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PERSPECTIVE

A pragmatic approach for integrating molecular tools into biodiversity conservation

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Abstract

Molecular tools are increasingly applied for assessing and monitoring biodiversity and informing conservation action. While recent developments in genetic and genomic methods provide greater sensitivity in analysis and the capacity to address new questions, they are not equally available to all practitioners:

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There is considerable bias across institutions and countries in access to technologies, funding, and training. Consequently, in many cases, more accessible traditional genetic data (e.g., microsatellites) are still utilized for making conservation decisions. Conservation approaches need to be pragmatic by tackling clearly defined management questions and using the most appropriate methods available, while maximizing the use of limited resources. Here we present some key questions to consider when applying the molecular toolbox for accessible and actionable conservation management. Finally, we highlight a number of important steps to be addressed in a collaborative way, which can facilitate the broad integration of molecular data into conservation.

KEYWORDS
conservation, management, molecular tools

1 | INTRODUCTION

Molecular methods are now widely used for monitoring biodiversity and guiding conservation decisions (Hoban et al., 2022). In addition, management plans increasingly include genetic considerations (Pierson et al., 2016). However, broad-scale implementation of management plans that are informed by molecular data remains challenging (Taylor et al., 2017), especially because financial and human resources are limited and most threatened species are located in low- and middle-income countries (Di Marco et al., 2017; Waldron et al., 2013).

Genetic information can contribute to conservation management and policy in two principal ways. First, it can be applied for identifying individuals, conservation units, or species, describing family relationships — including parentage, population structure and connectivity, hybridization, and assessing historical population size (Hohenlohe et al., 2021; Kardos, 2021). Second, as genetic diversity is strongly linked to the fitness of individuals, as well as adaptive potential of populations, it forms a basis for informing current and future planning of conservation actions intended to maximize population persistence (Frankham et al., 2017; Kardos et al., 2021). Whereas historically, there has been a strong focus on single locus datasets (e.g., mitochondrial or chloroplast DNA) and on a relatively low number of hypervariable loci (e.g., allozymes, microsatellites), genomes are now sampled more widely by identifying variable positions (single nucleotide polymorphism (SNPs)) from reduced-representation sequencing (RRS) or whole genome sequencing (WGS) (Figure 1). Such broader sampling of the genome allows for higher resolution and more precise inferences that can be beneficial for conservation decisions (Allendorf et al., 2010). However, genomics typically has higher costs and resource requirements and relies more strongly on available capacity to analyze and interpret the results (Shafer et al., 2015). Genomic tools can provide important information on the history of populations, the genomic consequences of small population size, and provide more statistical power to estimate individual and population fitness. However, for overall diversity estimates and the inference of population structure, genome-scale datasets often confirm results obtained from traditional genetic datasets, and many metrics relevant to conservation can also be derived from traditional genetic markers (Hoban et al., 2022; O'Brien et al., 2022). The relevance of applying molecular tools depends greatly on the specific conservation context, including the nature of threats and the urgency to mitigate them. The best course of action regarding research setup, including marker choice, therefore depends on the conservation issue, the level of precision and certainty needed, and the available capacity and resources. For these reasons, clear communication about what can be achieved with various types of datasets is key.

Recent developments have led to an impressive increase in genomic resources for a wide range of species and genomic tools have accelerated the impact of genetic data and concepts on policy and conservation action. Some conservation-oriented organizations have decisively and successfully taken up applying genetic concepts in their conservation policies or actions (e.g., National Oceanic and Atmospheric Administration, IUCN SSC Conservation Planning Specialist Group, Nature Scot, International Whaling Commissions, Australian Wildlife Conservancy, New Zealand Department of Conservation and others). However, the degree to which genetic considerations and molecular data have been integrated into conservation and management programs varies greatly across the world, and within nations (Pierson et al., 2016). This variation is, in part, due to suboptimal communication between geneticists and policymakers, with considerable important data remaining dispersed, inaccessible, or misunderstood (Cook et al., 2021; Laikre et al., 2020; Sandström

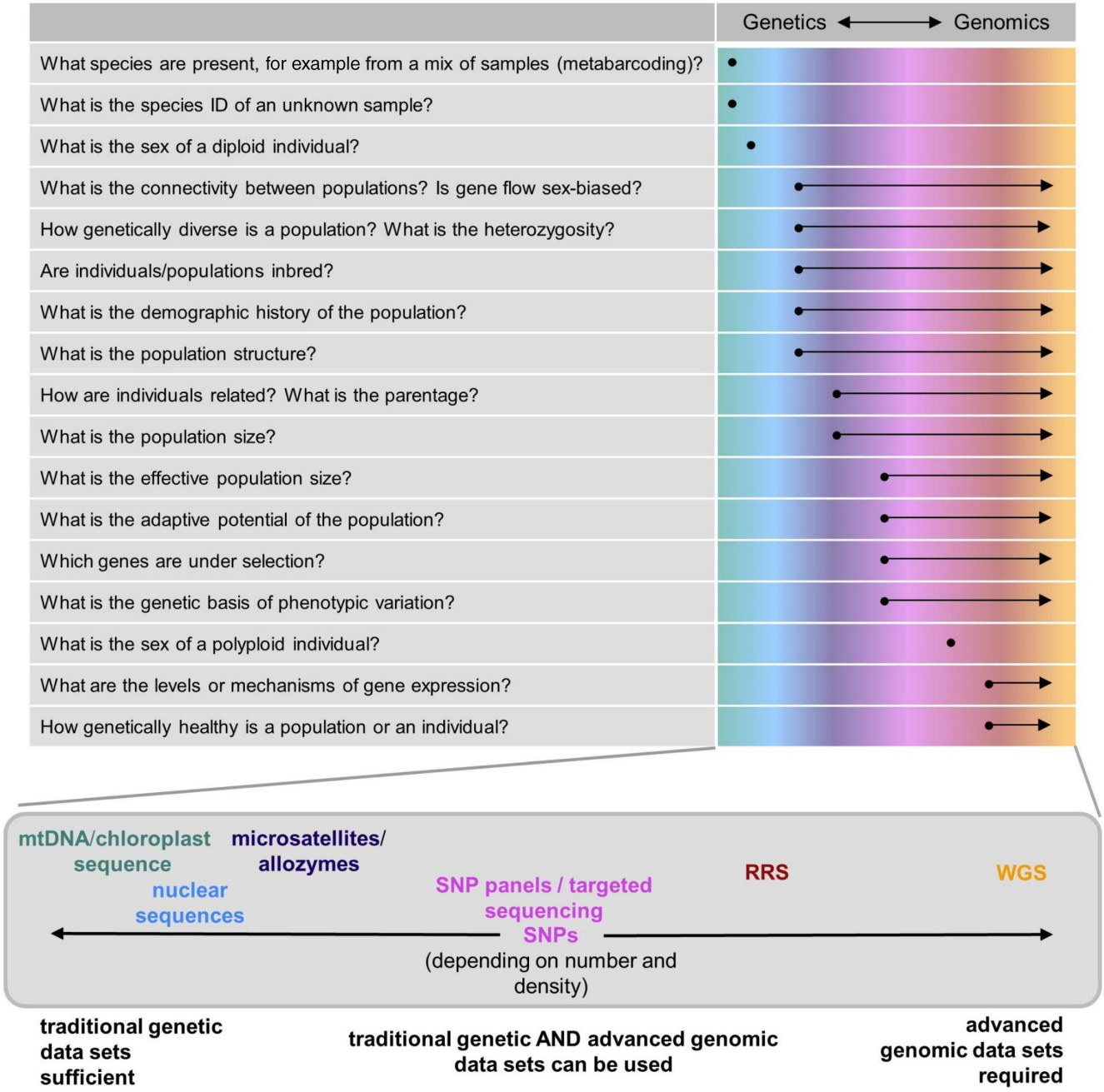

FIGURE 1 Summary of conservation questions and the application of different tools across the genetics/genomics continuum. Genetic tools have been changing rapidly over time, from targeting organellar, single locus markers, to a few genetic markers in the nuclear DNA, to genome-scale analyses including thousands of markers or even full genomes of individuals. There is no clear line differentiating genetics from genomics as this presents a continuum of possibilities. The amount of data needed to address a question satisfactorily, that is, the exact placement on the genetics/genomics continuum depends on the required resolution, precision, and certainty, and is, therefore, highly context-specific. Therefore, the dot should be seen as the minimum data requirement, with the arrow indicating the applicability of other markers, depending on specific data requirements. mtDNA, mitochondrial DNA; SNPs, Single Nucleotide Polymorphisms; RRS, Reduced-Representation Sequencing (e.g., restriction site-associated DNA sequencing, RADseq; Genotyping-By-Sequencing, GBS); WGS, Whole Genome Sequencing.

et al., 2019; Torres-Florez et al., 2018). In addition, even though the costs of genetic analyses have fallen rapidly, it is still considered costly and relies on specialized expertise, making it less accessible. Differences in the availability of specialized facilities and the capacity to generate, analyze, and interpret genetic and genomic data are key considerations. Such facilities, including high throughput sequencing equipment and high-performance computing clusters, are not available in all institutions or countries or are not readily accessible to

local conservation researchers and practitioners. International collaborations may enable access to such facilities; however, countries are also bound by stringent regulations regarding the export of samples (e.g., Convention on International Trade in Endangered Species [CITES]). Studies may also be subject to permits or regulations associated with the Nagoya Protocol on Access and Benefit Sharing (https://www.cbd.int/abs/) to ensure the fair and equitable use of genetic resources. Outsourcing components of the workflow (e.g., DNA sequencing) is typically more cost-effective; however, generating and analyzing data locally have several significant benefits: sample and data ownership remains with local researchers and practitioners, training and expertise transfers into the country, and direct connections to local management and policy needs can be encouraged (Holderegger et al., 2020).

Even if specialized facilities are available in a country, it often remains unclear to conservation practitioners which technological advances are beneficial for conservation projects and whether the additional costs associated with generating genome-scale datasets are an effective investment. Conservation researchers and practitioners require standardized and optimized approaches with demonstrated potential for broad-field application, while in academic research the incentives to achieve this, both in the form of funding and publications, are often lacking (van Oosterhout, 2020). Despite this, several recent initiatives have aimed to bridge the gap between geneticists and practitioners by providing well-informed decision-support tools tailored toward end-users (Funk et al., 2019; Hoffmann et al., 2015; Hogg et al., 2022; Holderegger et al., 2019; Nielsen et al., 2022). Although there is a need for best practice recommendations regarding suitable data generation and analysis, these are highly context-specific and may change as technologies develop. Thus, it is challenging to articulate guidelines that are broadly applicable across a variety of conservation questions, taxa, and technologies.

To facilitate the integration of genetic and genomics research into applied conservation, here, we discuss the conservation questions that can benefit from molecular tool applications and provide guidance on which tools are suitable, depending on the conservation context. This is illustrated by a number of case studies, which show how a growing body of genetic and genomic literature has influenced conservation decisions. We conclude by highlighting a number of steps for improving accessibility and inclusion in the field of conservation genetics: Effectively addressing these challenges will help to ensure that those involved in conservation policy and management around the world can access the information and resources they need to apply appropriate molecular tools to conservation questions.

2 | PRAGMATIC DECISIONS FOR INTEGRATING MOLECULAR DATA INTO CONSERVATION

To bolster the uptake of molecular methods in conservation, identifying pragmatic approaches can allow for efficient data collection and integration to more rapidly address specific conservation questions (Figure 2). A number of key questions related to appropriate sampling design, data requirements, and data availability can provide guidance, but it is important to acknowledge that the ability to access funding, resources, or analysis capacity also influences the choice of methods. Genetic information can be integrated through the application of proxies, repurposing previously collected data, and/or the collection of new data.

When molecular data are not available, whether through limited access to samples or facilities, or limited funding for this type of research, conservation decisions can be informed by genetic considerations through the use of proxy data. Careful assessment of risks and limitations can help to ensure the appropriate applications of proxy data. Examples where proxy data have been used include the freely available environmental and geographic distance variables which can be used as surrogates for both neutral and adaptive genetic variation in prioritizing protected area acquisitions (Hanson et al., 2017). If a population of interest has not been genotyped, genetic information from neighboring populations, such as their assignment to a phylogeographic clade, can be used to guide decisions regarding the choice of suitable source and target populations for translocations, as was recently illustrated in the case of lions (Bertola, Miller, et al., 2022; Bertola, Sogbohossou, et al., 2022). In general, comparative phylogeography can be used to explore whether patterns across species are congruent, for instance, due to similar evolutionary histories, such as shared glacial refugia (Bertola et al., 2016; Willis et al., 2004). Delineations or data from ecologically similar and co-occurring species can thus be suitable proxies to determine boundaries between phylogeographic lineages and evolutionary relationships between populations, providing relevant insights into overall biodiversity patterns. This means that differentiation and isolation between populations can be integrated into conservation decisions for populations for which genetic data do not yet exist.

Proxies for other components of within-species genetic diversity can also be used (Figure 2). Recently, Hoban et al. (2021) proposed the following indicators for assessing genetic diversity in a global biodiversity conservation framework: (1) the ratio of populations with an effective population size (*Ne*) above versus below 500, (2) the proportion of populations maintained relative to a historic baseline, and (3) the number of populations/species for

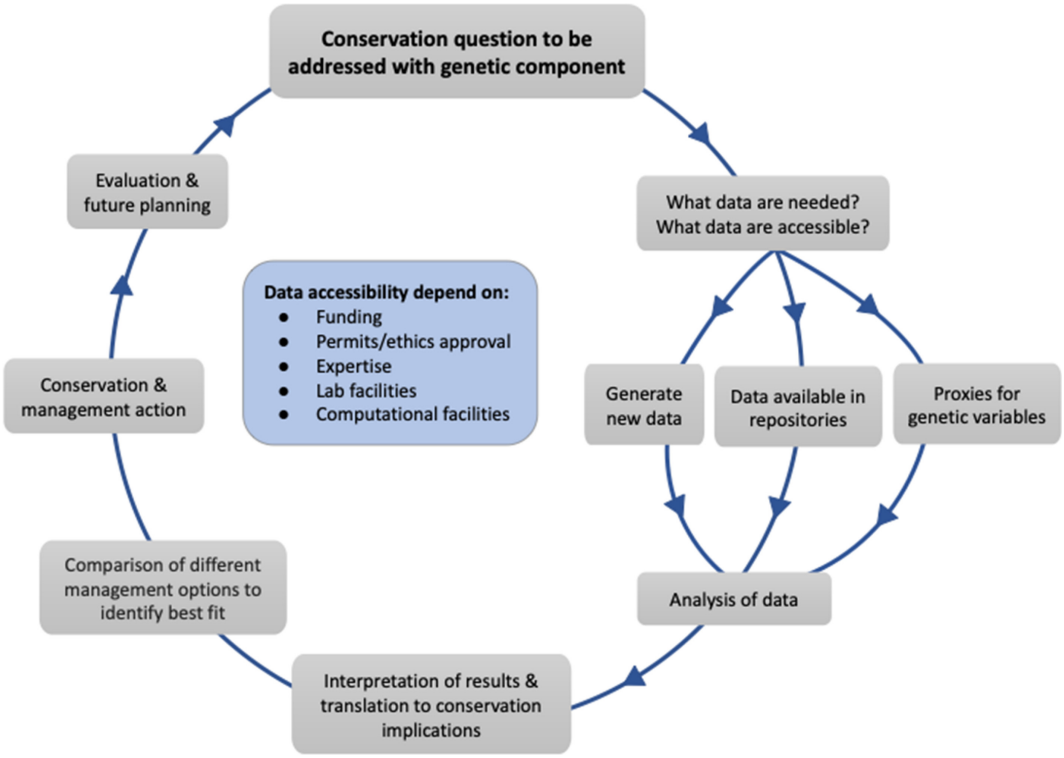

FIGURE 2 Flowchart listing decisions and considerations when integrating genetic information into conservation.

which genetic diversity is monitored. These indicators, for which actual genetic data are not a prerequisite, have been shown to be applicable in several countries and will provide information for monitoring genetic diversity (Hoban et al., 2023). Furthermore, O'Brien et al. (2022) have proposed a framework for bringing together different reporting mechanisms in a way that is suitable for all countries, including lower-income countries.

If genetic resources do already exist, for example, as publicly available data, and there is capacity to repurpose these, they may provide a good source of information to guide and support conservation decisions without requiring additional sequencing or genotyping. Many studies make genetic data available through online repositories (e.g., Genbank and NCBI). At present, the majority of publicly accessible data represents traditional genetic studies, although the number of species for which whole genome-scale data are available is steadily increasing. Traditional genetic datasets are still useful in that they may add insight to specific research questions, or enhance the utility of new datasets by building on existing baselines (Hauser et al., 2021; Nielsen et al., 2020; Saha et al., 2022; Stronen et al., 2022). A useful collaboration between genetics researchers and practitioners could be in aiding the translation of existing genomic resources, for example, data available in the scientific literature, to relevant conservation applications, or using that information to develop fit-for-purpose tools that can address on-the-ground conservation needs. Traditional genetic markers can further be used to calculate recently proposed Essential Biodiversity Variables (EBVs) for genetic composition, covering genetic diversity, genetic differentiation, inbreeding, and effective population size (*Ne*) (Hoban et al., 2022). Defining these EBVs specifically aims to improve aggregation, harmonization, and interpretation of biodiversity observations.

Finally, project teams may decide to generate new data to obtain the information necessary to address a specific research question. In the past, it has been challenging to ensure that new molecular datasets are comparable across different laboratories, or compatible with previously generated data, for example, for use in temporal monitoring or other applications. Calibration of equipment and workflows may differ between laboratories and change through time. This has been particularly challenging for microsatellite datasets, which have been widely used for conservation purposes. Genomic markers, such as SNPs, have been heralded as more consistent than traditional genetic markers; but, depending on the methods used to select, genotype, and analyze SNPs, these datasets can also vary widely (Wright et al., 2019). Compatibility issues are especially relevant for long-term genetic monitoring projects, which re-assess genetic diversity over time (i.e., multi-generational studies and historical/ancient DNA) and may alert us to changes

such as increasing inbreeding or genomic erosion (Díez-Del-Molino et al., 2018; Jensen et al., 2022). However, apart from some limited geographies (e.g., California or Sweden) and species (e.g., whales managed by the International Whaling Commission), long-term genetic monitoring is not yet widely applied to wild species (Pierson et al., 2016). This is often due to funding being sporadic and opportunistic, making long-term projects more challenging to implement and maintain. Relying on a validated panel of markers, or including overlap with a previously used marker set when designing a new panel, allows for expanding a shared baseline across countries. In addition, archiving of DNA samples and associated metadata is important for future calibration or other updates to methods. This allows conservation projects to build upon previous observations, either corroborating past results or providing new insights that can be used to change the course of action.

For many species of conservation concern, new studies build upon previously derived results and can utilize simulations to inform population changes (case studies in Figure 3 and Table S1; two worked-out examples in Boxes 1 and 2). Leveraging new technologies and the decreasing costs of genomic analysis enables comparison of results obtained with different methods and re-evaluation of previous conservation recommendations. Two case studies, with black and white rhinoceros (*Diceros bicornis* and *Ceratotherium simum*, resp.) and with Macquarie perch (*Macquaria australasica*) are described in more detail to highlight how various molecular resources have been combined to help guide conservation decisions in these species (Boxes 1 and 2).

3 | COMMUNICATION AND INTEGRATION

The integration of genetics into management plans and policy has been hampered by limited resources and suboptimal communication between geneticists and policy-makers (Cook et al., 2021; Laikre et al., 2020; Sandström

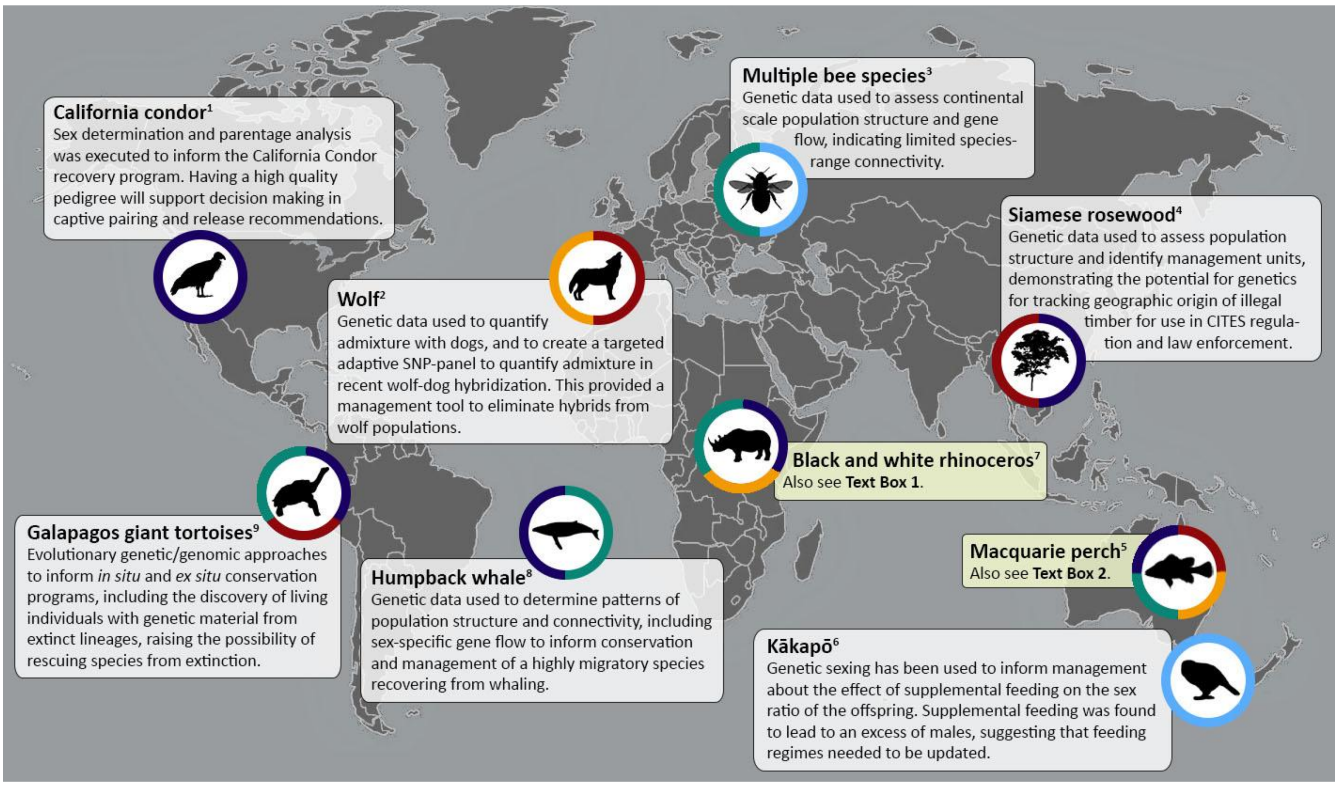

FIGURE 3 Case study examples in which conservation management is informed by genetic or genomic data (more case studies and additional details can be found in Table S1). These examples do not provide a complete review of all genetic studies executed on the species shown but rather refer to specific studies. Two cases are worked out in more detail: black and white rhinoceros (Box 1) and Macquarie perch (Box 2). Colors indicate data types: yellow, Whole Genome Sequencing (WGS); red, Reduced-Representation Sequencing (RRS); pink, Single Nucleotide Polymorphisms (SNP), dark blue, microsatellites/AFLP; light blue, nuclear sequences; green, mtDNA/chloroplast DNA (Case study references: 1: Moran et al., 2021; 2: Harmoinen et al., 2021; Smeds et al., 2021; 3: Lecocq et al., 2017; 4: Hartvig et al., 2020; 5: Pavlova et al., 2017; Lutz et al., 2021; Pavlova et al., 2022; 6: Clout et al., 2002; 7: Moodley et al., 2017; Moodley et al., 2018; Moodley et al., 2020; Sánchez-Barreiro et al., 2021; 8: Kershaw et al., 2017; 9: Poulakakis et al., 2008; Edwards et al., 2013; Jensen et al., 2015; Gaughran et al., 2018).

BOX 1 Black and white rhinoceros.

The well-documented poaching and demographic collapse of black rhinoceros (*Diceros bicornis)* has raised concern regarding the survival of the species. Despite a wide historical distribution, the black rhinoceros now survives in only five countries in Africa. Moodley et al. (2017) aimed to assess genetic variation by comparing historical and modern black rhinoceros samples in both the mtDNA (control region of 477 bp) and 11 nuclear microsatellites. The results showed a staggering loss of 69% of the species' mtDNA variation with diversity lower toward the limits of the species' range. The levels of nuclear diversity were also higher in historic samples and most ancestral lineages are now absent from the modern populations; genetically unique populations no longer exist (Nigeria, Cameroon, Chad, Eritrea, and Angola).

White rhinoceros (*Ceratotherium simum*) has a discontinuous African distribution which is limited to the extent of sub-Saharan grasslands. Both southern and northern populations have declined but the southern population has recovered. In contrast, for the northern population, only two post-reproductive females remain. Moodley et al., 2018 assessed the species' demographic history by analyzing 419 bp of the mtDNA control region for 63 individuals across the species' range. In addition, 232 individuals were genotyped for 10 microsatellites. Nuclear microsatellite diversity was low to moderate and only three mtDNA haplotypes were identified. Results showed little change in genetic diversity over time, but both populations showed a decline in effective population size. The decline of the southern population corresponded with the colonial period and the northern population showed a bottleneck during the time of the Bantu migration.

In Moodley et al. (2020), authors sequenced and annotated the first black rhinoceros genome. In addition, East African black rhinoceros and northern white rhinoceros genomes were re-sequenced and previously published data were included to investigate levels of heterozygosity. For black rhinoceros, more recent genetic contact across the Zambezi Valley between 125 and 150 KYA has been reported. At least one East African mtDNA haplotype was sampled on the southern banks of the Zambezi River and one southern African haplotype was sampled north of the Zambezi River. This result appears to be in contrast with the strong mtDNA and microsatellite (nuclear) discontinuity on either side of the Zambezi (Moodley et al., 2017). The Zambezi River may act as a barrier, but it is periodically permeable for black rhinoceros. White rhinoceros populations also came into secondary contact (100–220 KYA), which is consistent with gene flow estimates derived from microsatellite data (Moodley et al., 2018). In addition, gene flow continued long after the initial divergence and cessation of panmixia within black and white rhinoceros lineages. The expansion and contraction of habitats with glacial cycles appear to have maintained gene flow. In addition, Sánchez-Barreiro et al. (2021) presented a temporal white rhinoceros genomic data set, including 52 individuals to uncover additional patterns of population structure and within-subspecies genomic erosion.

These papers illustrate how the analysis of different markers (genetics to genomics) can help to answer questions at either a higher evolutionary level or at the phylogeographic, phylogenetic, or population level. Genome-level analysis often reveals finer scale patterns that are not observed when using mtDNA or microsatellite data, however, here, the overall patterns of diversity were supported by all marker types.

et al., 2019; Torres-Florez et al., 2018). Balanced collaborations and two-way communication between researchers, conservation practitioners, and policymakers are necessary to effectively integrate genetic information into conservation management (see e.g., Di Marco et al. (2017); Waldron et al. (2013)). We recommend improving connections for both genetics researchers and management practitioners to share relevant knowledge and resources and encouraging, or even facilitating close collaborations between stakeholders with different backgrounds. Already established initiatives can provide guidance on how such approaches can be implemented and transferred to other geographic regions. For example, in Victoria, Australia, the State government environment department, in collaboration with researchers, has developed a Genetic Risk Index (GRI) used for biodiversity management planning and investment decisions (https://www.environment.vic.gov.au/biodiversity/genetic-risk-index). The GRI applies evolutionary genetic principles to rank species in terms of the likelihood that they are experiencing loss of genetic

BOX 2 Macquarie perch.

The Macquarie perch (*Macquaria australasica*) is a freshwater fish once common and widespread through the Murray-Darling Basin of Eastern Australia, but it experienced severe population declines and isolation due to human impacts. Genetic and genomic methodologies play an important role in the conservation and management at the population level and individual level, respectively.

Pavlova et al. (2017) explored the consequences of habitat loss and fragmentation on population-level genetic diversity and future population trajectories of *M. australasica*. Using an 844 bp mtDNA fragment for 339 individuals across 17 populations and 19 microsatellites for 871 individuals from 20 populations, In combination with simulations, the authors estimated Ne across the species range, evaluated levels of genetic diversity for each population, and identified populations requiring genetic rescue/genetic restoration, as well as potential donor sources. It demonstrated that within a few decades, smaller populations are likely to suffer genetic erosion and inbreeding unless diversity is restored and maintained by translocations. Augmented gene flow was recommended as an urgent management action and subsequently adopted by the species-wide recovery plan.

The consequences of genetic augmentation were evaluated by Lutz et al. (2021) using RRS markers for the *M. australasica* population reintroduced into the Ovens River, comprising individuals originating from the genetically diverse Yarra source population and the moderately diverse Dartmouth population. For the individual-level analyses, 1679 individuals were scored for 1204 SNPs for parentage, kinship, and sibship analysis, and data for 92 individuals scored for 735 SNPs to assess individual genetic diversity and genetic dissimilarity between broodstock parents. For the population-level analyses, 564 individuals were scored for 1003 SNPs and reduced data sets were then used to calculate population structure and undertake genetic cluster assignment and hybrid analysis. Lutz et al. (2021) found that cross-type strongly predicted the survival of stocked offspring, with offspring of two Yarra parents having the highest survival and the majority of fish surviving in the Ovens River having at least one Yarra parent, despite the majority of fish originating from Dartmouth. The authors determined that, while Yarra offspring had the highest fitness, the Yarra x Dartmouth cross-type also had relatively high survival, and combining compatible stocks as part of the implementation of the recovery plan is of overall benefit to the restoration of *M. australasica*. Sex determination is an important tool for conservation and management, however, rapid sex-chromosome turnover in fish hinders the development of markers to sex-monomorphic species. Pavlova et al. (2022) used annotated genomes and RRS data (1,492,004 SNPs) for the *M. australasica* and the golden perch *M. ambigua*, and WGS of 50 *M. australasica* of each sex, to identify a sex-determination and develop an affordable sexing assay. Whereas the RRS approach yielded few sex-linked SNPs, WGS data revealed a small genomic region (146 bp) inherited in a predominantly XY fashion. A test of a molecular sexing assay targeting a SNP with a male-specific allele in the sex-linked region, and amplicon sequencing data for four Percichthyid species indicated that the *M. australasica* sexing region is species-specific and either specific to populations related to those in which it was detected or can be influenced by environment. The identification of sex-linked markers will assist practitioners in monitoring the recovery of Macquerie perch populations by providing a tool to determine genetic sex in some populations and to interpret those results in the context of other influencing factors, such as environmental conditions.

diversity likely to impact population persistence and is informed by genetic data if they are available. In the absence of genetic data, as is the case in a substantial proportion of the 1155 species initially assessed, pragmatic proxies, such as population size estimates, area of occupancy, estimated dispersal capacity, etc., are applied. In North America, genetic data have been used to identify Evolutionary Significant Units (ESUs) for purposes of applying the Endangered Species Act in Pacific salmon (*Oncorhynchus* spp) for the past 30 years (Waples, 1991). In Scotland, the first report on genetic diversity, published in 2020 by NatureScot, the statutory nature conservation body, provides a scorecard to assess the threats to genetic diversity within wild species (Hollingsworth et al., 2020). This scorecard was designed to be transferable to any country or region regardless of economic status or the

accessibility of direct genetic or genomic data for their species (O'Brien et al., 2022). Although the published scorecard uses information from molecular data, it can also be completed using assessments based on pragmatic proxies and genetic principles if genetic data are not available.

4 | A COMMUNITY EFFORT TO MOVING FORWARD

It is crucial that we, as a community, embrace the diverse contexts in which researchers and practitioners operate, improve accessibility, address inequities, and prioritize inclusivity in conservation genetics. Key points common to conservation genetic projects include data storage, accessibility, and stewardship (McCartney et al., 2021; Toczydlowski et al., 2021). Capacity-building can not only focus on the generation and interpretation of genomic data but also on the incorporation of genetic principles in the absence of genetic data. Two-way communication between the various stakeholders is crucial for connecting research questions and data to on-the-ground conservation needs (Pärli et al., 2021). This requires closing the communication gap by making the literature and datasets more broadly available, through Open Access and in a variety of languages (Karam-Gemael et al., 2018; Torres-Florez et al., 2018), consistent with FAIR (Findability, Accessibility, Interoperability, and Reusability) and CARE (Collective Benefit, Authority to control, Responsibility, Ethics) principles (Carroll et al., 2021; Wilkinson et al., 2016).

As a way forward, we suggest the following steps to facilitate the uptake of molecular data in conservation management and policy. They cover the following topics: (1) training and capacity building, (2) data generation, storage, and analysis, (3) communication, and (4) implementation.

1. *Encourage co-creation of conservation genetics projects*: Involve all relevant parties, including Indigenous Peoples and local communities, early in the project co-design phase to ensure that decisions are pragmatic and cost-effective, and partnerships are balanced and equitable, consistent with the Nagoya protocol (see also https://www.cbd.int/abs/; also see Hogg et al. (2017); Rayne et al. (2022); Taft et al. (2020); Taylor et al. (2017); Russo et al. (2023)).
2. *Develop in-person laboratory training programs*: Standardize the training program curricula, ingredient lists, and laboratory exercises for workshops that increase the adoption of genomic technology (including portable technology) and field-sequencing pipelines; strive for approaches that can be used as widely as possible; also see Watsa et al. (2020).
3. *Enhance in-country capacity for data generation*: Increase support to develop and operationalize low-cost and flexible laboratory facilities in countries or regions without established molecular biology research infrastructure: This includes (1) ensuring genetic dataset creation and data analysis can remain within the scope of in-country scientists, (2) accounting for the prohibitive costs and challenges with in-country availability of reagents, and (3) considering limited or no access to reliable cold chains; also see Ebenezer et al. (2022); Pomerantz et al. (2018).
4. *Build in-country capacity for data analysis*: Support in-country access to analysis tools, computing resources, and data storage, as well as sustainable strategies for financing these; also see Rodríguez et al. (2007); Wilson et al. (2016).
5. *Provide training in genetic concepts and theory*: Integrate foundational genetic training into curricula available to conservation practitioners and policymakers to empower their use of genetic data interpretation for management applications, especially in low- and middle-income countries, where opportunities for conservation genetics training may be limited; also see Schweizer et al. (2021).
6. *Establish central knowledge hubs for conservation genetics*: Provide "one-stop-shops" to make relevant resources findable and accessible (e.g., the webpage of the Coalition for Conservation Genetics: https://www.coalitionforconservationgenetics.org/); also see Hoban et al. (2013); Kershaw et al. (2022); Russo et al. (2023).
7. *Commit to long-term storage and availability of samples, data, and metadata*: Enable future research, consistent with both the FAIR and CARE guiding principles, with clear agreements regarding sample, data, and metadata ownership and conditions of use. Ensure data and metadata availability in public data repositories where appropriate; also see Crandall et al. (2023); Kitchener et al. (2021); Strand et al. (2020).
8. *Commit to long-term engagement across the research-policy-practice interface*: Maintain connections between researchers, policymakers, and practitioners, including Indigenous Peoples and local communities, to facilitate evaluation of conservation actions and follow-up studies; also see Cook et al. (2021); Lundmark et al. (2019); Thompson et al. (2023).
9. Develop open-access educational resources: Increase the scope and range of open-access conservation genetics resources online (e.g., recorded lectures, textbooks, field and laboratory protocols, GitHub repositories, and hands-on exercises); also see Kurelovic (2015); Roche et al. (2022).
10. *Establish platforms for networking and communication*: Connect practitioners with those who can

provide guidance, data, or access to reagents required for in-country genetic studies to address management and policy needs; also see Pärli et al. (2021); Sandström et al. (2019); Taft et al. (2020); Russo et al. (2023).

11. *Encourage communication across laboratories/institutions/countries*: Explore opportunities to align work, and increase standardization and compatibility of datasets, allowing for continuous expansion of shared baselines; also see Hindrikson et al. (2017); Taylor et al. (2017); Shaffer et al. (2022).
12. *Break down language barriers*: Ensure the availability of resources in multiple languages and make sure that communication follows mutual and inclusive principles avoiding technical jargon; Also see (Amano et al., 2016; Amano et al., 2021; Márquez & Porras, 2020; Torres-Florez et al., 2018).

5 | CONCLUSION

To facilitate the uptake of genetic considerations and serve conservation management and policy needs most pragmatically, it is important to assess the necessary molecular information and how it can be obtained most cost-effectively. Cutting-edge genomic research leads to critical new insights, as well as to the development of resources and methods that allow more precise and accurate inferences. Simultaneously, traditional genetic markers or genetic indicators provide sufficient data to address many management questions, despite the possible lack of incentives to generate and utilize these data in new academic research projects. There usually is a tradeoff between cost and precision, and practitioners may be faced with limitations related to sample availability/quality, access to genetic facilities, capacity to process and interpret the data, and compatibility issues with data collected at earlier time points or by alternative means. It is crucial that we acknowledge the local conditions and strive for broad incorporation of molecular data and concepts into policy and management decisions. Improving opportunities for communication and collaboration between genetics researchers and decision-makers is an essential component of achieving this goal. The CBD and other policy mechanisms requesting genetic diversity monitoring can also help to identify and allocate the necessary capacity-building resources and funding to support this. Failing to do so will only lead to further widening of the gap between conservation genetics and applied conservation, and risks slowing down existing initiatives to make conservation science more equitable.

AUTHOR CONTRIBUTIONS

The perspective has been initiated by LB and GS, and further developed with AB-O, FK, I-RR, AM, and PS. All authors have commented on the manuscript and been involved in reviewing.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

DATA AVAILABILITY STATEMENT

The data availability statement does not apply for this article.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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