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EDITORIAL

Advancing Species Conservation and Management Through Omics Tools

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Received: 30 April 2025 | **Accepted:** 2 May 2025

Handling Editor: Shawn R Narum

1 | Introduction

The conservation of biological resources has become a priority worldwide, exacerbated by the negative effects of a growing human population and related impacts on the structure, function and composition of ecosystems. A plethora of species and populations across terrestrial, freshwater and marine environments are experiencing reductions in population sizes, some of which are more susceptible to demographic and genetic stochasticity than others (Exposito-Alonso et al. 2022). The era of omics has inspired thought-provoking possibilities in the field of conservation biology. Access to and application of large-scale omics datasets (e.g., genomics, epigenomics, transcriptomics, proteomics, metabolomics, metagenomics) can shed novel insights on and resolve aspects of wildlife species biology and demography relevant to conservation assessments, management actions and monitoring (Allendorf et al. 2010; Schweizer et al. 2021; Zamudio 2023). The compilation and analysis of omics datasets can also inform management strategies for threatened wild and captive populations by, for example, identifying genetically vulnerable populations, adaptive loci, or uncovering interactions between host and symbiotic microbiota. These approaches contribute to a better understanding of local adaptation, introgression, inbreeding depression and genetic mechanisms of disease susceptibility and resistance. To this extent, the use of omics data to maximise effective actions for conservation and management is critical, particularly for species on the verge of extinction.

Halting climate change and the ongoing anthropogenic pressures that impact biodiversity is mandatory to curb the extinction crisis, but the loss of species and populations requires additional novel approaches for their conservation and management. To this end, the Special Issue 'Advancing species conservation and management through omics tools' was launched to bring attention to scientists interested in demonstrating how innovative techniques are useful to safeguard and manage biodiversity. In this editorial, we highlight how omics tools can help preserve biological diversity across space and time and across a wide range of biodiversity, encompassing authors from across the globe (Figure 1). Topics in this Special Issue include conservation surveys using genomics, epigenomics, metagenomics, transcriptomics, the development of computational models, novel pipelines related to best practices for sampling design and wet lab procedures, as well as genomic resources for wildlife species and their applicability to guide conservation and management strategies. Overall, our special issue provides a timely collection of research across broad themes that expand the application of omics tools across the tree of life. In doing so, we not only showcase contemporary development of the field but also provide an opportunity for engagement with stakeholders interested in using these tools and the associated knowledge to enhance biodiversity conservation and management.

2 | Reduced Representation Genome Approaches Supporting Conservation Science

Reduced representation genome sequencing (RRS) has been a popular approach to help inform and guide conservation and management programmes for wild and commercial species for

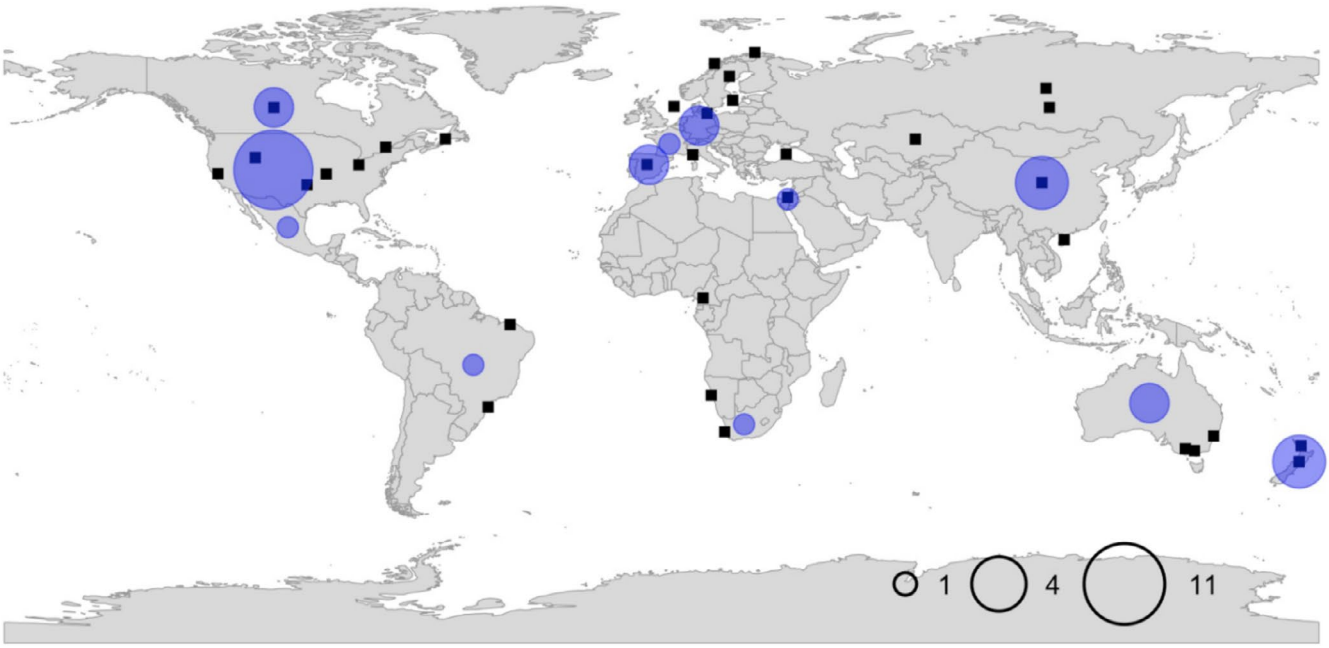

FIGURE 1 | Map showing the geographical distribution of affiliations of first authors (purple circles). The black squares indicate locations from which samples were collected and analysed for studies contributing to this Special Issue.

some time (Allendorf 2010; Narum et al. 2013), including species experiencing population declines. One of the advantages of using reduced genome sequencing (compared to molecular datasets using a handful of markers) pertains to obtaining accurate population genetic parameters. As accuracy of genetic parameters is sampling-dependent, attempts to identify rules of thumb for high-throughput sequencing data have been investigated (Aguirre-Liguori et al. 2023; Nazareno et al. 2017; Nugent et al. 2023; Scaketti et al. 2025). In this issue, Aguirre-Liguori et al. (2023) investigated the effects of sampling (i.e., number of individuals, populations, molecular markers) on genetic offsets for populations facing climate change. By identifying genetic-environmental associations for loci putatively under selection derived from high-throughput sequencing methods, Aguirre-Liguori et al. (2023) highlighted that the number of populations, rather than individuals, may be prioritised in studies predicting maladaptation to climate change. Besides the effects of sample size and number of markers, Nugent et al. (2023) evaluated the sensitivity of nuclear markers with distinct polymorphism levels in detecting admixture in Atlantic salmon. Applying the result that the number of SNP markers rather than the number of individuals matters and Nugent et al. (2023) designed an informative SNP panel to aid Atlantic salmon conservation actions. Informative SNP panels were also developed to inventory and monitor genetic diversity in brook trout (Mamoozadeh et al. 2023) and to inform fisheries management strategies for two commercial fish species in the southern Atlantic (Forde et al. 2023). Genomic resources to investigate evolutionary processes and to help assist effective conservation and management programmes for threatened animal and plant species were also developed (Madeira et al. 2023; Morales-González et al. 2023). Mimicking the allelic frequencies of remaining populations of the threatened Iberian lynx on simulated populations, Morales-González et al. (2023) compared distinct genomic coancestry matrices to identify the most accurate relatedness estimator that maximises genetic diversity and reduces inbreeding. Remarkably, Morales-González et al. (2023) highlighted the importance of creating putative evolutionary scenarios to establish long-term conservation programmes. Leveraging simulations to inform population genomics, Madeira et al. (2023) integrated their SNP dataset with oceanographic simulations to expand and improve current knowledge of mangrove connectivity and dispersal to guide marine conservation planning. Flamio Jr. et al. (2023) utilised ddRADseq to produce a novel genomic reference for polyploid pallid sturgeon, whose genetic integrity is under threat through hybridisation with shovelnose sturgeon. Through the identification of SNPs with alleles unique to each species, Flamio Jr. et al. (2023) were able to more robustly identify between the two sturgeon species and their hybrids in two management units. Moving from population to individual-based landscape genomics was the subject of Chambers et al. (2023), who provided a conservation-based perspective on individual-based sampling, whilst introducing a novel R package, ALGATR, to support researchers interested in landscape genomic analyses.

3 | The Expansion and Application of Whole Genome Sequencing

The broadening accessibility of high-throughput technologies (although there remains unequal access globally; Carneiro et al. 2025; von der Heyden 2023) has considerably advanced the transition from single markers to RRS to whole genome sequencing (WGS) (Allendorf 2010; Fuentes-Pardo and Ruzzante 2017) and allowed novel insights to address species conservation. In this special issue, a number of contributions used WGS to support species conservation. Dodge et al. (2023) assembled the genomes of the only two skink species listed as 'Extinct in the Wild' to support initiatives such as conservation reintroductions. Importantly, the authors were able to

infer an XY sex determination system for one of the species and showed high levels of heterozygosity. However, there was also evidence of recent inbreeding, which likely originated prior to the captive breeding programme aimed at maintaining viable populations of both skink species. Through comparisons of male and female genomes of the 'Vulnerable' stitchbird (also known as hihi), Bailey et al. (2023) identified the hihi W chromosome, thus contributing to broadening the genomic resources for this bird, as well as supporting future research into identifying inbreeding dynamics and adaptive potential. Jiang et al. (2023) generated genomes for 10 fungi species in the genus *Ganoderma*, including 224 individuals from a range of ecoregions. These data resulted in a better understanding of the phylogenetic and evolutionary dynamics of *Ganoderma*, provided additional insights into chromosome numbers and revealed widespread genomic introgression, with potential impacts on the synthesis of secondary metabolites. Focussing on the white mangrove, a successful pioneer species that has been extensively utilised for mangrove restoration, Zhu et al. (2023) showed that *Laguncularia*, to which the white mangrove belongs, originated during a period of global warming and that the genome is characterised by numerous tandem gene duplications. There were also signals of adaptive evolution in gene regions associated with salt stress resistance and nitrogen transport, which may underpin the ability of white mangroves to outcompete other mangrove species. Importantly, the availability of a genome, whether annotated or not, can raise additional questions, particularly at the population level. Wold et al. (2023) focussed on the 'Critically Endangered' kākāpō and utilised six approaches for the discovery of structural variants (SVs), where they showed that measures of SV such as count and size distribution differed between each of the SV discovery tools. Further, the data showed both intra and inter-generational differences in the mean number of SVs, suggesting that realising the power of WGS and SVs will entail further considerations and development of the method. Finally, high coverage WGS may be prohibitively expensive depending on the research environment. Therefore, Watowich et al. (2023) investigated the accuracy of low coverage WGS (with reference to available panels) and showed that associated genotypes could calculate genetic relatedness and population genetic structure with high accuracy, thus highlighting the potential of low coverage WGS for generating large data sets including for nonmodel species. Within the context of minimising sequencing costs, pooling multiple individuals for sequencing provides a viable alternative to sequencing individual samples (Schlötterer et al. 2014). However, analyses of pooled sequences (pool-seq) can be challenging. In this issue, Willis et al. (2023) update a popular pipeline for working with pool-seq data or indexed DNA samples, provide an applied example of the strength of pool-seq data and highlight how PoolParty2 is complementary to other bioinformatic resources.

4 | Epigenomic, Transcriptomic and Methylome Approaches

Genomic variation extends beyond sequence variation to the functionality of the genome via epigenomics and transcription. Environmental changes, including diet, toxins and abiotic factors, can influence epigenetic characteristics such as CpG methylation and histone modifications, resulting in changes to gene expression and thus phenotype (Ballard et al. 2024). Epigenomics and its consequent effects on variation in gene expression (transcriptomics) are, therefore, key mechanisms by which physiological plasticity and variation can manifest beyond genomic DNA variation, and in some cases, these processes can be passed from one generation to the next (Kronholm and Collins 2015).

Because epigenomic variation can drive phenotypic variation, and thus facilitate phenotypic plasticity in response to environmental pressures, species that have very low genetic variation may have the capacity to respond and persist in a changing environment. These patterns have been proposed to explain the success of bottlenecked invasive species (e.g., Marin et al. 2020). Within threatened species, the degree to which epigenomic resilience can prevent extinction by compensating for low genetic adaptive potential is a promising new line of enquiry in omics research. Williams et al. (2023) investigated these relationships in plants, using experimental lines of four threatened species of *Leavenworthia*, under variable watering treatments, and by examining a range of phenotypic traits alongside whole-genome DNA methylation data. They found that species varied in methylation and phenotypic responses to the environmental stressor, with variation potentially driven by species range size. Williams et al. (2023) conclude that these data add an important dimension to the assessment of species and population extinction risks and conservation prioritisation. Between species, epigenomics can be used to characterise essential life-history traits informative for population management. An example is the study of lifespan, because ageing and DNA methylation are correlated (e.g., Wilkinson et al. 2021). In fish, lifespan can vary through several orders of magnitude, up to 400 years, and despite this parameter being an essential variable in biodiversity monitoring and designing sustainable fisheries programmes, lifespan is poorly estimated for many species. Budd et al. (2023) used epigenomic analysis to improve the lifespan estimates for 442 fish species. A model incorporating genomic CpG density data was strongly predictive of species' lifespan, providing an essential tool for estimating this key demographic parameter. Furthermore, Venney et al. (2023) explored the effects of captive rearing on the methylome in Atlantic salmon and reported considerable sex-specific effects of hatchery rearing and few epigenetic changes due to parental hatchery rearing that persisted in the F1 offspring. These results suggest minimal epigenetic inheritance and rapid loss of epigenetic changes associated with hatchery rearing, an observation that has a number of implications for captive rearing for conservation efforts.

Transcriptomic variation in natural populations can also inform biological responses of species to environmental change. For example, variation in responsiveness to disease, extreme weather events, habitat variables or toxins can inform species' resilience, or lack thereof, in the face of escalating anthropogenic threats. Keagy et al. (2023) provide an overview of the theory, mechanisms, hypotheses and methods for constructively exploring these processes in real-world biodiversity settings. Through a balanced appraisal of challenges and opportunities, options and constraints, the review and examples provide a road map for landscape transcriptomics for measuring and understanding

biodiversity. A unique example, which also demonstrates a key technical advancement, is the use of formalin-fixed paraffin-embedded (FFPE) archival samples for investigating wildlife disease, as reported by Miller et al. (2023). The authors successfully conducted transcriptomic analysis from such difficult samples and found differential expression associated with an unknown pathology in lampreys, alongside clear-sighted recommendations for the use of similar samples in future studies, greatly widening the potential of such work.

5 | Museomics and Other Historical Approaches

Genomic sampling of wild populations allows the monitoring of biodiversity for conservation, and the testing of historical biogeographical hypotheses that have influenced the origin, distribution and maintenance of biodiversity. Using a whole-genome data set, Celemín et al. (2023) reconstructed the postglacial demographic history and clarified levels of diversity, inbreeding and divergence for subspecies and populations of the North Atlantic harbour porpoise. They also used a seascape genomics approach to assess how environmental heterogeneity (including the strong salinity gradient in the Baltic Sea) impacted the adaptive divergence of populations. Their findings have implications for the conservation management of both endangered and critically endangered populations of this small species of cetacean.

Genomic studies of contemporary wild populations and DNA databases can benefit from incorporating genomic time series obtained from specimens in natural history collections (NHCs). Museums and NHCs are a powerful source of material to directly examine evolutionary change and to improve the application of DNA databases for biodiversity monitoring and conservation. Clark et al. (2023) reviewed the literature on temporal genomics, focusing on studies that measured evolutionary responses to anthropogenic pressures in the past 200 years. The authors discussed best practices related to sampling design, marker choice, statistical and analytical power for studies of temporal genomics. With the goal of utilising NHCs for rapid generation of reference databases, Dopheide et al. (2023) developed a sensitive and efficient laboratory and bioinformatic approach to process 100 s of invertebrate specimens simultaneously. The method recovered full-length or partial COI barcodes even from NHC specimens that produced low-yield DNA and no visible PCR bands. Their taxonomy-informed pipeline is expected to help develop databases to support regional and national biodiversity surveys.

6 | Methodological Advances and New Analytical Tools in Conservation Omics Research

In this section, we highlight methodological advances and new analytical tools (e.g., software, scripts, pipelines) developed to obtain and analyse high-throughput sequencing data. The optimisation of lab-wet procedures and protocols has been reported as best practices and recommendations, facilitating the acquisition of reliable omics data. Taking into account the variation among sequencing platforms (e.g., throughput, cost and read length), species uniqueness (e.g., genome size and content), levels of genome representativeness (i.e., reduced or whole genome sequencing) and their associated techniques (e.g., GBS, RADseq, ddRADseq), further studies are still needed to reduce sequencing costs and enhance sequencing data quality. In this special issue, best practices and recommendations to improve genomic library quality were reported by Lajmi et al. (2023) and López et al. (2023). For instance, López et al. (2023) performed in silico digestion analyses using multiple restriction enzymes and species, stressing that enzyme choice is study goals dependent to obtain high-quality sequencing data. In a similar study, Lajmi et al. (2023) analyse diverse datasets from the literature and carry out controlled experiments to understand the effects of enzyme choice and size selection on sequencing efficiency. Lajmi et al. (2023) also report the user-friendly webtool ddgRADer to assist experimental design while optimising sequencing efficiency. Through the novel package vcfpop, Huang et al. (2023) provide solutions when working with polyploid organisms, such as plants that include analyses of Bayesian clustering, parentage analyses and analyses of molecularvariation. As the movement of species is impacted by barriers, both natural and anthropogenic, it becomes important to model resistance to dispersal to help inform conservation decisions. Vanhove & Launey (2023) adapted and tested a gradient forest model (resGF) allowing for multiple environmental predicators to generate maps of gene flow across landscapes and showed that resGF can be applied across different marker types.

Best-practice recommendations for genetic studies of noninvasive samples (gNIS) were reported by Arantes et al. (2023). They highlighted the potential of using gNIS for large-scale genetic monitoring based on SNPs and demonstrated how to improve control over genomic library preparation. However, large datasets can be computationally challenging to analyse; Chi et al. (2023) provide a solution through FastHaN, a novel programme for constructing haplotype networks from large datasets that is up to 5800 times faster than other haplotype network reconstruction software.

A set of analytical tools was developed to analyse reduced and whole genome sequencing data. Robledo-Ruiz et al. (2023) presented new R functions to identify and separate sex-linked loci and infer the genetic sex of individuals based on these loci for two bird and one mammal species, with the authors emphasising that these R functions would enhance confident results for a minimum sample size of 15 known-sex individuals of each sex. Further, Baerwald et al. (2023) developed a CRISPR-based assay following noninvasive swabs of Chinook salmon mucous, to distinguish with high accuracy between different runs of fish. Notably, this method can be deployed in-field and has a rapid turnaround of <1 h, thus facilitating biomonitoring.

7 | Molecular Diet Analysis

The development of molecular technology also significantly contributes to dietary analysis of wild animals. Shi et al. (2023) explored the utility of microhaplotypes for DNA mixture analysis in the diet of Chinook salmon. They found that mock DNA mixtures of up to 10 smolts that had been predated by salmon could reliably be resolved using microhaplotypes, and that increasing the molecular marker panel size would likely facilitate the identification of more individuals. However, the authors also indicated that poor and variable DNA quality prevented accurate genotyping and abundance estimation. Dick et al. (2023) assessed the effects

of prey ration size, predator species and temperature on digestion rates by feeding two rations of Chinook salmon to two piscivorous fish species. They found that all three measures influenced digestion rate, and that metabarcoding and qPCR methods can identify prey after much longer digestion than visual methods. These studies demonstrate the increasing application of molecular methods in fine-resolution diet composition analysis and that genome-based metabarcoding studies will provide more comprehensive and efficient insights into the diet and food web of wild animals.

8 | The Importance of Curation—From Samples to Data

One of the most crucial aspects of any type of omics or ecological work is the reporting of the provenance of samples, how these were obtained and the resulting workflow around these samples. For example, the Genomic Observatories Metadatabase (GeOMe) was developed to easily integrate spatiotemporal context of samples utilised for generating genetic data (Deck et al. 2017), given that many studies do not report even basic geospatial data. In this issue, Vaughan et al. (2023) examined associated metadata of 199 whole genome assemblies for 89 invasive species and found that for 47 assemblies, there was no reporting of spatial data. Of assemblies that derived from field-collected data, only 27 provided location data, noting that missing field data can seriously impact the invasion biology.

9 | Some Final Perspectives on Omics and Species Conservation

This special issue highlights a wide variety of omics tools and applications within the context of conservation of wild species and their populations. Although by no means exhaustive, the research collated within this issue provides an overview to researchers and decision-makers alike to realise the integration between omics research and conservation and showcases how omics tools can support conservation and management efforts globally. This includes strengthening accessibility to ensure equitable access to research infrastructure. For this issue, the majority of contributions came from the global north, with a minority of papers from Africa and South America (New Zealand and Australia were relatively well represented), a pattern that has been mirrored elsewhere (Carneiro et al. 2025). Addressing challenges associated with this divide in research is beyond the scope of this issue, but numerous colleagues provide perspectives and solutions (Beheregaray 2008; Carneiro et al. 2025; Hirsch et al. 2024; von der Heyden 2023). Finally, while we present a broad swathe of methods and tools to help guide conservation and management programmes, these were still limited to only a few taxa. As such, extending applicability and increasing the number of species is necessary to better understand and safeguard species uniqueness, particularly under increasing anthropogenic and climate change pressures.

Acknowledgements

We thank Tiaan Engelbrecht for helping with the map and the EICs of Molecular Ecology Resources for hosting the special issue.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

No data availability statement needed for editorial.

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