Harmonising genomics research excellence and stakeholder needs in conservation management

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Abstract

Biodiversity resilience relies on genetic diversity, which sustains the persistence and evolutionary potential of organisms in dynamic ecosystems. Genomics is a powerful tool for estimating genome-wide genetic diversity, offering precise and accurate estimates of the status and trajectory of genetic diversity within species and populations. However, the widespread integration of genomic information into biodiversity conservation and management efforts faces challenges due to a lack of standardised genome-wide data generation methods and applications. The heterogeneity of approaches can make it difficult to consistently interpret the results and clearly communicate key information to stakeholders such as practitioners and decision-makers. To begin to address these challenges, the European Reference Genome Atlas (ERGA) promotes the standardisation of methodologies for high-quality reference genome sequencing and analysis as part of the global network of the Earth BioGenome Project. ERGA is also proactively developing best practices to engage stakeholders in biodiversity genomics research, starting with examining case studies and conducting mapping efforts to familiarise researchers with pathways to effective engagement. An emerging theme is the researchers' experience of variable perceptions amongst stakeholders of the value and utility of reference genomes and genomics data in biodiversity conservation and management. Addressing this issue calls for consensus on standardised genome-wide data generation methods and applications that will help to deliver the highest standards for accuracy, interpretability, and comparability. We believe converging on consensus methods standardisation is essential for fostering the stakeholder trust and confidence required to successfully promote widespread adoption of genome-wide genetic diversity assessments in biodiversity conservation and management.

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Running title

Genetic Diversity: Standards and Stakeholders

Abstract

Biodiversity resilience relies on genetic diversity, which sustains the persistence and evolutionary potential of organisms in dynamic ecosystems. Genomics is a powerful tool for estimating genome-wide genetic diversity, offering precise and accurate estimates of the status and trajectory of genetic diversity within species and

populations. However, the widespread integration of genomic information into biodiversity conservation and management efforts faces challenges due to a lack of standardised genome-wide data generation methods and applications. The heterogeneity of approaches can make it difficult to consistently interpret the results and clearly communicate key information to stakeholders such as practitioners and decision-makers. To begin to address these challenges, the European Reference Genome Atlas (ERGA) promotes the standardisation of methodologies for high-quality reference genome sequencing and analysis as part of the global network of the Earth BioGenome Project. ERGA is also proactively developing best practices to engage stakeholders in biodiversity genomics research, starting with examining case studies and conducting mapping efforts to familiarise researchers with pathways to effective engagement. An emerging theme is the researchers' experience of variable perceptions amongst stakeholders of the value and utility of reference genomes and genomics data in biodiversity conservation and management. Addressing this issue calls for consensus on standardised genome-wide data generation methods and applications that will help to deliver the highest standards for accuracy, interpretability, and comparability. We believe converging on consensus methods standardisation is essential for fostering the stakeholder trust and confidence required to successfully promote widespread adoption of genome-wide genetic diversity assessments in biodiversity conservation and management.

Keywords

biodiversity genomics; conservation genomics; genome-wide genetic diversity; methods standardisation; reference genomes; stakeholder engagement

1. Introduction

Genetic diversity is central to species resilience and adaptability, playing a crucial role in enabling organisms to respond to environmental changes and anthropogenic pressures, as well as determining their evolutionary potential for long-term survival and adaptability within dynamic ecosystems (Kardos et al., 2023; Kardos & Luikart, 2021). Being able to assess genetic diversity is therefore an essential requirement for building informed strategies for conservation and management of biodiversity and ecosystem services. Several direct and indirect methods can be employed to assess genetic diversity. However, high levels of accuracy and precision, as well as true comparability across assessments, can only be achieved through the analysis of genome-wide data at the population level. This approach combining reference quality genome assemblies with **whole genome re-sequencing (WGS)** data, which we refer to as the assessment of **genome-wide genetic diversity** , can substantially enhance the resolution and accuracy of evidence available to practitioners and other stakeholders to inform the development of practical biodiversity conservation applications (Fuentes-Pardo & Ruzzante, 2017; Hogg, 2024). Despite the many opportunities offered by using WGS data, the integration of genomic information into conservation efforts to study genetic diversity within and between species, or conservation genomics, faces many challenges. Some of these include the costs involved, the need for specialised expert knowledge, and the difficulties of interpreting and communicating results to stakeholders (Cook et al., 2023; Shafer et al., 2015). Efforts to integrate genomics data are further hampered by the lack of standardised procedures for data generation, processing, and analysis on the one hand, and the regional disparities in access to genomics resources and technologies on the other (Gomez-Cabrero et al., 2014; Mulder et al., 2017). This means that working towards achieving the highest standards for accuracy, interpretability, and comparability could further widen the feasibility gap for adoption and implementation in resource-limited regions (Wilson et al., 2016). Beyond practical considerations, the priorities and preferred approaches of different scientific and stakeholder communities also often vary (Grill, 2021; Taylor et al., 2017), which further complicates the standardised integration of genomic information to achieve common conservation and management objectives. Routes to address these challenges must be sought to enable the widespread and effective use of WGS data within global biodiversity research and conservation management frameworks. While researchers have an important role to play especially on the methodological and technological side, to fully succeed it is also essential to engage with stakeholders effectively to co-develop pathways to achieve meaningful genomics data integration. Stakeholders are people or organisations who affect or are affected

by species conservation and management decisions. These may include policymakers, conservationists, natural site managers, non-governmental organisations, landowners, farmers, environment agencies, the general public or other entities. A chequered history of stakeholder engagement provides both positive and negative foundations on which to build fruitful interactions, but an important first step for researchers is to recognise the importance of understanding stakeholder needs and limitations to be able to effectively communicate the value of integrating standardised genomics approaches in applied species conservation and management (Bateman & Balmford, 2023; Supple & Shapiro, 2018). Key to the success of stakeholder engagement and the integration of genomic information is to first build consensus within the scientific community on harmonised genomics research standards and best practices. Promoting broadly standardised and validated genomics methodologies to define a unified approach to genomics data across the scientific community could substantially advance the acceptance of genomics and its application by stakeholders, especially policymakers. Recognising this, the international community of researchers driving **reference genome** generation for eukaryotic biodiversity, connected through the**Earth BioGenome Project (EBP)** , has been building consensus on standards for reference resources (Lawniczak et al., 2022; Lewin et al., 2018). Regional initiatives that form part of the EBP network, including the **African BioGenome Project (AfricaBP)** (Ebenezer et al., 2022), Australia's **Threatened Species Initiative (TSI)** (Hogg et al., 2022) and the **European Reference Genome Atlas (ERGA)** (Mazzoni et al., 2023) bring diversity of experience to the consensus building process. This community-driven agreement on reference genome resources and standards greatly facilitates communicating their importance and utility to stakeholders. However, despite increasing recognition by the scientific community (Formenti et al., 2022; Hogg, 2024; Theissinger et al., 2023), when it comes to genetic diversity assessments the necessary advances are yet to be achieved. To begin to address these needs, we start by outlining the aspirations and practicalities of employing genome-wide genetic diversity assessments for within-species monitoring. Next we examine how standards support the production and use of reference genomes and contrast this with the status of community consensus on standards for the production and use of WGS data in biodiversity research and conservation management. This appraisal is supported by reviewing the context of key barriers that need to be overcome to achieve the standardisation necessary for proper integration and widespread deployment of genome-wide genetic diversity assessments. Finally, we explore the landscape of stakeholder engagement with applied genomics research using results from a workshop and interviews mapping stakeholders involved in biodiversity conservation research projects from several European countries. While it is clear that many challenges arise from the heterogeneity of methods, data, approaches, resources, and other factors, community consensus on standards is urgently required to improve alignments of biodiversity genomics research with real-world conservation demands and stakeholder needs.

2 Genome-wide genetic diversity for within-species monitoring

At the Conference of the Parties (COP) to the Convention on Biological Diversity (CBD), the importance of maintaining genetic diversity within and between populations was recognised and emphasised as being critical for species adaptability and survival (COP 15, 2022). Complementing other biodiversity data, building a comprehensive understanding of species genetic information is key to monitoring and understanding biodiversity, which can be leveraged for species conservation and management (DeWoody et al., 2021; Hogg, 2024; Lewin et al., 2018; Mazzoni et al., 2023; Supple & Shapiro, 2018; Theissinger et al., 2023), as well as for sustainable **bioeconomy** (D'Amato et al., 2020; Huddart et al., 2022) and **biosecurity** applications (Glidden et al., 2021; Marselle et al., 2021; Robinson et al., 2024). A variety of direct and indirect methods can be employed to assess genetic diversity, however, comprehensive within-species genetic monitoring requires reference genome assemblies with WGS data for genome-wide genetic diversity assessments.

2.1 Genomics informs collation of Essential Biodiversity Variables

To monitor biodiversity changes, the CBD endorses two levels of metric abstraction: Essential Biodiversity Variables (EBVs) and Biodiversity Indicators. EBVs are direct interpretations of scientific or observational data, presented in a harmonised, standardised, and scalable manner (Pereira et al., 2013). Biodiversity Indicators, derived from EBVs, are designed to be intuitive and widely understood measures that form the basis of consistent species and ecosystem monitoring. A subset of EBVs is dedicated to capturing spatial and temporal variability in intraspecific genetic composition, i.e. measuring the status and trajectory of genetic diversity within species. The Group on Earth Observations Biodiversity Observation Network (GEO BON) has proposed four genetic composition EBVs: (i) intraspecific genetic diversity, (ii) genetic differentiation, (iii) effective population size (N_e), and (iv) inbreeding. The group's technical descriptions and feasibility assessments of these genetic EBVs acknowledge the increasing importance of DNA-based data for deriving accurate estimates (Hoban et al., 2022). Proposed improvements to overcome the limitations of the current genetic diversity goals and targets also advocate tracking the number of populations or species being monitored with DNA-based methods (Hoban, Bruford, et al., 2023). Nevertheless, concerns have been raised about how the lack of standardisation and scalability of various genetic and genomic approaches impact the feasibility of widespread employment of DNA-based methods for collating genetic EBVs. Recent progress has been made in integrating genetic composition EBVs into the CBD's Global Biodiversity Framework (GBF) goals and targets, albeit with the incorporation to date of only a limited set of Biodiversity Indicators (Hoban, Bruford, et al., 2023). These include the headline indicator focused on N_e as an indirect measure of genetic diversity monitoring, specifically the proportion of populations within species with an effective population size greater than 500. This headline indicator is supported by the complementary indicator focused on species demography as an indirect measure of population differentiation, specifically the proportion of distinct populations maintained within species. These key indicator proxies for genetic diversity and differentiation, respectively, can be estimated using various non-DNA-based methods. While these methods can provide temporally informative data at a local level (e.g. through changes in N_e of a certain population measured with the same proxies), true genetic diversity and population differentiation levels can only be accurately measured through DNA data analysis. DNA-based metrics can be estimated using data from single loci to entire genomes, where the marker type and density typically depend on specific research questions and available resources. As technologies have advanced, approaches for accessing genetic content and estimating genetic diversity have evolved over time (**Figure 1**). Regardless of the sequencing method and number of markers employed, the use of reference genomes increases accuracy and reproducibility for DNA-based estimates (Anilkumar et al., 2023). Used as universal points of comparison for each species, reference genomes serve as critical benchmarks in genetic composition analysis: the common backbone onto which population-derived DNA marker data are mapped. However, while marker-derived data across sparse genomic regions can be informative for estimating several measures of genetic diversity, genome-wide genetic diversity screening is needed to study genetic variation at fine-scale resolution (e.g. for current levels of inbreeding), as well as for understanding the demographic and evolutionary forces shaping the observed variation (Suchačková Bartoňová et al., 2023; Sundell et al., 2023; Van Der Valk et al., 2024).

2.2 Genome-wide data offer key advantages over proxies or markers

The full potential of WGS data can be exploited when anchored on chromosome-level genome assemblies for accurate and comprehensive estimations of genetic indices. First, by capturing the complete genetic variation along the genome, WGS approaches provide a detailed account of the evolutionary variance underlying every estimate, and take advantage of the large amount of data to deliver precise and accurate estimates. Second, using genome-wide data enables the incorporation of linkage disequilibrium as a property to estimate genetic indices, such asN_e or runs of homozygosity (RoH, useful for inbreeding estimations), and to understand and estimate phenomena that leave regional/local signatures on the genome and are outliers when compared to the genome-wide norm, such as selection or introgression (Allendorf et al., 2024; Gargiulo et al., 2024). An important outcome of these two key advantages of using genome-wide data is that the resulting genetic composition EBV estimates are much more comparable across species. For instance, heterozygosity within

a population can serve as a valuable metric for estimatingN_e, which is essential for assessing the threat of genetic drift in small populations and the associated extinction risk - a key factor influencing management prioritisations (Hoban, Da Silva, et al., 2023; Waples, 2022; Willi et al., 2020).N_e also determines the efficacy of positive natural selection, influencing the ability of a species to respond to environmental changes (Charlesworth, 2009; Flanagan et al., 2018). Therefore, species with reduced N_e are often associated with an increased risk of inbreeding depression (Duntsch et al., 2023; Ruiz-Lopez et al., 2012). WGS approaches have the advantage of accurately and precisely estimating inbreeding in species without known pedigrees (Hedrick & Garcia-Dorado, 2016; Kardos et al., 2015), thereby increasing their applicability for near-inaccessible species like those present in underwater habitats (Kardos et al., 2023). Genome-wide data can also help identify the genetic basis of inbreeding depression (Kardos et al., 2016), which can improve the implementation of genetic rescue plans (Fitzpatrick et al., 2020). Beyond nucleotide-based variation, genome-wide genetic diversity can provide insights into more complex variation, such as structural variants, which can be manifested as variations in copy number (deletions, insertions, and duplications), orientation (inversions) or chromosomal position (translocations) (Bhati et al., 2023; Lee et al., 2023). In addition, WGS data can answer important questions about the molecular basis of qualitative and quantitative traits that remain largely unresolved. These questions include analysing gene interactions (epistasis; (Carre et al., 2024)) as well as connections among genomes of other species inhabiting the same ecosystem (community genomics; (Bernatchez et al., 2024)). Studying genome-wide genetic diversity also enables powerful assessments of local adaptation (Hoban et al., 2016; Sang et al., 2022). In addition, between-population genome-wide genetic diversity helps determine species and population boundaries, quantifying differentiation that is crucial for developing conservation strategies and defining conservation units (Coates et al., 2018; Lehnert et al., 2023; Pearman et al., 2024). Taken together, the advantages offered by genome-wide data and reference genomes provide compelling arguments for the integration of such genomic information into conservation management efforts to study genetic diversity within and between species. Increased access to genome-wide genetic diversity estimates should also extend future integrated analyses of genetic diversity data with ecological and environmental data for characterising key trends impacting how species respond to environmental changes and anthropogenic pressures (**Figure 1**). This will form the foundation for building informed strategies for conservation and management of biodiversity and ecosystem services that respond to real-world conservation demands and stakeholder needs.

2.3 Bioeconomy and biosecurity also benefit from genome-wide approaches

The **One Health** framework, which emphasises the links between human, animal, and environmental health, highlights the importance of incorporating genomics approaches in protecting human health and wellbeing (Marselle et al., 2021; Urban et al., 2023). In this context it is important to recognise that beyond conservation management applications, genome-wide approaches are equally relevant to the bioeconomy and biosecurity sectors. Understanding the genetic diversity of populations and species can guide the sustainable management of natural resources, including fisheries, forestry, agriculture, and management of wild carnivorous populations (Andersson et al., 2024; Aronsson et al., 2023). For example, knowledge of the genetic basis of desired phenotypic traits, including biomass and resistance to pathogens, can be used for genomics-informed breeding and selection programmes (Norman et al., 2018). Similarly, in the context of biosecurity and disease, having access to genome-wide genetic diversity data could help understand how species evolve and adapt to pathogen pressures, providing valuable insights into transmission dynamics and resistance mechanisms (Alves et al., 2022; Hessenauer et al., 2020; O'Hanlon et al., 2018). Planetary changes driven by human activities are greatly affecting global infectious disease distribution and prevalence (Nova et al., 2022), with potentially devastating consequences for many species of direct bioeconomic relevance and more broadly for key ecosystem services providers. Considering such applications of genome-wide genetic diversity monitoring and assessments beyond species of conservation concern substantially broadens the variety of potential stakeholders. This diversity cannot be ignored when building strategies to effectively communicate the value of integrating standardised genomics approaches in applied species conservation and management.

3 Consensus methods and standards advance science and enhance confidence

3.1 Reference genome methods standardisation is promoting their production and use

Recent advances in long-read sequencing and assembly scaffolding technologies have substantially enhanced the scale and quality of data production for reference genome generation (Li & Durbin, 2024; Marx, 2023). Consequently, chromosome-scale reference genomes are now becoming the standard for studies aiming to understand genome structure and organisation, as well as species and population genetics and evolution (Blaxter et al., 2022; Formenti et al., 2022; Theissinger et al., 2023). In response to these new technologies and decreasing costs, numerous reference genome initiatives have been established that focus on target species from different taxonomic groups or geographical regions. Collectively they contribute to the EBP's "moonshot" effort for biology (Lewin et al., 2018), to build reference genome resources for the vast majority of eukaryotic organisms that are currently not represented in public genome repositories (Stephan et al., 2022). As part of the global EBP network of reference genome projects, this scientific community exemplifies how large international collaborative efforts can work towards consensus to establish standards and best practices for producing high-quality reference genomes (Lewin et al., 2022). Through the EBP community work coordinated by five technical standards committees, reference genome methods standardisation has converged on common best practices and recommendations for all stages of production, from sampling to sequencing and assembly through to deposition in open international data repositories (Lawniczak et al., 2022). For example, quantitative assembly standards include achieving the highest quality assemblies with an error rate of less than 1/10,000, megabase N50 contig continuity, and chromosome-scale N50 scaffolding (N50: half of the genome is assembled in contigs or scaffolds of length N50 or more). The practical importance of standards - the use of existing ones and the development of new ones where needed - was recently highlighted through the ERGA Pilot Project's implementation of a decentralised approach for the large-scale production of reference genomes (Mc Cartney et al., 2023). ERGA's work on standards has continued through the**Biodiversity Genomics Europe (BGE)** project, supported by the European Union's Horizon Europe programme for research and innovation. Developing and promoting such standards is essential to build community consensus. This needs to go hand in hand in providing guidance on how to achieve them, for example through training platforms like the ERGA Knowledge Hub (ERGA Knowledge Hub, 2024). In the face of changing technologies and methods, such standards are not immutable, however, setting standards provides a clear target towards which the community can aim. This encourages streamlining and standardisation of the best practices, combinations of methods, and quality control procedures, that mostly routinely enable the attainment of the high-quality target standards. In the field of reference genome generation, community efforts towards defining consensus methods and standards are promoting the scaled-up production and use of chromosome-scale reference genome assemblies.

3.2 Genetic diversity assessments would benefit from enhanced methods standardisation

Genetic diversity assessment approaches in conservation management have a long-standing history that started with the introduction of allozymes in the early 1970s (Prakash et al., 1969). These markers enabled researchers to analyse genetic variation and relatedness among individuals, informing species conservation and management decisions (Allendorf, 2017). The advent of genomics and next-generation sequencing technologies has revolutionised conservation practices relying on genetic data. Estimates that were once based on only a few genetic loci are now made with millions of markers across the whole genome (Allendorf, 2017; McMahon et al., 2014; Supple & Shapiro, 2018). These technological advances have provided conservation biologists with unprecedented accuracy and precision in understanding the genetic makeup of populations, identifying adaptive genetic variations, and detecting subtle evolutionary changes over time (Hogg et al.,

2022; Supple & Shapiro, 2018). Furthermore, data that support establishing correlations between variation along the genome and environmental parameters and/or adaptive phenotypes enable the prediction of future evolutionary gaps and identify means to mitigate them (Capblancq et al., 2020; Ferreira et al., 2023; Hoste et al., 2024; Razgour et al., 2019; Waldvogel et al., 2020). Combining WGS data with high-quality reference genomes is empowering researchers to examine genetic diversity at an ever finer scale and providing precise estimates of population health, crucial for effective management (Hogg et al., 2022; Shafer et al., 2015; Supple & Shapiro, 2018). Despite these advances in technologies and methods for DNA-based approaches, several challenges remain to be overcome to achieve community consensus on methods and standards, which are necessary to advance the science and enhance stakeholder confidence. The main challenges arise from the variety of sampling strategies, library preparation protocols, and sequencing techniques used, the different degrees to which the whole genome is represented by the data, the variable consistency of analysis stringencies applied, and the potential biases these and other variables may each introduce (Hoban et al., 2016; Lachance & Tishkoff, 2013; Meirmans, 2015; Schmidt et al., 2024). Techniques that target subsets of the entire genome, such as medium- to high-density single nucleotide polymorphism (SNP) panels (Helyar et al., 2011) or reduced representation sequencing techniques like restriction site-associated DNA (RAD) sequencing (Baird et al., 2008), are not designed to detect fine-scale genomic variation. These methods provide an incomplete picture of the genetic landscape and introduce substantial heterogeneity across studies due to variations in choices of molecular laboratory techniques, the specific genomic regions being targeted, and variable approaches to circumvent analytical challenges (Cariou et al., 2016; Davey et al., 2011, 2013; Shafer et al., 2017). Alternative low-coverage whole genome sequencing (lcWGS) approaches have gained popularity for their cost-effectiveness and potential to provide meaningful data (Lou et al., 2021). However, when read depths are too low to confidently call individual genotypes, lcWGS requires specialised analysis tools to account for genotype uncertainty. Additionally, the sequencing effort distribution design, number of samples, and per-sample sequencing depths all affect the accuracy of estimating genetic diversity, linkage disequilibrium, and allele frequency, as well as detecting population structure and signatures of selection. This variety of DNA-based approaches to conduct genetic diversity assessments contributes to the difficulties of consistently interpreting the results and clearly communicating key information to stakeholders (Taylor et al., 2017). Community consensus on methods standardisation is therefore essential for accurate and comparable applied population genomics studies to deliver results that can meaningfully inform conservation and management actions. Focusing on approaches that use WGS data to assess genome-wide genetic diversity offers an effective means to reduce heterogeneity across studies and establish robust frameworks for obtaining comparable indices of population health and status. When properly implemented, WGS approaches can be robust to different technologies, library preparations, and other methodological variations, whereas achieving similar robustness with other DNA-based methods is much more challenging. Consensus standards on analysis best practices are equally critical, from the perspective of research scientists but also considering practitioners and other stakeholders to ensure translatability into applied actions (Hogg, 2024; Hogg et al., 2022). This should include working towards a common understanding of how to best take advantage of machine learning and artificial intelligence (AI) approaches to exploit the high dimensional input data for accurate population genetics inferences (Korfmann et al., 2023; Schrider & Kern, 2018; Van Oosterhout, 2024). Converging on consensus community standards also needs to consider the importance of providing training and guidance on how to achieve them, for example through platforms like the TSI's Applied Conservation Genomics Hub (TSI Applied Conservation Genomics Hub, 2024). Notwithstanding other important barriers to standardisation in applied research (**Box 1**), in the same manner as for the field of reference genome generation, defining scientific community consensus on methods and standards will greatly promote the scaled-up production and use of WGS data for genome-wide genetic diversity assessments.

4 ERGA stakeholder mapping workshop: first steps towards engagement

Expanding and improving the scope of genomics research in biodiversity conservation requires involving relevant stakeholders and rights holders (Leventon et al., 2016; Segelbacher et al., 2022; Supple & Shapiro, 2018). This involves the cooperative participation of local communities, policymakers, and scientists in conservation efforts to ensure their effectiveness and sustainability (Reed, 2008). Such collaborative approaches are designed to align conservation objectives with socio-economic interests and generate a sense of ownership and responsibility (Skarlatidou et al., 2019; Sterling et al., 2017). Additionally, inclusive stakeholder engagement can lead to more accurate and context-specific solutions to biodiversity challenges that enhance ecosystem resilience (Cumming et al., 2022; Reed et al., 2009; Spooner et al., 2021). When the ERGA Citizen Science Committee launched its stakeholder identification survey in 2022, biodiversity genomics researchers missed crucial information about their potential stakeholders. The survey collected responses from researchers across Europe and revealed that identifying and involving relevant stakeholders remains a substantial challenge, which prevents the establishment of effective relationships between researchers and stakeholders. This highlighted the need to continue efforts to map and engage stakeholders to build pathways towards comprehensive and meaningful involvement. The survey also revealed that some scientists currently perceive the idea of imposing a requirement of stakeholder participation in their research projects as a burden rather than an opportunity. This highlighted the need for training within the ERGA community on the importance of stakeholder engagement, starting by providing tools to recognise and map stakeholders according to guidelines in the BiodivERsA Stakeholder Engagement Handbook (Durham et al., 2014). This is the initial phase of building a conceptual framework for best practices for stakeholder engagement in biodiversity genomics. It will include interviews with stakeholders from various sectors, such as politics, industry, practitioners, local communities, and citizens. The final phase of the project will involve developing a comprehensive plan to describe clear pathways to effective stakeholder participation throughout the research process. Here we present our approach to the initial phase of how to recognise and map relevant stakeholders for biodiversity genomics research through a stakeholders mapping workshop involving researchers from across Europe.

4.1 Materials and methods

As part of the development of the distributed genomics infrastructure supporting reference genome generation for the ERGA community, the ERGA Citizen Science Committee, in collaboration with the ERGA Pilot Project (Mc Cartney et al., 2023) and members of the BGE Project, organised a workshop aimed at strengthening researchers' capacities to recognise relevant stakeholders. The online workshop involved 39 researchers participating in the ERGA Pilot Project with a broad geographical representation covering 23 European countries. The goals were to identify, prioritise, and map international, national, and local stakeholders involved in or potentially interested in their biodiversity genomics research projects. During the workshop, participants were randomly assigned to six groups, each with a dedicated mediator, in order to foster interactions and discussions in smaller groups and promote the collection of opinions and ideas. Each group was presented with instructions for completing the three main goals: first, to identify stakeholders and stakeholder groups potentially interested in their projects; second, to prioritise the relevant stakeholders by their perceived interest and influence with respect to their projects; and third, to map the stakeholders by their interests and influence, as well as local, regional, and international dimensions. To prioritise putative engagement actions, during the online stakeholder mapping workshop participants wrote the names of identified stakeholder groups on virtual stickers. They then placed them in one of four categories based on their perceived influence and interest levels. The categories and the stakeholder identification stages are described in the BiodivERsA Stakeholder Engagement Handbook (Durham et al., 2014), summarised here as: *Involve* , High influence and low interest - keep these stakeholders adequately informed and maintain regular contact to ensure no major issues arise; *Inform* , Low influence and low interest - monitor these stakeholders and keep them regularly updated as needed, tailoring communications to meet their needs;*Collaborate* , High influence and high interest - essential stakeholders that must be fully engaged, enlist their full help, create

partnerships, galvanise support for the project, and keep them satisfied; *Consult* , High interest and low influence - provide these stakeholders with enough information and interaction to keep them updated and address their concerns, but avoid overwhelming them with too much information. This exercise aimed to encourage the participating researchers to consider not only what categories of stakeholders and stakeholder groups might potentially be interested in their research projects, but also to begin to consider how engagement priorities and strategies could differ depending on the perceived influence and interest levels of different stakeholders. Following the workshop, each mediator prepared a summary report detailing the main points of discussion and comments collected from the participants, as well as a list of identified stakeholders mapped during the workshop and the prioritisation categories to which they were assigned (*Involve* , *Inform* , *Collaborate* ,*Consult*). Data were then aggregated into a single dataset for analysis, and the mediators further categorised the list of stakeholders by *Class* and by *Country status* , based on the following criteria: *Class* - *Citizens nonprofit* denotes nonprofit organisations that engage with the public, including community groups, citizen science organisations, and local community associations;*Industry* - private sector companies involved in relevant industries, such as biotech firms, environmental consultancies, and agricultural companies; *Protected areas* - organisations that manage or oversee protected natural areas, such as national parks, marine protected areas, and nature reserves; *Public institution* - government agencies or public bodies involved in environmental management, scientific research, and policy-making, including environmental protection agencies and public research institutes;*Research communities* - collaborative groups composed of multiple research entities, such as universities, research institutes, and other scientific organisations working together on common projects; *Zoo aquarium* - zoos, aquariums, botanical gardens, and other facilities that manage living collections of animals and plants for conservation, research, and public education purposes; and for *Country status* -*Strengthening countries* or *Widening countries* , based on the EU country designations as part of the strategy for widening participation and spreading excellence, with stakeholder groups being assigned to the country where they are based or officially registered. This allowed for the testing (χ-squared tests) of associations between *Country status* and *Class* , as well as further explorations of potential associations with pairwise comparisons between *Country status* and each *Class* conducted using two-proportion z-tests. Data analyses were performed using R*v.4.4.1* (R Core Team, 2024).

4.2 Results and discussion

In total, the workshop activities resulted in the successful identification and mapping of 384 stakeholders (Additional File 1). After categorisation by the mediators by *Class* and by*Country status* there remained 283 stakeholders in the dataset for analysis as 101 were identified as international bodies and therefore could not be assigned to a specific country. While the excluded stakeholders represent important organisations in the landscape of relevant bodies to consider for comprehensive mapping, here the focus was on national-level stakeholders to be able to compare across countries. Across the categories, there were 167 stakeholders from 12 Strengthening countries and 116 from 11 Widening countries, with the majority of both Strengthening (59%) and Widening (53%) countries being classed as public institutions (**Figure 2**). This predominance may be explained by the familiarity of researchers with public institutions as a result of their frequent interactions and collaborations with them. These interactions and collaborations are often an integral part of the research process. It follows therefore to suppose that researcher awareness or familiarity with other stakeholder classes is much lower, which emphasises the utility of activities that strengthen researchers' capacities to recognise relevant stakeholders. For four of the six classes, the numbers and proportions of identified stakeholders were greatest for Strengthening countries, while for the classes *Protected areas* and *Zoo aquariums* there were more identified in Widening countries (**Figure 2**), with a statistically significant association between *Country status* and*Class* ($\mathrm{df} = 5$, $N = 283$: $\mathrm{Z} = 15.71$, $p = 0.007$). Pairwise comparisons showed a significantly higher proportion of the two classes with more stakeholders in Widening countries compared to Strengthening countries - *Protected areas* ($\mathrm{Z} = -2.38$, $p = 0.018$) and *Zoo aquarium* ($\mathrm{Z} = -2.95$, $p = 0.003$). No significant differences were found for the remaining classes (*Citizens nonprofit* : $\mathrm{Z} = 0.95$, $p = 0.340$; *Public institution* : $\mathrm{Z} = 1.12$, $p= 0.260$; *Industry* : $\mathrm{Z} = 0.74$,$p = 0.460$; *Research community* : $\mathrm{Z} = 0.72$, $p = 0.470$). The higher proportion of *Protected areas* and *Zoo aquariums* with more stakeholders in

Widening countries can be attributed to several factors. Firstly, Widening countries often feature biodiversity hotspots, regions with exceptionally high levels of species diversity and endemism. Researchers may therefore be more likely to consider bodies such as natural parks protecting these unique ecosystems as relevant stakeholders for their projects. Secondly, Widening countries may prioritise conservation efforts as part of their development strategies, recognising the ecological, economic (e.g. tourism), and social value of their natural resources, which leads to increased researcher engagement with or knowledge of stakeholders focused on conservation. The process of interactively grouping stakeholders based on their perceived influence and interest levels into four stage categories (*Inform* , *Consult* , *Collaborate* , and *Involve*) stimulated discussions that prompted participants to evaluate how they recognise and prioritise relevant stakeholders. Across all 384 identified stakeholders, the largest groups were *Inform* (31%) and *Collaborate* (30%) and the smallest group was *Consult* (15%), with *Involve* accounting for 24%. When considering only national stakeholders the proportions remained almost identical, with 30% for *Inform* and *Collaborate* , 15% for *Consult* , and 25% for *Involve* (**Figure 3**). Unlike the categorisations of stakeholders by *Class* , there was no statistically significant association between *Country status* and stage category, and there were no statistically significant differences between Strengthening and Widening countries for any of the four stage categories. Discussions during the categorisation process revealed that stakeholders could be grouped into different stage categories depending on the current status of their research projects. This fluidity suggests that stakeholders' roles can evolve as projects progress, for example transitioning from *Involve* (high influence and low interest) to *Collaborate* (high influence and high interest) when the project has succeeded in generating more tangible results. Another important point that was raised repeatedly with respect to assessing a stakeholder's interest level was the highly variable perception of the value and utility of reference genomes and WGS data in conservation and biodiversity management. Participants described how they noted a growing positive consideration of the importance of genetic diversity assessments. However, they also recognised a disconnection between this and the perceived relevance of genome-wide genetic diversity assessments amongst practitioners. Taken together, these quantitative and qualitative observations, based on input from 39 researchers representing 23 European countries considering 384 identified national and transnational stakeholders, suggest a need for additional efforts that aim to improve researcher-stakeholder interactions. On the one hand, researcher awareness of and capacity to recognise relevant stakeholders in biodiversity genomics is an area that would benefit from further development. On the other hand, a demystification of genomics-based approaches to applied conservation and management would help to foster wider and more meaningful stakeholder engagement. In this regard, developing and promoting community-consensus standardised and validated genomics methodologies for assessing genome-wide genetic diversity could substantially advance the integration of genomic information in the conservation and management of biodiversity and ecosystem services.

5 Case studies of stakeholder engagement in biodiversity genomics

To provide concrete examples of how stakeholder engagement and genomics data integration can enhance conservation efforts, we conducted interviews with representatives of three research projects. These case studies highlight the practical challenges and successes of applying genomics to conservation and management, in partnership with stakeholders. They demonstrate the value of collaboration between researchers and various stakeholders, including conservation organisations, citizen scientists, and policymakers. Through the sharing of their experiences, these case studies illustrate how genomic insights can inform conservation strategies, influence policy decisions, and support biodiversity management. The following summaries detail the goals, methodologies, and outcomes of these projects emphasising the role of genomics and stakeholder engagement in advancing conservation efforts.

5.1 Genomic insights for fungal conservation

Project goals and methodology: Sweden is home to some 5300 fungal species identified in forests (Knutsson et al., 2020). Despite protection programmes for some fungi, their genetic diversity is not thoroughly explored, and genomics data are not yet integrated into their conservation efforts. This project used reference genomes and WGS data to understand population structure and inform three specific conservation programmes, including contributions to red list assessments. The Swedish Species Information Centre (SSIC) served as a key stakeholder, collaborating with local county administrations responsible for implementing the conservation measures. The project involved generating high-quality reference genomes and sequencing multiple samples from three species of conservation concern. To achieve a broad geographical sampling of the analysed species, citizen scientists were engaged, providing valuable contributions to the collection process. Despite challenges in DNA extraction, the study successfully applied population genomics methods (principal component analysis - PCA, Admixture) to characterise population structure. The results highlighted a spectrum of diversity among fungal species, ranging from distinct taxa to intraspecific diversity. These diversity level assessments are essential for future conservation efforts.**Importance of genomics and stakeholder engagement:** The project used genomics due to its efficiency in resolving population structure in relation to monitored distributions of the selected target species. Genomics can provide a comprehensive picture of genetic diversity, essential for understanding population structure and informing conservation strategies, where comprehensive coverage, accuracy, and long-term value make it the preferred method. A total of approximately 100 samples were analysed per species. The Science for Life Laboratory (SciLifeLab) conducted the genomics work, ensuring high-quality data through standardised protocols and repeated extractions. Obtaining high quality and quantity of DNA and RNA from different samples such as annual fleshy fruit bodies and perentail thicker fruit bodies was challenging due to the presence of secondary compounds and a rich community of associated bacteria, fungi, and algae. SciLifeLab's expertise was invaluable in overcoming these difficulties, producing near-chromosome-level assemblies for all three species using the tools and standards advocated by the EBP. The possibility for extensive method development and testing to optimise extractions was critical for producing reliable data and allowed for the standardisation of genomics methodologies across different species. Assembly and annotation were performed by the National Bioinformatics Infrastructure Sweden (NBIS), following community standards to ensure high-quality results. Stakeholder engagement was a key component of the project, involving non-academic partners such as the SSIC, county boards, and citizen scientists. The stakeholders initiated the species selection and sampling design, asking the questions they needed genomic information for, and SciLifeLab produced the necessary data. This collaboration allowed stakeholders to contribute valuable field knowledge, conduct sample collection, and work with researchers to interpret genomics data for conservation strategies. Because the initiative comes from the stakeholders, the collaboration can influence policy decisions and will eventually support Swedish Red List updates and species action programmes. The project demonstrated the effectiveness of WGS in conservation genomics as well as the importance of adapting extraction protocols to allow for standardising sequencing and assembly methodologies to obtain high-quality data. For fungi, and many other groups, obtaining high-quality DNA and RNA extracts for chromosome-level assemblies is a substantial challenge. Due to their complex biological structures and life processes, many fungi present unique challenges in obtaining sufficient DNA compared to other eukaryotes. Highlighting this aspect is crucial for advancing genomics research across all eukaryotes.

5.2 Genomic research on Swiss butterflies

Project goals and methodology: Switzerland is home to over 200 butterfly species, yet their cryptic diversity remains largely unexplored. This project used WGS data to identify the evolutionary relationships of putative cryptic species that are often labelled as distinct subspecies, and to potentially resolve them. This research, important for the upcoming Swiss butterfly book that is a community-based not-for-profit effort of Swiss lepidopterists, involved sequencing approximately 200 individuals across seven species complexes to perform population genomics inferences. Despite challenges in balancing the number of pairs and individuals, the study successfully applied population genomics methods (PCA and Admixture) to characterise gene flow and population structure. The results highlighted a spectrum of diversity among cryptic species, ranging

from distinct taxa to intraspecific diversity and postglacial lineages, but also highlighted that further studies are needed beyond the Swiss scale (e.g. for the*Phengaris alcon /P. rebeli* complex (Lucek et al., 2024). These diversity level assessments are essential for future conservation efforts and for revising the Swiss Red List in collaboration with national stakeholders. The researchers' experience underscores the importance of standardising genomics methodologies to ensure reliable data. Standardisation is critical in conservation genomics, where various techniques compete. The interviewed researcher emphasised that while many in the scientific community advocate for different methods, WGS remains the most reliable technique. This is due to its comprehensive coverage, accuracy, and long-term value. This point was stressed in the interview, highlighting that stakeholders and policymakers prefer a single, straightforward approach over a multitude of options. This simplifies decision-making processes and enhances research outcomes. This preference aligns with the project's choice to focus on WGS, which has become more cost-effective and less labour-intensive with advancements in sequencing technologies.**Importance of genomics and stakeholder engagement:** The project focused on genomics due to its ability to resolve taxonomic issues that traditional barcoding and other genetic resources could not. Previous studies, e.g. (Litman et al., 2018). revealed barcoding limitations, which may be resolved with low-density genomics data (Jospin et al., 2023), but only between strongly divergent lineages. This prompted the shift to WGS, which offers higher resolution and more comprehensive data. In this context, benefits from the use of genomics include a better understanding of cryptic biodiversity, enhanced data quality, and future-proofing the data for further research. However, challenges such as financial constraints, computational needs, and limited analytical support were addressed by outsourcing library preparation to standardised centres. In addition, they were addressed by using standardised data processing pipelines. Stakeholder engagement was integral, involving hobbyists, museums, consultants, and cantonal offices. Their collaboration contributed substantially by providing valuable field knowledge, facilitating the application of genomics data through species background and interpretation for conservation strategies, and influencing policy decisions. This was exemplified by the recognition of newly identified species and Red List updates, e.g.*Erebia bubastis,* (Jospin et al., 2023). This partnership demonstrated the effectiveness of standardised genomics methods in conservation genomics. It underscored the importance of continued efforts to promote such practices for transnational biodiversity conservation. Additionally, the researcher noted evolving attitudes within the scientific community, where younger generations and international collaborators recognise the value of genomics data. This shift suggests a growing acceptance of standardised genomics approaches. This could further enhance the integration of comprehensive genomic data into conservation efforts globally.

5.3 Genomic insights into aspen adaptation

Project goals and methodology: This project investigates the genetic adaptation of aspen (*Populus tremula*) in Sweden and Norway. To gain new insights, transects running from north-to-south and east-to-west were sampled. Following previous work, this study examines adaptations to varying environmental factors, such as day length and temperature. A primary aim of the project is to identify genetic variation contributing to these adaptations using Genome-Wide Association Studies (GWAS) to understand the adaptive potential of aspen trees to future climate conditions. While having only limited economic value, aspen plays a key role in biodiversity and ecosystem services, supporting various insect communities. This ecological role makes the findings crucial for informing conservation efforts. Population genetics data enables a holistic understanding of the ecosystem by studying the interaction of tree genotype and the hosted insect populations within a Planetary Biology framework. Generating a reference genome was essential for this study. To generate the reference genome, whole genome sequencing methods including PacBio and optical mapping were used, while population re-sequencing was performed using Illumina short-read data. The expertise of the SciLifeLab was essential to the success of all stages of the project. The main challenges faced were ensuring high-quality DNA extraction and sufficient sequencing depth. Overall, the genomics data provided understanding of population structure and adaptation mechanisms, and provided actionable insights for conservation and biodiversity management.**Importance of genomics and stakeholder engagement:** Whole genome re-sequencing data were used as this offers extensive possibilities and is relatively

easy to generate. Moreover, genomics approaches provide a deeper understanding of genetic adaptations and biodiversity, which traditional methods cannot achieve. However, the use of whole genome data presented practical challenges, such as data storage, computational complexity, managing metadata, and ensuring data accessibility. Despite these challenges, genomics data offered invaluable insights into the species. The demand for genomics data in the project was initially driven by purely basic research interests. The National Institute for Tree Breeding (Skogforsk) was the main stakeholder, who provided practical insights and helped implement and maintain the field trials comprising all genotypes that were re-sequenced. Skogforsk also faced very practical challenges, such as dealing with moose in field settings, which informed the experimental approaches. Stakeholder engagement was crucial throughout the project.

6 Discussion

A comprehensive understanding of species genetic composition is essential to monitor and understand biodiversity, complementing other biodiversity biomonitoring data for integrated and effective species conservation and management. Assessments of genetic diversity are performed using a variety of direct and indirect methods. However, the heterogeneity of methods, data, approaches, resources, and other factors, can make it difficult to consistently interpret the results and clearly communicate key information to stakeholders. As set out above, the advantages offered by using reference genomes and genome-wide data for genetic diversity assessments provide compelling arguments for the widespread integration of such genomic information into biodiversity conservation and management efforts. Community consensus on methods and standards can greatly advance biodiversity research and enhance stakeholder confidence, through promoting the scaled-up production and use of WGS data for genome-wide genetic diversity assessments. Consensus on standardised genome-wide data generation methods and applications will help to build a framework that supports achieving the highest standards for accuracy, interpretability, and comparability. This process comes with several challenges, such as responding to changing technologies and methodologies, but particularly with respect to overcoming barriers to the adoption and implementation of standardised best practices worldwide. Nevertheless, demonstrating to stakeholders that the research community is converging on standardised genome-wide genetic diversity assessments is a key step towards fostering trust and confidence to promote widespread adoption. In this regard, initiating stakeholder mapping efforts such as those presented here through the work of the ERGA Citizen Science Committee is important for the establishment of effective relationships between researchers and stakeholders. As well as highlighting several common concerns amongst researchers and some differences across the 23 European countries involved, an emerging theme was the researchers' experience of variable perceptions amongst stakeholders of the value and utility of reference genomes and WGS data in conservation and biodiversity management. The three presented case studies on fungi, butterflies, and trees therefore likely represent the positive end of the perception spectrum, as they each highlight how effective stakeholder engagement and genomics data integration can enhance conservation and management efforts. Altogether, we conclude that researchers have an important task ahead to address methods standardisation for genome-wide genetic diversity assessments, and that to achieve widespread adoption, enhanced engagement with stakeholders is necessary to co-develop pathways for the meaningful integration of genomics data in biodiversity conservation and management.

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1 Conflict of interest

BOX 1. Achieving standardisation in applied research requires overcoming barriers

Research community consensus is required to achieve the necessary methods and technology standardisation that would facilitate proper integration and widespread deployment of genome-wide genetic diversity assessments for within-species monitoring. However, the success of the integration of genomic information and meaningful stakeholder engagement further depends on taking into account additional barriers to achieving standardisation in applications research worldwide (Wilson et al., 2016). Building a framework that supports achieving the highest standards for accuracy, interpretability, and comparability must therefore also seek routes to overcome barriers to their adoption and implementation in resource-limited regions.

Access to genomics data needs to be more evenly distributed

Standardising conservation genomics data generation methods and applications is challenging due to the uneven distribution of access to genomics data worldwide. Particularly in resource-limited regions, access to and the ability to generate comprehensive genomics data are often severely limited, resulting in an incomplete understanding of global biodiversity. This imbalance in the availability of genomics data limits efforts to identify and protect threatened species and genetically distinct populations, which is essential for developing standardised conservation management strategies (Pearman et al., 2024). The implementation of universal standards and methodologies to enhance accuracy and comparability will be near-impossible without support for equitable access to genomics resources and the means to generate them. Open access to data archived at public repositories like the European Nucleotide Archive (Yuan et al., 2024) provide the means to share and use relevant genomics datasets like reference genomes and WGS data. However, not all produced data are archived in such repositories, and the use or reuse of public datasets is complicated by the lack of standardised methods and reporting (metadata) for data generation. To begin to address these disparities, international collaborations and funding initiatives must prioritise enhanced access to and local ability to generate data in underrepresented regions. Robust biodiversity genomics data analyses require access to consistent and high-quality data from diverse geographical and ecological contexts. Advancing methods standardisation and reporting is therefore needed to improve access to genomics data and abilities to contribute to data production, promoting an equitable distribution that reduces barriers to achieving standardisation in applied research on genetic diversity.

Communication needs strengthening to maximise impact and reach

Clear communication of conservation genomics endeavours and outcomes is challenging, and when it fails it can lead to misunderstandings and biases in stakeholder and public perception. Constructive stakeholder engagement is needed as the research community builds consensus on methods and technology standardisation for genome-wide genetic diversity assessments, and for this to be effective clear communication is essential (Kadykalo et al., 2020). The numerous different DNA-based genetics or genomics techniques used in biomonitoring can easily cause confusion to non-specialist researchers, stakeholders, or laypersons (Garner et al., 2016). For example, one common source of confusion is the misunderstanding of the resolution of different techniques, i.e. between species identification through DNA barcoding, or community species characterisation through DNA metabarcoding, and assessments of within-species genetic diversity through RAD sequencing, lcWGS, or WGS approaches. Species identification and community characterisation for biomonitoring are essential for observations data collection efforts that support large-scale modelling of species

distributions across time and space, however, there are inherent limits to the extended application of such data for population genetics that could lead to false expectations and incorrect inferences (Couton et al., 2023). These and other misconceptions can hamper public and stakeholder understanding of the distinct and complementary roles each different method plays in biodiversity conservation and management. Effective scientific mediation is therefore an important tool that cannot be ignored, especially when communicating with policymakers to inform decision-making and resource allocation. Professional science communicators and accessible communication strategies can bridge the gap between complex genomics-based approaches and practical conservation policies. Ensuring that the nuances and specific applications of different techniques are clearly understood and easily distinguishable will help to achieve standardisation in applications research worldwide.

Glossary

African BioGenome Project (AfricaBP): this initiative is a coordinated pan-African effort to build capacity and infrastructure to generate, analyse, and deploy genomics data for the improvement and sustainable use of biodiversity and agriculture across Africa (Ebenezer et al., 2022).**Biodiversity Genomics Europe (BGE):** this project is a joint effort of two genomics communities: iBOL Europe, which focuses on DNA barcoding, and the European Reference Genome Atlas (ERGA), which focuses on genome sequencing, collectively aiming to accelerate the use of genomic science to enhance understanding of biodiversity (https://biodiversitygenomics.eu/).**Bioeconomy:** a concept at the policy and industry levels that entails the usage of renewable biological resources from land and sea, like crops, forests, fish, animals, and microorganisms, to produce food, materials, and energy (D'Amato et al. 2020).**Biosecurity:** a concept that encompasses the policy and regulatory frameworks that analyse and manage risk in the sectors of food safety, animal and plant life and health, including associated environmental risks, as well as mitigation and prevention strategies.**CARE principles:** the acronym stands for Collective Benefit, Authority to Control, Responsibility, and Ethics, a set of principles aiming to address concerns related to protecting the rights and interests of people and the purpose of data to ensure equitable outcomes (Carroll et al., 2020).**Earth BioGenome Project (EBP):** an international initiative that aims to coordinate global efforts to sequence, catalogue, and characterise reference-quality genomes of all of Earth's eukaryotic biodiversity (Lewin et al., 2018).**Effective population size (N_e)** : in population genetics, N_e measures the number of individuals in a population who contribute offspring to the next generation, with values often far lower than the number of individuals (census size), and is crucial in determining the level of variability in a population and the effectiveness of selection relative to drift (Charlesworth, 2009).**European Reference Genome Atlas (ERGA):** a pan-European scientific community of experts in genome sequencing and analysis that aims to coordinate the generation of reference-quality genomes for all eukaryotic species in Europe (Mazzoni et al., 2023).**FAIR principles:** the acronym stands for Findability, Accessibility, Interoperability, and Reuse, a set of principles used to assess the capacity of computational systems to find, access, interoperate, and reuse data with no or minimal human intervention (Wilkinson et al., 2016).**Genome-wide genetic diversity:** the total diversity (or variation) found across the entire genome of a species, encompassing all types of genetic variations, including single nucleotide polymorphisms (SNPs), insertions and deletions (indels), copy number variations, and structural variants.**One Health:** a concept centred on an approach that recognises that human, animal, plant, and ecosystem health are inextricably interconnected and because of this, should be sustainably balanced and optimised (Marselle et al., 2021).**Reference genome:** the digital representation of the complete DNA sequence of a species, typically obtained from assembling contiguous sequences produced by long-read technologies into complete, high-quality chromosome-level genome assemblies (Li & Durbin, 2024; Marx, 2023).**Strengthening countries:** European Union member states and countries associated to the Horizon Europe Programme designated as well-performing in research and innovation indicators, generally characterised by stronger research institutional frameworks and support.**Threatened Species Initiative (TSI):** Australia's national project to improve conservation practices through the use of cutting-edge genomics technology and advanced computational biology to transform the way the conservation

industry manages wildlife recovery programs (Hogg et al., 2022).**Whole-genome re-sequencing (WGS):** the sequencing of an individual's entire genome content to identify genetic variation by comparing it to a reference genome, ranging from single nucleotide polymorphisms (SNPs), to insertions, deletions, and copy number variations (Bentley, 2006).**Widening countries:** European Union member states and countries associated to the Horizon Europe Programme designated as under-performing in research and innovation indicators, generally characterised by weaker research institutional frameworks and support.

References

Allendorf, F. W. (2017). Genetics and the conservation of natural populations: Allozymes to genomes. *Molecular Ecology* ,*26* (2), 420–430. https://doi.org/10.1111/mec.13948Allendorf, F. W., Hössjer, O., & Ryman, N. (2024). What does effective population size tell us about loss of allelic variation? *Evolutionary Applications* , *17* (6), e13733. https://doi.org/10.1111/eva.13733Alves, J. M., Carneiro, M., Day, J. P., Welch, J. J., Duckworth, J. A., Cox, T. E., Letnic, M., Strive, T., Ferrand, N., & Jiggins, F. M. (2022). A single introduction of wild rabbits triggered the biological invasion of Australia.*Proceedings of the National Academy of Sciences* , *119* (35), e2122734119. https://doi.org/10.1073/pnas.2122734119Andersson, L., Bekkevold, D., Berg, F., Farrell, E. D., Felkel, S., Ferreira, M. S., Fuentes-Pardo, A. P., Goodall, J., & Pettersson, M. (2024). How fish population genomics can promote sustainable fisheries: A road map.*Annual Review of Animal Biosciences* , *12* (1), 1–20. https://doi.org/10.1146/annurev-animal-021122-102933Anilkumar, C., Muhammed Azharudheen, T. P., Sah, R. P., Sunitha, N. C., Devanna, B. N., Marndi, B. C., & Patra, B. C. (2023). Gene based markers improve precision of genome-wide association studies and accuracy of genomic predictions in rice breeding. *Heredity* , *130* (5), 335–345. https://doi.org/10.1038/s41437-023-00599-5Aronsson, M., Andrén, H., Low, M., & Persson, J. (2023). Wolverine denning behaviour and its implications for monitoring reproductive females. *Wildlife Biology* , *2023* (4), e01079. https://doi.org/10.1002/wlb3.01079Baird, N. A., Etter, P. D., Atwood, T. S., Currey, M. C., Shiver, A. L., Lewis, Z. A., Selker, E. U., Cresko, W. A., & Johnson, E. A. (2008). Rapid SNP discovery and genetic mapping using sequenced RAD markers. *PLoS ONE* , *3* (10), e3376. https://doi.org/10.1371/journal.pone.0003376Bateman, I., & Balmford, A. (2023). Current conservation policies risk accelerating biodiversity loss. *Nature* , *618* (7966), 671–674. https://doi.org/10.1038/d41586-023-01979-xBentley, D. R. (2006). Whole-genome re-sequencing. *Current Opinion in Genetics & Development* , *16* (6), 545–552. https://doi.org/10.1016/j.gde.2006.10.009Bernatchez, L., Ferchaud, A.-L., Berger, C. S., Venney, C. J., & Xuereb, A. (2024). Genomics for monitoring and understanding species responses to global climate change.*Nature Reviews Genetics* , *25* (3), 165–183. https://doi.org/10.1038/s41576-023-00657-yBertola, L. D., Brüniche-Olsen, A., Kershaw, F., Russo, I. M., MacDonald, A. J., Sunnucks, P., Bruford, M. W., Cadena, C. D., Ewart, K. M., De Bruyn, M., Eldridge, M. D. B., Frankham, R., Guayasamin, J. M., Grueber, C. E., Hoareau, T. B., Hoban, S., Hohenlohe, P. A., Hunter, M. E., Kotze, A., ... Segelbacher, G. (2024). A pragmatic approach for integrating molecular tools into biodiversity conservation. *Conservation Science and Practice* , *6* (1), e13053. https://doi.org/10.1111/csp2.13053Bhati, M., Mapel, X. M., Lloret-Villas, A., & Pausch, H. (2023). Structural variants and short tandem repeats impact gene expression and splicing in bovine testis tissue. *GENETICS* , *225* (3), iyad161. https://doi.org/10.1093/genetics/iyad161Blaxter, M., Archibald, J. M., Childers, A. K., Coddington, J. A., Crandall, K. A., Di Palma, F., Durbin, R., Edwards, S. V., Graves, J. A. M., Hackett, K. J., Hall, N., Jarvis, E. D., Johnson, R. N., Karlsson, E. K., Kress, W. J., Kuraku, S., Lawniczak, M. K. N., Lindblad-Toh, K., Lopez, J. V., ... Lewin, H. A. (2022). Why sequence all eukaryotes? *Proceedings of the National Academy of Sciences* , *119* (4), e2115636118. https://doi.org/10.1073/pnas.2115636118Capblancq, T., Fitzpatrick, M. C., Bay, R. A., Exposito-Alonso, M., & Keller, S. R. (2020). Genomic prediction of (mal)adaptation across current and future climatic landscapes. *Annual Review of Ecology, Evolution, and Systematics* ,*51* (1), 245–269. https://doi.org/10.1146/annurev-ecolsys-020720-042553Cariou, M., Duret, L., & Charlat, S. (2016). How and how much does RAD-seq bias genetic diversity estimates? *BMC Evolutionary Biology* , *16*

(1), 240. https://doi.org/10.1186/s12862-016-0791-0Carre, C., Carluer, J. B., Chaux, C., Estoup-Streiff, C., Roche, N., Hosy, E., Mas, A., & Krouk, G. (2024). Next-Gen GWAS: Full 2D epistatic interaction maps retrieve part of missing heritability and improve phenotypic prediction. *Genome Biology* , *25* (1), 76. https://doi.org/10.1186/s13059-024-03202-0Carroll, S. R., Garba, I., Figueroa-Rodriguez, O. L., Holbrook, J., Lovett, R., Materechera, S., Parsons, M., Raseroka, K., Rodriguez-Lonebear, D., Rowe, R., Sara, R., Walker, J. D., Anderson, J., & Hudson, M. (2020). The CARE principles for indigenous data governance. *Data Science Journal* , *19* , 43. https://doi.org/10.5334/dsj-2020-043Charlesworth, B. (2009). Effective population size and patterns of molecular evolution and variation. *Nature Reviews Genetics* , *10* (3), 195–205. https://doi.org/10.1038/nrg2526Coates, D. J., Byrne, M., & Moritz, C. (2018). Genetic diversity and conservation units: Dealing with the species-population continuum in the age of genomics. *Frontiers in Ecology and Evolution* , *6* , 165. https://doi.org/10.3389/fevo.2018.00165Cook, C. N., Redford, K. H., & Schwartz, M. W. (2023). Species conservation in the era of genomic science. *BioScience* , *73* (12), 885–890. https://doi.org/10.1093/biosci/biad098COP 15. (2022). *Conference of the Parties to the Convention on Biological Diversity: Kunming-Montreal Global Biodiversity Framework* . Fifteenth meeting – Part II, Montreal, Canada, 7–19 December 2022. https://www.cbd.int/meetings/COP-15Couton, M., Viard, F., & Altermatt, F. (2023). Opportunities and inherent limits of using environmental DNA for population genetics. *Environmental DNA* ,*5* (5), 1048–1064. https://doi.org/10.1002/edn3.448Cumming, G., Campbell, L., Norwood, C., Ranger, S., Richardson, P., & Sanghera, A. (2022). Putting stakeholder engagement in its place: How situating public participation in community improves natural resource management outcomes. *GeoJournal* , *87* (S2), 209–221. https://doi.org/10.1007/s10708-020-10367-1D'Amato, D., Bartkowski, B., & Droste, N. (2020). Reviewing the interface of bioeconomy and ecosystem service research. *Ambio* , *49* (12), 1878–1896. https://doi.org/10.1007/s13280-020-01374-0Davey, J. W., Cezard, T., Fuentes-Utrilla, P., Eland, C., Gharbi, K., & Blaxter, M. L. (2013). Special features of RAD sequencing data: Implications for genotyping.*Molecular Ecology* , *22* (11), 3151–3164. https://doi.org/10.1111/mec.12084Davey, J. W., Hohenlohe, P. A., Etter, P. D., Boone, J. Q., Catchen, J. M., & Blaxter, M. L. (2011). Genome-wide genetic marker discovery and genotyping using next-generation sequencing. *Nature Reviews Genetics* ,*12* (7), 499–510. https://doi.org/10.1038/nrg3012DeWoody, J. A., Harder, A. M., Mathur, S., & Willoughby, J. R. (2021). The long-standing significance of genetic diversity in conservation.*Molecular Ecology* , *30* (17), 4147–4154. https://doi.org/10.1111/mec.16051Di Marco, M., Chapman, S., Althor, G., Kearney, S., Besancon, C., Butt, N., Maina, J. M., Possingham, H. P., Rogalla Von Bieberstein, K., Venter, O., & Watson, J. E. M. (2017). Changing trends and persisting biases in three decades of conservation science. *Global Ecology and Conservation* , *10* , 32–42. https://doi.org/10.1016/j.gecco.2017.01.008Di Tommaso, P., Chatzou, M., Floden, E. W., Barja, P. P., Palumbo, E., & Notredame, C. (2017). Nextflow enables reproducible computational workflows. *Nature Biotechnology* , *35* (4), 316–319. https://doi.org/10.1038/nbt.3820Duntsch, L., Whibley, A., De Villemereuil, P., Brekke, P., Bailey, S., Ewen, J. G., & Santure, A. W. (2023). Genomic signatures of inbreeding depression for a threatened Aotearoa New Zealand passerine. *Molecular Ecology* , *32* (8), 1893–1907. https://doi.org/10.1111/mec.16855Durham, E., Baker, H., Smith, M., Moore, E., & Morgan, V. (2014). *The BiodivERsA Stakeholder Engagement Hand-book* . BiodivERsA.Ebenezer, T. E., Muigai, A. W. T., Nouala, S., Badaoui, B., Blaxter, M., Buddie, A. G., Jarvis, E. D., Korlach, J., Kuja, J. O., Lewin, H. A., Majewska, R., Mapholi, N., Maslamoney, S., Mbo'o-Tchouawou, M., Osuji, J. O., Seehausen, O., Shorinola, O., Tiambo, C. K., Mulder, N., ... Djikeng, A. (2022). Africa: Sequence 100,000 species to safeguard biodiversity.*Nature* , *603* (7901), 388–392. https://doi.org/10.1038/d41586-022-00712-4ERGA Knowledge Hub. (2024).*ERGA Knowledge Hub- Training material for Biodiversity Genomics* . https://knowledge.ergabiodiversity.euFerreira, M. S., Thurman, T. J., Jones, M. R., Farelo, L., Kumar, A. V., Mortimer, S. M. E., Demboski, J. R., Mills, L. S., Alves, P. C., Melo-Ferreira, J., & Good, J. M. (2023). The evolution of white-tailed jackrabbit camouflage in response to past and future seasonal climates. *Science* , *379* (6638), 1238–1242. https://doi.org/10.1126/science.ade3984Fitzpatrick, S. W., Bradburd, G. S., Kremer, C. T., Salerno, P. E., Angeloni, L. M., & Funk, W. C. (2020). Genomic and fitness consequences of genetic rescue in wild populations. *Current Biology* , *30* (3), 517-522.e5. https://doi.org/10.1016/j.cub.2019.11.062Flanagan, S. P., Forester, B. R., Latch, E. K., Aitken, S. N., & Hoban, S. (2018). Guidelines for planning genomic assessment and monitoring of locally adaptive variation to inform species conservation. *Evolutionary Applications*

,*11* (7), 1035–1052. https://doi.org/10.1111/eva.12569Formenti, G., Theissinger, K., Fernandes, C., Bista, I., Bombarely, A., Bleidorn, C., Ciofi, C., Crottini, A., Godoy, J. A., Hoglund, J., Malukiewicz, J., Mouton, A., Oomen, R. A., Paez, S., Palsboll, P. J., Pampoulie, C., Ruiz-Lopez, M. J., Svardal, H., Theofanopoulou, C., ... Zammit, G. (2022). The era of reference genomes in conservation genomics. *Trends in Ecology & Evolution* , *37* (3), 197–202. https://doi.org/10.1016/j.tree.2021.11.008Fuentes-Pardo, A. P., & Ruzzante, D. E. (2017). Whole-genome sequencing approaches for conservation biology: Advantages, limitations and practical recommendations. *Molecular Ecology* , *26* (20), 5369–5406. https://doi.org/10.1111/mec.14264Gargiulo, R., Decroocq, V., Gonzalez-Martinez, S. C., Paz-Vinas, I., Aury, J., Lesur Kupin, I., Plomion, C., Schmitt, S., Scotti, I., & Heuertz, M. (2024). Estimation of contemporary effective population size in plant populations: Limitations of genomic datasets. *Evolutionary Applications* ,*17* (5), e13691. https://doi.org/10.1111/eva.13691Garner, B. A., Hand, B. K., Amish, S. J., Bernatchez, L., Foster, J. T., Miller, K. M., Morin, P. A., Narum, S. R., O'Brien, S. J., Roffler, G., Templin, W. D., Sunnucks, P., Strait, J., Warheit, K. I., Seamons, T. R., Wenburg, J., Olsen, J., & Luikart, G. (2016). Genomics in Conservation: Case Studies and Bridging the Gap between Data and Application. *Trends in Ecology & Evolution* , *31* (2), 81–83. https://doi.org/10.1016/j.tree.2015.10.009Glidden, C. K., Nova, N., Kain, M. P., Lagerstrom, K. M., Skinner, E. B., Mandle, L., Sokolow, S. H., Plowright, R. K., Dirzo, R., De Leo, G. A., & Mordecai, E. A. (2021). Human-mediated impacts on biodiversity and the consequences for zoonotic disease spillover. *Current Biology* , *31* (19), R1342–R1361. https://doi.org/10.1016/j.cub.2021.08.070Gomez-Cabrero, D., Abugessaisa, I., Maier, D., Teschendorff, A., Merkenschlager, M., Gisel, A., Ballestar, E., Bongcam-Rudloff, E., Conesa, A., & Tegner, J. (2014). Data integration in the era of omics: Current and future challenges. *BMC Systems Biology* , *8* (Suppl 2), I1. https://doi.org/10.1186/1752-0509-8-S2-I1Grill, C. (2021). Involving stakeholders in research priority setting: A scoping review. *Research Involvement and Engagement* , *7* (1), 75. https://doi.org/10.1186/s40900-021-00318-6Hedrick, P. W., & Garcia-Dorado, A. (2016). Understanding inbreeding depression, purging, and genetic rescue. *Trends in Ecology & Evolution* ,*31* (12), 940–952. https://doi.org/10.1016/j.tree.2016.09.005Helyar, S. J., Hemmer-Hansen, J., Bekkevold, D., Taylor, M. I., Ogden, R., Limborg, M. T., Cariani, A., Maes, G. E., Diopere, E., Carvalho, G. R., & Nielsen, E. E. (2011). Application of SNPs for population genetics of nonmodel organisms: New opportunities and challenges. *Molecular Ecology Resources* ,*11* (s1), 123–136. https://doi.org/10.1111/j.1755-0998.2010.02943.xHessenauer, P., Fijarczyk, A., Martin, H., Prunier, J., Charron, G., Chapuis, J., Bernier, L., Tanguay, P., Hamelin, R. C., & Landry, C. R. (2020). Hybridization and introgression drive genome evolution of Dutch elm disease pathogens. *Nature Ecology & Evolution* , *4* (4), 626–638. https://doi.org/10.1038/s41559-020-1133-6Hoban, S., Archer, F. I., Bertola, L. D., Bragg, J. G., Breed, M. F., Bruford, M. W., Coleman, M. A., Ekblom, R., Funk, W. C., Grueber, C. E., Hand, B. K., Jaffe, R., Jensen, E., Johnson, J. S., Kershaw, F., Liggins, L., MacDonald, A. J., Mergeay, J., Miller, J. M., ... Hunter, M. E. (2022). Global genetic diversity status and trends: Towards a suite of Essential Biodiversity Variables (EBVs) for genetic composition. *Biological Reviews* , *97* (4), 1511–1538. https://doi.org/10.1111/brv.12852Hoban, S., Bruford, M. W., Da Silva, J. M., Funk, W. C., Frankham, R., Gill, M. J., Grueber, C. E., Heuertz, M., Hunter, M. E., Kershaw, F., Lacy, R. C., Lees, C., Lopes-Fernandes, M., MacDonald, A. J., Mastretta-Yanes, A., McGowan, P. J. K., Meek, M. H., Mergeay, J., Millette, K. L., ... Laikre, L. (2023). Genetic diversity goals and targets have improved, but remain insufficient for clear implementation of the post-2020 global biodiversity framework. *Conservation Genetics* , *24* (2), 181–191. https://doi.org/10.1007/s10592-022-01492-0Hoban, S., Da Silva, J. M., Mastretta-Yanes, A., Grueber, C. E., Heuertz, M., Hunter, M. E., Mergeay, J., Paz-Vinas, I., Fukaya, K., Ishihama, F., Jordan, R., Koppa, V., Latorre-Cardenas, M. C., MacDonald, A. J., Rincon-Parra, V., Sjogren-Gulve, P., Tani, N., Thurfjell, H., & Laikre, L. (2023). Monitoring status and trends in genetic diversity for the Convention on Biological Diversity: An ongoing assessment of genetic indicators in nine countries. *Conservation Letters* , *16* (3), e12953. https://doi.org/10.1111/conl.12953Hoban, S., Kelley, J. L., Lotterhos, K. E., Antolin, M. F., Bradburd, G., Lowry, D. B., Poss, M. L., Reed, L. K., Storfer, A., & Whitlock, M. C. (2016). Finding the genomic basis of local adaptation: Pitfalls, practical solutions, and future directions. *The American Naturalist* , *188* (4), 379–397. https://doi.org/10.1086/688018Hogg, C. J. (2024). Translating genomic advances into biodiversity conservation. *Nature Reviews Genetics* ,*25*

(5), 362–373. https://doi.org/10.1038/s41576-023-00671-0Hogg, C. J., Ottewell, K., Latch, P., Rossetto, M., Biggs, J., Gilbert, A., Richmond, S., & Belov, K. (2022). Threatened Species Initiative: Empowering conservation action using genomic resources.*Proceedings of the National Academy of Sciences* , *119* (4), e2115643118. https://doi.org/10.1073/pnas.2115643118Hoste, A., Capblancq, T., Broquet, T., Denoyelle, L., Perrier, C., Buzan, E., Šprem, N., Corlatti, L., Crestanello, B., Hauffe, H. C., Pellissier, L., & Yannic, G. (2024). Projection of current and future distribution of adaptive genetic units in an alpine ungulate. *Heredity* ,*132* (1), 54–66. https://doi.org/10.1038/s41437-023-00661-2Huddart, J. E. A., Crawford, A. J., Luna-Tapia, A. L., Restrepo, S., & Di Palma, F. (2022). EBP-Colombia and the bioeconomy: Genomics in the service of biodiversity conservation and sustainable development. *Proceedings of the National Academy of Sciences* , *119* (4), e2115641119. https://doi.org/10.1073/pnas.2115641119Jospin, A., Chittaro, Y., Bolt, D., Demergès, D., Gurcel, K., Hensle, J., Sanchez, A., Praz, C., & Lucek, K. (2023). Genomic evidence for three distinct species in the Erebia manto complex in Central Europe (Lepidoptera, Nymphalidae).*Conservation Genetics* , *24* (3), 293–304. https://doi.org/10.1007/s10592-023-01501-wKadykalo, A. N., Cooke, S. J., & Young, N. (2020). Conservation genomics from a practitioner lens: Evaluating the research-implementation gap in a managed freshwater fishery. *Biological Conservation* , *241* , 108350. https://doi.org/10.1016/j.biocon.2019.108350Kardos, M., & Luikart, G. (2021). The genetic architecture of fitness drives population viability during rapid environmental change. *The American Naturalist* ,*197* (5), 511–525. https://doi.org/10.1086/713469Kardos, M., Luikart, G., & Allendorf, F. W. (2015). Measuring individual inbreeding in the age of genomics: Marker-based measures are better than pedigrees.*Heredity* , *115* (1), 63–72. https://doi.org/10.1038/hdy.2015.17Kardos, M., Taylor, H. R., Ellegren, H., Luikart, G., & Allendorf, F. W. (2016). Genomics advances the study of inbreeding depression in the wild. *Evolutionary Applications* ,*9* (10), 1205–1218. https://doi.org/10.1111/eva.12414Kardos, M., Zhang, Y., Parsons, K. M., A, Y., Kang, H., Xu, X., Liu, X., Matkin, C. O., Zhang, P., Ward, E. J., Hanson, M. B., Emmons, C., Ford, M. J., Fan, G., & Li, S. (2023). Inbreeding depression explains killer whale population dynamics. *Nature Ecology & Evolution* , *7* (5), 675–686. https://doi.org/10.1038/s41559-023-01995-0Knutsson, T., Krikorev, M., Ottosson, E., Dahlberg, A., Edman, M., Hansen, K., Jeppson, M., Karström, M., Larsson, E., Nitare, J., Nordén, B., Svensson, S., & Tedebrand, J.-O. (2020). *Rödlista 2020 – expertkommittén för svampar* [Dataset].Korfmann, K., Gaggiotti, O. E., & Fumagalli, M. (2023). Deep Learning in Population Genetics.*Genome Biology and Evolution* , *15* (2), evad008. https://doi.org/10.1093/gbe/evad008Lachance, J., & Tishkoff, S. A. (2013). SNP ascertainment bias in population genetic analyses: Why it is important, and how to correct it. *BioEssays* , *35* (9), 780–786. https://doi.org/10.1002/bies.201300014Larivière, D., Abueg, L., Brajuka, N., Gallardo-Alba, C., Grüning, B., Ko, B. J., Ostrovsky, A., Palmada-Flores, M., Pickett, B. D., Rabbani, K., Antunes, A., Balacco, J. R., Chaisson, M. J. P., Cheng, H., Collins, J., Couture, M., Denisova, A., Fedrigo, O., Gallo, G. R., … Formenti, G. (2024). Scalable, accessible and reproducible reference genome assembly and evaluation in Galaxy. *Nature Biotechnology* , *42* (3), 367–370. https://doi.org/10.1038/s41587-023-02100-3Lawniczak, M. K. N., Durbin, R., Flicek, P., Lindblad-Toh, K., Wei, X., Archibald, J. M., Baker, W. J., Belov, K., Blaxter, M. L., Marques Bonet, T., Childers, A. K., Coddington, J. A., Crandall, K. A., Crawford, A. J., Davey, R. P., Di Palma, F., Fang, Q., Haerty, W., Hall, N., … Richards, S. (2022). Standards recommendations for the Earth BioGenome Project.*Proceedings of the National Academy of Sciences* , *119* (4), e2115639118. https://doi.org/10.1073/pnas.2115639118Lee, Y.-L., Bosse, M., Takeda, H., Moreira, G. C. M., Karim, L., Druet, T., Oget-Ebrad, C., Coppieters, W., Veerkamp, R. F., Groenen, M. A. M., Georges, M., Bouwman, A. C., & Charlier, C. (2023). High-resolution structural variants catalogue in a large-scale whole genome sequenced bovine family cohort data. *BMC Genomics* , *24* (1), 225. https://doi.org/10.1186/s12864-023-09259-8Lehnert, S. J., Bradbury, I. R., Wringe, B. F., Van Wyngaarden, M., & Bentzen, P. (2023). Multifaceted framework for defining conservation units: An example from Atlantic salmon (*Salmo salar*) in Canada. *Evolutionary Applications* , *16* (9), 1568–1585. https://doi.org/10.1111/eva.13587Leventon, J., Fleskens, L., Claringbould, H., Schwilch, G., & Hessel, R. (2016). An applied methodology for stakeholder identification in transdisciplinary research. *Sustainability Science* , *11* (5), 763–775. https://doi.org/10.1007/s11625-016-0385-1Lewin, H. A., Richards, S., Lieberman Aiden, E., Allende, M. L., Archibald, J. M., Bálint, M., Barker, K. B., Baumgartner, B., Belov, K., Bertorelle, G., Blaxter, M. L., Cai, J., Caperello, N. D., Carlson, K., Castilla-Rubio, J. C.,

Chaw, S.-M., Chen, L., Childers, A. K., Coddington, J. A., ... Zhang, G. (2022). The Earth BioGenome Project 2020: Starting the clock.*Proceedings of the National Academy of Sciences* , *119* (4), e2115635118. https://doi.org/10.1073/pnas.2115635118Lewin, H. A., Robinson, G. E., Kress, W. J., Baker, W. J., Coddington, J., Crandall, K. A., Durbin, R., Edwards, S. V., Forest, F., Gilbert, M. T. P., Goldstein, M. M., Grigoriev, I. V., Hackett, K. J., Haussler, D., Jarvis, E. D., Johnson, W. E., Patrinos, A., Richards, S., Castilla-Rubio, J. C., ... Zhang, G. (2018). Earth BioGenome Project: Sequencing life for the future of life. *Proceedings of the National Academy of Sciences* , *115* (17), 4325–4333. https://doi.org/10.1073/pnas.1720115115Li, H., & Durbin, R. (2024). Genome assembly in the telomere-to-telomere era. *Nature Reviews Genetics* . https://doi.org/10.1038/s41576-024-00718-wLitman, J., Chittaro, Y., Birrer, S., Praz, C., Wermeille, E., Fluri, M., Stalling, T., Schmid, S., Wyler, S., & Gonseth, Y. (2018). A DNA barcode reference library for Swiss butterflies and forester moths as a tool for species identification, systematics and conservation. *PLOS ONE* ,*13* (12), e0208639. https://doi.org/10.1371/journal.pone.0208639Lou, R. N., Jacobs, A., Wilder, A. P., & Therkildsen, N. O. (2021). A beginner's guide to low-coverage whole genome sequencing for population genomics.*Molecular Ecology* , *30* (23), 5966–5993. https://doi.org/10.1111/mec.16077Lucek, K., Blattner, L., Cornet, C., Chittaro, Y., Erhardt, A., Jaun, A., Jost, B., Winiger, N., Wymann, H.-P., & Dušej, G. (2024). Towards a genomic resolution of the Phengaris alcon species complex. *Conservation Genetics* ,*25* (3), 823–834. https://doi.org/10.1007/s10592-024-01605-xMarselle, M. R., Hartig, T., Cox, D. T. C., De Bell, S., Knapp, S., Lindley, S., Triguero-Mas, M., Böhning-Gaese, K., Braubach, M., Cook, P. A., De Vries, S., Heintz-Buschart, A., Hofmann, M., Irvine, K. N., Kabisch, N., Kolek, F., Kraemer, R., Markevych, I., Martens, D., ... Bonn, A. (2021). Pathways linking biodiversity to human health: A conceptual framework.*Environment International* , *150* , 106420. https://doi.org/10.1016/j.envint.2021.106420Marx, V. (2023). Method of the year: Long-read sequencing. *Nature Methods* , *20* (1), 6–11. https://doi.org/10.1038/s41592-022-01730-wMazzoni, C. J., Ciofi, C., & Waterhouse, R. M. (2023). Biodiversity: An atlas of European reference genomes. *Nature* , *619* (7969), 252–252. https://doi.org/10.1038/d41586-023-02229-wMc Cartney, A. M., Formenti, G., Mouton, A., De Panis, D., Marins, L. S., Leitao, H. G., Diedericks, G., Kirangwa, J., Morselli, M., Salces, J., Escudero, N., Iannucci, A., Natali, C., Svardal, H., Fernandez, R., De Pooter, T., Joris, G., Strazisar, M., Wood, J., ... Mazzoni, C. J. (2023). *The European Reference Genome Atlas: Piloting a decentralised approach to equitable biodiversity genomics* . https://doi.org/10.1101/2023.09.25.559365McMahon, B. J., Teeling, E. C., & Höglund, J. (2014). How and why should we implement genomics into conservation? *Evolutionary Applications* , *7* (9), 999–1007. https://doi.org/10.1111/eva.12193Meirmans, P. G. (2015). Seven common mistakes in population genetics and how to avoid them. *Molecular Ecology* , *24* (13), 3223–3231. https://doi.org/10.1111/mec.13243Mölder, F., Jablonski, K. P., Letcher, B., Hall, M. B., Tomkins-Tinch, C. H., Sochat, V., Forster, J., Lee, S., Twardziok, S. O., Kanitz, A., Wilm, A., Holtgrewe, M., Rahmann, S., Nahnsen, S., & Köster, J. (2021). Sustainable data analysis with Snakemake. *F1000Research* , *10* , 33. https://doi.org/10.12688/f1000research.29032.2Mulder, N., Adebamowo, C. A., Adebamowo, S. N., Adebayo, O., Adeleye, O., Alibi, M., Baichoo, S., Benkahla, A., Fadlelmola, F. M., Ghazal, H., Ghedira, K., Matimba, A., Moussa, A., Mungloo-Dilmohamud, Z., Owolabi, M. O., Radouani, F., Rotimi, C. N., Stein, D. J., & Souiai, O. (2017). Genomic Research Data Generation, Analysis and Sharing – Challenges in the African Setting.*Data Science Journal* , *16* , 49. https://doi.org/10.5334/dsj-2017-049Norman, A., Taylor, J., Edwards, J., & Kuchel, H. (2018). Optimising genomic selection in wheat: Effect of marker density, population size and population structure on prediction accuracy. *G3 Genes|Genomes|Genetics* , *8* (9), 2889–2899. https://doi.org/10.1534/g3.118.200311Nova, N., Athni, T. S., Childs, M. L., Mandle, L., & Mordecai, E. A. (2022). Global Change and Emerging Infectious Diseases. *Annual Review of Resource Economics* , *14* (1), 333–354. https://doi.org/10.1146/annurev-resource-111820-024214O'Hanlon, S. J., Rieux, A., Farrer, R. A., Rosa, G. M., Waldman, B., Bataille, A., Kosch, T. A., Murray, K. A., Brankovics, B., Fumagalli, M., Martin, M. D., Wales, N., Alvarado-Rybak, M., Bates, K. A., Berger, L., Böll, S., Brookes, L., Clare, F., Courtois, E. A., ... Fisher, M. C. (2018). Recent Asian origin of chytrid fungi causing global amphibian declines.*Science* , *360* (6389), 621–627. https://doi.org/10.1126/science.aar1965Pärli, R., Lieberherr, E., Holderegger, R., Gugerli, F., Widmer, A., & Fischer, M. C. (2021). Developing a monitoring program of genetic diversity: What do stakeholders say? *Conservation Genetics* , *22* (5), 673–684. https://doi.org/10.1007/s10592-021-01379-6Pearman, P. B., Broennimann, O., Aavik, T., Albayrak, T., Alves, P. C., Aravanopoulos, F. A.,

Bertola, L. D., Biedrzycka, A., Buzan, E., Cubric-Curik, V., Djan, M., Fedorca, A., Fuentes-Pardo, A. P., Fussi, B., Godoy, J. A., Gugerli, F., Hoban, S., Holderegger, R., Hvilsom, C., ... Bruford, M. (2024). Monitoring of species' genetic diversity in Europe varies greatly and overlooks potential climate change impacts. *Nature Ecology & Evolution* , *8* (2), 267–281. https://doi.org/10.1038/s41559-023-02260-0Pereira, H. M., Ferrier, S., Walters, M., Geller, G. N., Jongman, R. H. G., Scholes, R. J., Bruford, M. W., Brummitt, N., Butchart, S. H. M., Cardoso, A. C., Coops, N. C., Dulloo, E., Faith, D. P., Freyhof, J., Gregory, R. D., Heip, C., Höft, R., Hurtt, G., Jetz, W., ... Wegmann, M. (2013). Essential Biodiversity Variables. *Science* , *339* (6117), 277–278. https://doi.org/10.1126/science.1229931Prakash, S., Lewontin, R. C., & Hubby, J. L. (1969). A molecular approach to the study of genic heterozygosity in natural populations. IV. Patterns of genic variation in central, marginal and isolated populations of Drosophila pseudoobscura. *Genetics* , *61* (4), 841–858. https://doi.org/10.1093/genetics/61.4.841R Core Team. (2024). *R: A language and environment for statistical computing* [Computer software]. R Foundation for Statistical Computing. https://www.r-project.org/Razgour, O., Forester, B., Taggart, J. B., Bekaert, M., Juste, J., Ibáñez, C., Puechmaille, S. J., Novella-Fernandez, R., Alberdi, A., & Manel, S. (2019). Considering adaptive genetic variation in climate change vulnerability assessment reduces species range loss projections. *Proceedings of the National Academy of Sciences* , *116* (21), 10418–10423. https://doi.org/10.1073/pnas.1820663116Reed, M. S. (2008). Stakeholder participation for environmental management: A literature review.*Biological Conservation* , *141* (10), 2417–2431. https://doi.org/10.1016/j.biocon.2008.07.014Reed, M. S., Graves, A., Dandy, N., Posthumus, H., Hubacek, K., Morris, J., Prell, C., Quinn, C. H., & Stringer, L. C. (2009). Who's in and why? A typology of stakeholder analysis methods for natural resource management.*Journal of Environmental Management* , *90* (5), 1933–1949. https://doi.org/10.1016/j.jenvman.2009.01.001Robinson, J. M., Breed, A. C., Camargo, A., Redvers, N., & Breed, M. F. (2024). Biodiversity and human health: A scoping review and examples of underrepresented linkages. *Environmental Research* , *246* , 118115. https://doi.org/10.1016/j.envres.2024.118115Ruiz-Lopez, M. J., Ganan, N., Godoy, J. A., Del Olmo, A., Garde, J., Espeso, G., Vargas, A., Martinez, F., Roldan, E. R. S., & Gomendio, M. (2012). Heterozygosity-fitness correlations and inbreeding depression in two critically endangered mammals. *Conservation Biology* ,*26* (6), 1121–1129. https://doi.org/10.1111/j.1523-1739.2012.01916.xSang, Y., Long, Z., Dan, X., Feng, J., Shi, T., Jia, C., Zhang, X., Lai, Q., Yang, G., Zhang, H., Xu, X., Liu, H., Jiang, Y., Ingvarsson, P. K., Liu, J., Mao, K., & Wang, J. (2022). Genomic insights into local adaptation and future climate-induced vulnerability of a keystone forest tree in East Asia.*Nature Communications* , *13* (1), 6541. https://doi.org/10.1038/s41467-022-34206-8Schiebelhut, L. M., Guillaume, A. S., Kuhn, A., Schweizer, R. M., Armstrong, E. E., Beaumont, M. A., Byrne, M., Cosart, T., Hand, B. K., Howard, L., Mussmann, S. M., Narum, S. R., Rasteiro, R., Rivera-Colon, A. G., Saarman, N., Sethuraman, A., Taylor, H. R., Thomas, G. W. C., Wellenreuther, M., & Luikart, G. (2024). Genomics and conservation: Guidance from training to analyses and applications. *Molecular Ecology Resources* , *24* (2), e13893. https://doi.org/10.1111/1755-0998.13893Schmidt, T. L., Thia, J. A., & Hoffmann, A. A. (2024). How can genomics help or hinder wildlife conservation? *Annual Review of Animal Biosciences* , *12* (1), 45–68. https://doi.org/10.1146/annurev-animal-021022-051810Schrider, D. R., & Kern, A. D. (2018). Supervised Machine Learning for Population Genetics: A New Paradigm. *Trends in Genetics* , *34* (4), 301–312. https://doi.org/10.1016/j.tig.2017.12.005Segelbacher, G., Bosse, M., Burger, P., Galbusera, P., Godoy, J. A., Helsen, P., Hvilsom, C., Iacolina, L., Kahric, A., Manfrin, C., Nonic, M., Thizy, D., Tsvetkov, I., Veličković, N., Vilà, C., Wisely, S. M., & Buzan, E. (2022). New developments in the field of genomic technologies and their relevance to conservation management. *Conservation Genetics* ,*23* (2), 217–242. https://doi.org/10.1007/s10592-021-01415-5Shafer, A. B. A., Peart, C. R., Tusso, S., Maayan, I., Brelsford, A., Wheat, C. W., & Wolf, J. B. W. (2017). Bioinformatic processing of RAD-seq data dramatically impacts downstream population genetic inference. *Methods in Ecology and Evolution* , *8* (8), 907–917. https://doi.org/10.1111/2041-210X.12700Shafer, A. B. A., Wolf, J. B. W., Alves, P. C., Bergstrom, L., Bruford, M. W., Brannstrom, I., Colling, G., Dalen, L., De Meester, L., Ekblom, R., Fawcett, K. D., Fior, S., Hajibabaei, M., Hill, J. A., Hoezel, A. R., Hoglund, J., Jensen, E. L., Krause, J., Kristensen, T. N., ... Zieliński, P. (2015). Genomics and the challenging translation into conservation practice. *Trends in Ecology & Evolution* , *30* (2), 78–87. https://doi.org/10.1016/j.tree.2014.11.009Sharaf, A., Nesengani, L. T., Hayah, I., Kuja, J. O., Mdyogolo, S., Omotoriogun, T. C., Odogwu, B. A., Beedessee, G., Smith, R. M.,

Barakat, A., Moila, A. M., Hamouchi, A. E., BenKahla, A., Boukteb, A., Elmouhtadi, A., Mafwila, A. L., Abushady, A. M., Elsherif, A. K., Ahmed, B., ... Ebenezer, T. E. (2024).*Establish grassroots genomics and bioinformatics programs to train 400 Africans yearly* . https://doi.org/10.31219/osf.io/c92rkSkarlatidou, A., Suskevics, M., Göbel, C., Prūse, B., Tauginienė, L., Mascarenhas, A., Mazzonetto, M., Sheppard, A., Barrett, J., Haklay, M., Baruch, A., Moraitopoulou, E.-A., Austen, K., Baïz, I., Berditchevskaia, A., Berényi, E., Hoyte, S., Kleijssen, L., Kragh, G., ... Wyszomirski, P. (2019). The value of stakeholder mapping to enhance co-creation in citizen science initiatives. *Citizen Science: Theory and Practice* , *4* (1), 24. https://doi.org/10.5334/cstp.226Spooner, E., Karnauskas, M., Harvey, C. J., Kelble, C., Rosellon-Druker, J., Kasperski, S., Lucey, S. M., Andrews, K. S., Gittings, S. R., Moss, J. H., Gove, J. M., Samhouri, J. F., Allee, R. J., Bograd, S. J., Monaco, M. E., Clay, P. M., Rogers, L. A., Marshak, A., Wongbusarakum, S., ... Lynch, P. D. (2021). Using Integrated Ecosystem Assessments to Build Resilient Ecosystems, Communities, and Economies. *Coastal Management* , *49* (1), 26–45. https://doi.org/10.1080/08920753.2021.1846152Stephan, T., Burgess, S. M., Cheng, H., Danko, C. G., Gill, C. A., Jarvis, E. D., Koepfli, K.-P., Koltes, J. E., Lyons, E., Ronald, P., Ryder, O. A., Schriml, L. M., Soltis, P., VandeWoude, S., Zhou, H., Ostrander, E. A., & Karlsson, E. K. (2022). Darwinian genomics and diversity in the tree of life.*Proceedings of the National Academy of Sciences* , *119* (4), e2115644119. https://doi.org/10.1073/pnas.2115644119Sterling, E. J., Betley, E., Sigouin, A., Gomez, A., Toomey, A., Cullman, G., Malone, C., Pekor, A., Arengo, F., Blair, M., Filardi, C., Landrigan, K., & Porzecanski, A. L. (2017). Assessing the evidence for stakeholder engagement in biodiversity conservation. *Biological Conservation* ,*209* , 159–171. https://doi.org/10.1016/j.biocon.2017.02.008Sucháčková Bartoňová, A., Linke, D., Klečková, I., De G. Ribeiro, P., & Matos-Maravi, P. (2023). Incorporating genomics into insect conservation: Butterflies as a model group. *Insect Conservation and Diversity* , *16* (4), 427–440. https://doi.org/10.1111/icad.12643Sundell, T., Kammonen, J. I., Mustanoja, E., Biard, V., Kunnasranta, M., Niemi, M., Nykanen, M., Nyman, T., Palo, J. U., Valtonen, M., Paulin, L., Jernvall, J., & Auvinen, P. (2023). Genomic evidence uncovers inbreeding and supports translocations in rescuing the genetic diversity of a landlocked seal population. *Conservation Genetics* , *24* (2), 155–165. https://doi.org/10.1007/s10592-022-01497-9Supple, M. A., & Shapiro, B. (2018). Conservation of biodiversity in the genomics era. *Genome Biology* , *19* (1), 131. https://doi.org/10.1186/s13059-018-1520-3Taylor, H. R., Dussex, N., & van Heezik, Y. (2017). Bridging the conservation genetics gap by identifying barriers to implementation for conservation practitioners.*Global Ecology and Conservation* , *10* , 231–242. https://doi.org/10.1016/j.gecco.2017.04.001The Galaxy Community, Abueg, L. A. L., Afgan, E., Allart, O., Awan, A. H., Bacon, W. A., Baker, D., Bassetti, M., Batut, B., Bernt, M., Blankenberg, D., Bombarely, A., Bretaudeau, A., Bromhead, C. J., Burke, M. L., Capon, P. K., Čech, M., Chavero-Díez, M., Chilton, J. M., ... Zoabi, R. (2024). The Galaxy platform for accessible, reproducible, and collaborative data analyses: 2024 update. *Nucleic Acids Research* , *52* (W1), W83–W94. https://doi.org/10.1093/nar/gkae410Theissinger, K., Fernandes, C., Formenti, G., Bista, I., Berg, P. R., Bleidorn, C., Bombarely, A., Crottini, A., Gallo, G. R., Godoy, J. A., Jentoft, S., Malukiewicz, J., Mouton, A., Oomen, R. A., Paez, S., Palsbøll, P. J., Pampoulie, C., Ruiz-López, M. J., Secomandi, S., ... Zammit, G. (2023). How genomics can help biodiversity conservation. *Trends in Genetics* ,*39* (7), 545–559. https://doi.org/10.1016/j.tig.2023.01.005TSI Applied Conservation Genomics Hub. (2024). *The Threatened Species Initiative- Applied Conservation Genomics Hub* . https://threatenedspeciesinitiative.com/Urban, L., Perlas, A., Francino, O., Martí-Carreras, J., Muga, B. A., Mwangi, J. W., Boykin Okalebo, L., Stanton, J. L., Black, A., Waipara, N., Fontsere, C., Eccles, D., Urel, H., Reska, T., Morales, H. E., Palmada-Flores, M., Marques-Bonet, T., Watsa, M., Libke, Z., ... Van Oosterhout, C. (2023). Real-time genomics for One Health. *Molecular Systems Biology* , *19* (8), e11686. https://doi.org/10.15252/msb.202311686Van Der Valk, T., Jensen, A., Caillaud, D., & Guschanski, K. (2024). Comparative genomic analyses provide new insights into evolutionary history and conservation genomics of gorillas. *BMC Ecology and Evolution* , *24* (1), 14. https://doi.org/10.1186/s12862-023-02195-xVan Oosterhout, C. (2024). AI-informed conservation genomics. *Heredity* , *132* (1), 1–4. https://doi.org/10.1038/s41437-023-00666-xWaldvogel, A.-M., Feldmeyer, B., Rolshausen, G., Exposito-Alonso, M., Rellstab, C., Kofler, R., Mock, T., Schmid, K., Schmitt, I., Bataillon, T., Savolainen, O., Bergland, A., Flatt, T., Guillaume, F., & Pfenninger, M. (2020). Evolutionary genomics can improve prediction of species' responses to climate change.*Evolution Letters* , *4* (1), 4–18.

https://doi.org/10.1002/evl3.154Waples, R. S. (2022). What Is *N* e, Anyway? *Journal of Heredity* , *113* (4), 371–379. https://doi.org/10.1093/jhered/esac023Wilkinson, M. D., Dumontier, M., Aalbersberg, Ij. J., Appleton, G., Axton, M., Baak, A., Blomberg, N., Boiten, J.-W., Da Silva Santos, L. B., Bourne, P. E., Bouwman, J., Brookes, A. J., Clark, T., Crosas, M., Dillo, I., Dumon, O., Edmunds, S., Evelo, C. T., Finkers, R., ... Mons, B. (2016). The FAIR guiding principles for scientific data management and stewardship.*Scientific Data* , *3* (1), 160018. https://doi.org/10.1038/sdata.2016.18Willi, Y., Fracassetti, M., Bachmann, O., & Van Buskirk, J. (2020). Demographic processes linked to genetic diversity and positive selection across a species' range.*Plant Communications* , *1* (6), 100111. https://doi.org/10.1016/j.xplc.2020.100111Wilson, K. A., Auerbach, N. A., Sam, K., Magini, A. G., Moss, A. St. L., Langhans, S. D., Budiharta, S., Terzano, D., & Meijaard, E. (2016). Conservation research is not happening where it is most needed. *PLOS Biology* , *14* (3), e1002413. https://doi.org/10.1371/journal.pbio.1002413Yuan, D., Ahamed, A., Burgin, J., Cummins, C., Devraj, R., Gueye, K., Gupta, D., Gupta, V., Haseeb, M., Ihsan, M., Ivanov, E., Jayathilaka, S., Kadhirvelu, V. B., Kumar, M., Lathi, A., Leinonen, R., McKinnon, J., Meszaros, L., O'Cathail, C., ... Cochrane, G. (2024). The European Nucleotide Archive in 2023. *Nucleic Acids Research* , *52* (D1), D92–D97. https://doi.org/10.1093/nar/gkad1067

Data Accessibility and Benefit-Sharing Section

Data Accessibility Statement

The data collected during the workshop are made available in Additional File 1.

Benefit-Sharing Statement

Benefits Generated: Benefits from this research accrue from the open sharing of our data and results as described above.

Author contributions

CdG and EB participated in the project conceptualisation and methodology and conducted stakeholder interviews with NRS, KL, and AR. CdG also contributed to the formal analysis and data curation, while EB co-led the supervision. CM played a role in supervision, conceptualisation, and methodology, and contributed to writing and editing the manuscript. AM helped with the investigation and contributed to the writing of the original draft and revisions. CB, NRS, KL, AR, LO, LSM, and MJR-L drafted and reviewed the manuscript. JM-F and EO provided input to the review of the manuscript, with EO providing the perspective as a stakeholder. RMW supervised the project, contributed to the conceptualisation, and prepared the final manuscript version.

Figure legends

Figure 1. Advancing horizons in biodiversity genomics. In the past, access to genetic content of species was limited and approached using many different protocols and markers. This has greatly advanced with the scaling up of reference genome production today and in the near future, with new genomics analysis tools in the future leveraging artificial intelligence (AI) and machine learning methods. With respect to genetic diversity estimates, these were built using "genetic proxies" and today with the initial use of DNA-based approaches through whole genome re-sequencing (WGS), single nucleotide polymorphism (SNP) panels, and restriction site-associated DNA sequencing (RADseq). Routine access to genome-wide genetic diversity estimates in the near future should stimulate the development of future methods that enable integrated analyses

of genetic diversity data with ecological and environmental data for identifying and understanding key trends. These advances need stakeholder engagement to translate the science into practical biodiversity conservation and management actions. Whereas in the past there was some resistance to using genetic information, today genetic approaches are more widely accepted and being implemented for species of high conservation concern. In the near future this should extend to genome-wide data supporting indicator estimates for monitoring essential biodiversity variables and species genetic diversity assessments. Longer-term future data integration efforts will demand new analysis techniques for complex datasets, where widespread adoption will require continued stakeholder engagement and the demonstration of key practical benefits of genome-wide genetic diversity assessments.**Figure 2.** Stakeholders identified during the workshop categorised by *Class* and *Country status* . The bars show numbers of stakeholders identified in 23 European countries categorised as Strengthening (N=12) and Widening (N=11) countries and categorised by Class. A total of 283 stakeholders that were assigned to a specific country (i.e. excluding international organisations) were identified, 167 from Strengthening and 116 from Widening countries. Country statuses are defined by the European Union's country designations and are indicated on the map in Figure 3. Definitions of the six classes of stakeholders are provided in the Materials and methods section.**Figure 3.** Proportions of the 283 identified stakeholders assigned to stage categories of influence and interest for 21 European countries. The categories and the stakeholder identification stages are described in the BiodivERsA Stakeholder Engagement Handbook (Durham et al., 2014): Inform (low influence and low interest), Consult (high interest and low influence), Collaborate (high influence and high interest), and Involve (high influence and low interest). Across all countries the categories with the most stakeholders were Collaborate and Inform, both with 84 stakeholders, followed by Involve with 72 and Consult with 43 stakeholders. Countries are labelled using their ISO 3166-1 alpha-2 codes. The total number of stakeholders mapped for each country is shown in parenthesis. Stakeholders from Luxembourg and Romania were also present in the dataset, but are not shown in the figure due to low sample size (N=2 for each).

Additional files

Additional File 1: Additional_File_1_Dataset_stakeholders_workshop.xlsx (Excel). This spreadsheet contains the data collected on identified stakeholders during the workshop and their categorisation.