because few studies are using MIG-seq for museum specimen samples. Furthermore, cost-effective target capture methods have also been developed (Knyshev et al., 2019; Linck et al., 2017; Suchan et al., 2016). These methods do not need genomic information for the genetic analysis of museum specimens. In the future, new low-cost and time-efficient analysis methods could also be developed.

### Table 2  Non-destructive DNA extraction methods used in each taxonomic group

| Taxonomic group | Specimens | Methods | References |
|-----------------|-----------|---------|------------|
| Chordata        | Aves      | Stuffed bird | Used from skin of feet and feathers with attached skin | Mundy et al. (1997) |
| Mammalia        | Bone, tooth, and skin samples | Incubated in extraction buffers | Rohland et al. (2004) |
| Arthropod       | Arthropod | Immersed body with 80% ethanol | Extracted in extraction buffer | Rowley et al. (2007) |
| Entognatha      | Preparation specimen for microscope | Immersed in lysis buffer | Porco et al. (2010) |
| Insecta         | Dried body | Distilled water and sonicated | Hunter, Goodall, Walsh, Owen, and Day (2008) |
|                 | Dried body | Extracted in extraction buffer | Andersen and Mills (2012); Gilbert et al. (2007); Tin et al. (2014) |
|                 | Frozen, immersed body with 70% ethanol, and dried | Extracted in extraction buffer | Santos, Ribeiro, Cabral, and Speranca (2018) |
| Other animals   | Freshwater invertebrates | Immersed body with 70% ethanol | Extracted in extraction buffer | Carew et al. (2018) |
| Plantae         | Plantae, Polypodiopsida, eudicots | Dried leaf | Placed extraction buffer on the leaf | Sugita et al. (2020) |
Second, utilizing genomic information is useful for understanding the temporal transition of mutations or methylations of functional genes (Gelabert et al., 2020; Irestedt et al., 2019; Rubi et al., 2020). This knowledge is also important for informing the conservation of endangered species. Genomic and epi-genomic information contributes to detailed demographic analysis and the identification of selected loci because of environmental changes. However, these analyses require genomic information and their target species are only model organisms for which the entire genomes are known. However, future cost reductions in determining whole genomes could reduce the hurdles and allow for the application of this approach to the study of conservation genomics.

Last, global guidelines for the use of specimens should also be constructed. If the frequency of specimen use increases, it is expected that the load on the curator would increase. Moreover, researchers who are not familiar with the uses of museum specimens could damage specimens. Zimkus and Ford (2014) proposed guidelines on the usage of museum specimens for genetic analysis. For instance, the integration and sharing of results including successes and failures of museum specimen analyses would provide important information for both researchers and curators as the condition of preserved specimens varies. Thus, the determination and standardization of more suitable genetic preservation methods are warranted to promote genetic analysis using museum specimens in the future.

There is no doubt that museum specimen DNA could be a valuable material for understanding biodiversity conservation in the future. Indeed, increasing the use of museum specimens might provide a new perspective on conservation genetics.

ACKNOWLEDGMENTS
This review is based on a presentation delivered at the seventh Suzuki Award at the 66th Annual Meeting of the Ecological Society of Japan, March 2019. I would like to thank Prof. Yuji Isagi, Prof. Motomi Ito, Prof. Atushi Ushimaru, members of the Laboratory of Forest Biology in Kyoto University, members of the Laboratory of Plant Evolution and Biodiversity in The University of Tokyo for various types of support in my research. I would also like to thank all the collaborating researchers, amateur collectors, and nature conservationists. This work was supported by JSPS KAKENHI grant numbers 15J00908, 17J00965, and 19K15856.

CONFLICT OF INTEREST
The authors declare no conflicts of interest.

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