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Review

The application gap: Genomics for biodiversity and ecosystem service management



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ABSTRACT

The conservation of biodiversity from the genetic to the community levels is fundamental for the continual provision of ecosystem services (ES), the benefits that ecosystems provide to people. Genetic and genomic diversity enhance the resilience of populations and communities that underpin the provision of ecosystem functions and services. We show that genomics applications are mostly limited to flagship species and that their benefits for biodiversity conservation and ES management are underachieved. We propose a framework on how genomics applications can guide management for biodiversity conservation and sustainable ES to bridge this genomics-ES management 'application gap'. We review how genomic knowledge in single species (relatedness, potentially adaptive variants) or in interacting species (host-microorganism coevolution, hybridization) can guide effective management actions. These include population supplementation, assisted migration or hybridization to promote climate-adapted variants or adaptive potential, control of invasives, delimitation of conservation or management areas, provenancing strategies for restoration, managing microbial function and solving conservation and ES trade-offs. Genomics-informed management actions for improved conservation and ES outcomes are supported through synergies between scientists and ES managers at local, regional and

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international levels, through the development of standardized genomic workflows, training to ES managers and incorporation of local information. Such actions facilitate the implementation of biodiversity conservation and ES policies such as the UN 2030 sustainable development goals and the EU Biodiversity strategy for 2030, and support the inclusion of ambitious biodiversity conservation goals in the development of new policies such as the CBD post-2020 Global Biodiversity Framework or conservation policies on hybrids.

1. Introduction

Managers of terrestrial or aquatic ecosystems increasingly use scientific evidence to design strategies for biodiversity conservation, its sustainable use and the sustainable provision of ecosystem services (Addison et al., 2017; Bland et al., 2017; Keith et al., 2013; Milner-Gulland and Rowcliffe, 2007; Perrings et al., 2011). Ecosystem services (ES) are the benefits that ecosystems provide to people (Haines-Young and Potschin, 2018). Sustainable ES and human well-being critically rely on biodiversity, which encompasses the diversity of ecosystems, species, and genes (Bennett et al., 2015; Díaz et al., 2018; Reid et al., 2005). Biodiversity drives ES through sustaining ecosystem functions and enabling the resilience of populations, species and communities (Breed et al., 2019; Mace et al., 2012; Stange et al., 2021). As global assessments document alarming rates of degradation of biodiversity, ES and the climate (CBD, 2020; Fao and Unep, 2020; IPBES, 2019; IPCC, 2020; WWF, 2020), there is an increasing urgency and necessity to preserve and restore life-sustaining biodiversity for ES management (Breed et al., 2019; Keith et al., 2013; Mace et al., 2012; Oliver et al., 2015; Stange et al., 2021).

Ecosystem managers have given different levels of attention to biodiversity among and within species. The diversity of species, their functions and interactions are regularly considered (Barbaro et al., 2017; Bockerhoff et al., 2017; Cadotte et al., 2011; Dee et al., 2019; Lavorel et al., 2013), but the underlying genetic diversity within species is less conspicuous and remains often overlooked (Hoban et al., 2021b; Laikre et al., 2010, 2020). Genomic diversity, i.e. genetic diversity at the genome-wide level, is composed of DNA variants that are mostly neutral to natural selection, and of variants that can respond to selection, affecting individual fitness and population adaptation. Genomic diversity is responsible for the level of adaptation of populations to their current environment, and for their adaptive potential (Derry et al., 2019; Hoffmann et al., 2017) which enables them to adapt to environmental change and increases their resilience to anthropogenic risks (Hoffmann and Sgrò, 2011; Hughes and Stachowicz, 2004; Sgrò et al., 2011; Wernberg et al., 2018). The natural resource manager can harness this genetic diversity information for an evolutionary management of populations, with relatively fast effects, in just one or a few generations, e.g., slowing down genetic erosion or producing a shift in adaptive allele frequencies (Hairston et al., 2005; Rudman et al., 2017). Recent reviews have highlighted the relevance and application potential of genomics for biodiversity, ecosystems and people (Breed et al., 2019; Stange et al., 2021). However, despite available scientific knowledge, methods and guidance, the integration of genetic and genomic information into international policy on biodiversity conservation and sustainable management is progressing slowly (Arlettaz et al., 2010; Dubois et al., 2020; Shafer et al., 2015), notably with regard to the post-2020 global biodiversity framework of the Convention on Biological Diversity (Hoban et al., 2021a, 2021b; Laikre et al., 2020) and the 2030 UN sustainable development goals (Huddart et al., 2022; Mondejar et al., 2021).

In this paper we focus on genomic variation and its applications to facilitate biodiversity conservation and management for the sustainable provision of ES. Using a literature keyword search and the review of papers relating to specific ES management goals, we illustrate how genomic applications appear to have poor representation in the ES literature and how their use is still largely focused on a few flagship species. Consequently, benefits from genomics are underachieved, a reality we can qualify as a genomics-management 'application gap' (see

also (Taylor et al., 2017)). We illustrate solutions to bridge this gap which extends beyond the earlier defined conservation genetics gap and its proposed solutions (Hoban et al., 2013a; Holderegger et al., 2019). We show how genomic data captures relevant conservation and management information in single and in interacting species (e.g., inbreeding, population structure, adaptive genetic variation, symbiotic interactions, co-evolutionary history) and how this information is actually or potentially used to support management actions to effectively attain ES-related management goals in a broad range of ecosystems.

Our paper comprises four sections: 1) A section on the concepts and our proposed framework relevant to genomic applications in natural and weakly to moderately managed ecosystems; 2) a Methods section that describes our approach of reviewing the literature; 3) a core section that addresses the application gap and illustrates with case studies how genomics can facilitate conserving biodiversity and achieving a large range of species-level and community-level management goals for ES; and 4) a Discussion section that summarizes our findings on genomics for biodiversity conservation and ES management and discusses their implications for improved research and biodiversity management in an international conservation context.

2. Concepts and framework for sustainable genomics-informed biodiversity conservation and ecosystem service management

2.1. Ecosystem services and a suggested framework for their sustainable management

Ecosystem services are defined by the Common International Classification of Ecosystem Services (CICES, supported by the European Environmental Agency) as the contributions that ecosystems make to human well-being, and are considered to be distinct from the goods and benefits that people subsequently derive from ES (Haines-Young and Potschin, 2018). The CICES v. 5.1 framework defines three ES Sections: Provisioning ES, Regulation and maintenance ES, and Cultural ES. The concept of ES was popularised in the Millennium Ecosystem Assessment (Reid et al., 2005) and was further developed into the concept of 'Nature's Contributions to People' (NCP) by the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) to explicitly recognize the role of culture and local knowledge in shaping the relationship between nature and people (Díaz et al., 2018); for correspondence between the ES and NCP frameworks, see Kadykalo et al. (2019). Since specific ES are relatively straightforward to identify from an ES management point of view, and since they are commonly linked to a particular species or function within an ecosystem, we mainly use the ES concept in this paper.

We propose a conceptual framework for effective and sustainable genomics-informed biodiversity conservation and management of ES as detailed in Fig. 1. The ecosystem manager first has to define a management goal that aims to maximise one or multiple ES (Villarreal-Rosas et al., 2020), while also preserving the ecosystem with a high level of biodiversity for future needs under uncertainty (Grêt-Regamey et al., 2013; Hamel and Bryant, 2017). To establish a management plan, they must identify ecosystem biodiversity reference points in time, such as i) the current biodiversity in the ecosystem before management actions are applied, and ii) the biodiversity at a specific future time point in which the targeted management goal will be achieved (Fig. 1). Indicators based on species diversity, genomic, phenotypic and environmental diversity

can be used to measure the biodiversity status and eco-evolutionary processes of the ecosystem and the ES it provides. This is useful to understand and predict effects of potential threats to biodiversity and the ES (Keith et al., 2013), to provide insights into the mitigation of these threats, and thus to contribute to designing management actions to achieve the management goal (Fig. 1). Monitoring the change in these ecological and evolutionary indicators and adjusting management action as necessary is key for successful biodiversity conservation and sustainable ES management (Hoban et al., 2020). Collaboration between managers and scientists is highly relevant in this process, to exchange information, samples and methods.

2.2. Evolutionary processes and the added value of genomics for biodiversity conservation and ES management

Different evolutionary processes affect biodiversity and thus ES provision: speciation and hybridization events shape species diversity, and mutation, genetic drift, gene flow and selection shape the genetic diversity within species (Fig. 1), with potential effects on species interactions (Whitham et al., 2006). Both these levels of genetic or genomic diversity, within single species and in systems of interacting species, are thus relevant for conservation and ES provision (Fig. 2, see also Methods).

High-throughput sequencing technologies have made it possible to study evolutionary processes at the genomic level in model and in non-model organisms (Ekblom and Galindo, 2011; Formenti et al., 2022; Rajora, 2019). The main advance compared to previous technologies is a 100–10,000 fold increase in the number of genetic markers assessed (e.g., single nucleotide polymorphisms, SNPs) which allows for more accurate estimation of evolutionary parameters and removes biases due to uneven genome sampling (Peterson et al., 2012). Intra-specific genomic data informs on the level of population genetic diversity (e.g., the risk of loss of genetic diversity through genetic drift), on the relatedness among individuals and substructure of populations, on their connectivity through gene flow, and on past demographic history including events such as population genetic bottlenecks or expansions (Gaut et al., 2018). In addition, the increased quantity and density of markers allow the

detection of genomic regions or genes potentially involved in adaptive genetic variation, for example, based on molecular signatures of selection (Nielsen, 2005; Pritchard et al., 2010) or their association with relevant phenotypes or putative environmental drivers of selection (Flood and Hancock, 2017; Rellstab et al., 2015).

The provision of sustainable ES depends on the persistence and continued performance of the species that provide the ES ('ES species'), which relies on the sustainability and adaptive evolution of biodiversity at all levels, as well as the ecosystem's stability (Hairston et al., 2005). Keystone species are species that exert very large effects on other associated species in a community (Paine, 1995). Their adaptive potential is therefore particularly important to consider for management alongside that of the co-occurring ES species. A cost-effective genomics-informed ES management requires the identification of keystone and ES species and populations, and a suitable study design, sampling strategy and choice of genomic markers to inform on evolutionary processes within species and, in some cases, in communities of co-occurring and/or interacting species (Angeloni et al., 2012; Blasco-Costa et al., 2021; Flanagan et al., 2018; Hoban et al., 2013b; Schielzeth and Wolf, 2021; Whitham et al., 2006).

3. Methods

To identify the best strategy to select the literature to review for this paper, we first evaluated the potential of a systematic literature extraction. We conducted a terminology research on Pubmed Central (www.ncbi.nlm.nih.gov/pmc/) to systematically and quantitatively examine the links between the keywords 'genom' (contained in genome, genomic, genomics), 'biodiversity' and 'ecosystem service' in the scientific literature. In over 6000 papers that contained at least two of the keywords in the full text, only nine mentioned 'genom' and 'ecosystem service' simultaneously in the abstract, although both keywords co-occurred hundreds of times with 'biodiversity' (details in Supplementary material S1). Studies on genomic applications that are relevant for ES management thus appear to lack visibility in the scientific literature, or match poorly the terminology of ES (details on terminology match with CICES V5.1 ES Sections and Classes in Supplementary material S1).

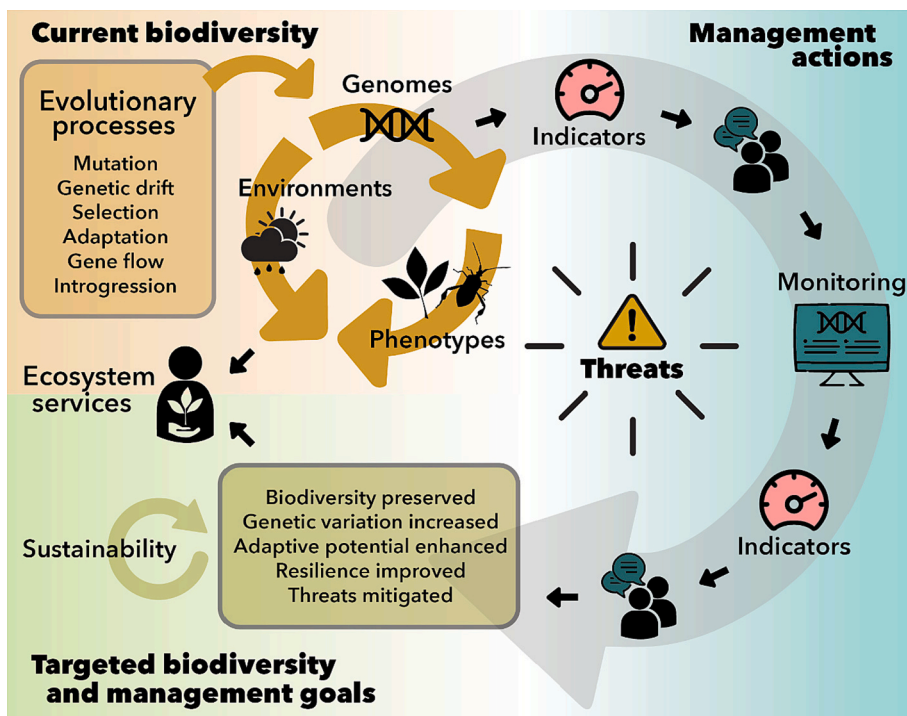


Fig. 1. Framework to reduce the application gap of genomics in biodiversity conservation and ecosystem service management. Current biodiversity and ecosystem services (ES) are affected by evolutionary processes that modulate genomic diversity. Managers can use indicators based on genomic, phenotypic and environmental diversity to assess and understand this current state of an ecosystem and to inform which management actions lead to the targeted management goals. Collaboration between managers and scientists is highly relevant in this process, to exchange information, samples and methods. Threats can affect all stages of the ecosystem and its management, but monitoring and adjustment of management actions will make it possible to achieve the management goals in which the targeted biodiversity can sustainably provide ecosystem services. The colour codes used are the same in Figs. 1, 2 and 3, i.e. orange for genomic and other data, blue for management actions and green for management goals. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

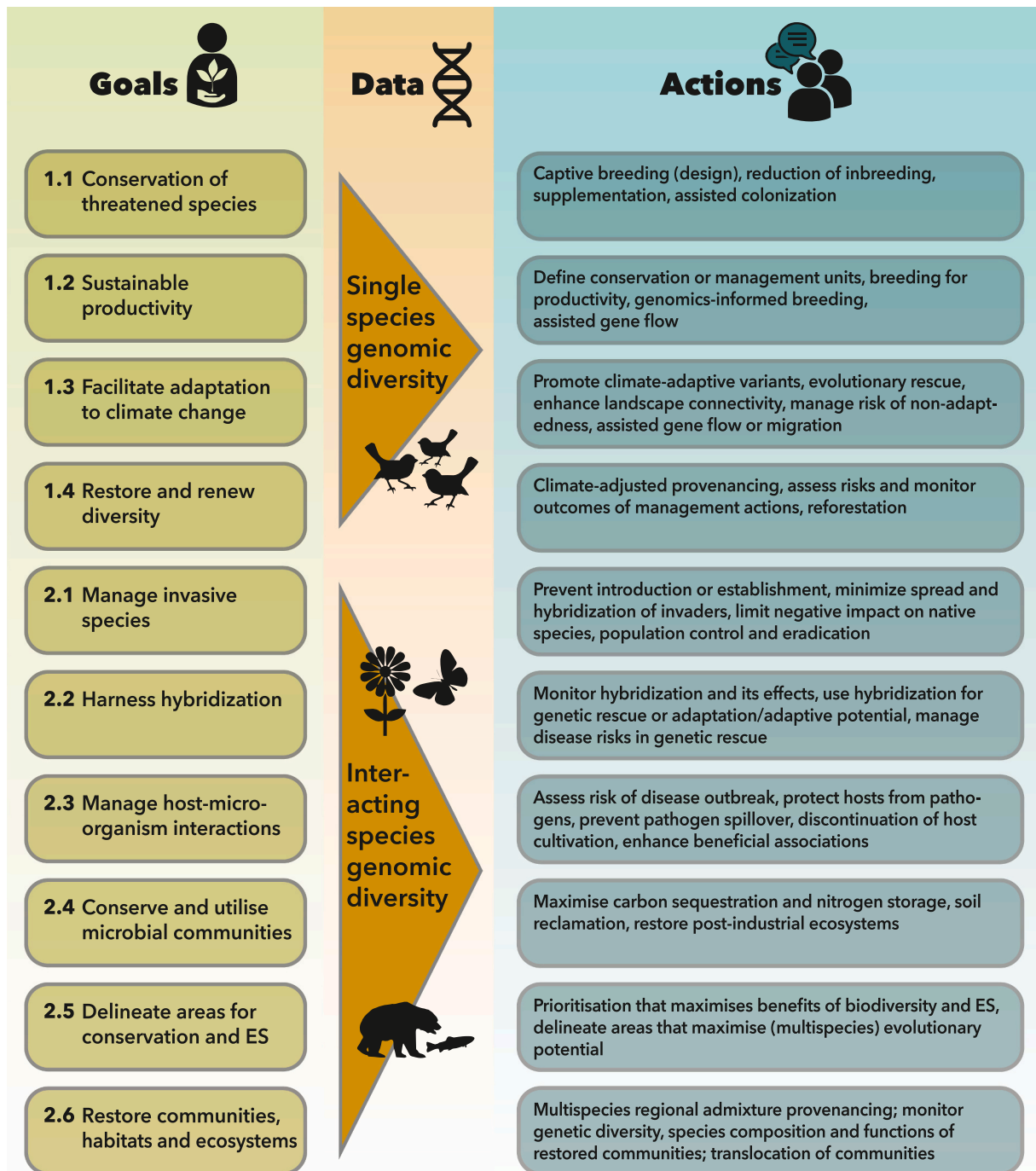


Fig. 2. The value of genomic diversity knowledge for biodiversity and ecosystem services management goals and associated management actions. Management actions can be connected to multiple management goals (see text).

The keyword search suggested limited power for a systematic literature extraction; we thus defined our literature search in consultation with natural resource managers. Based on our framework (Fig. 1), we developed a list of management goals (MGs) in ecosystems that derive from natural biodiversity (Fig. 2). We selected review papers and case studies pertaining to each MG, structured into the categories ‘Single species genomic diversity’ or ‘Interacting species genomic diversity’ to illustrate how management actions (MAs, in bold in the text) for these MGs benefit from genomic data on a single species, or on multiple interacting species (Fig. 2). We are conscious that some MGs are overlapping (Fig. 2) but list them separately on purpose to enhance their accessibility to natural resource managers. When possible, we preferred

case studies that implemented genomics-informed MAs over those that only suggested them. Given the wide scope of MGs, we did not aim to cover the literature on genomics and ES management exhaustively. The main workflows that link genomic and other data to MAs are summarised in Fig. 3.

4. Genomic applications to support biodiversity and ES management

4.1. Single species genomic diversity for biodiversity and ES management

Ecosystem managers have long recognized the importance of genetic

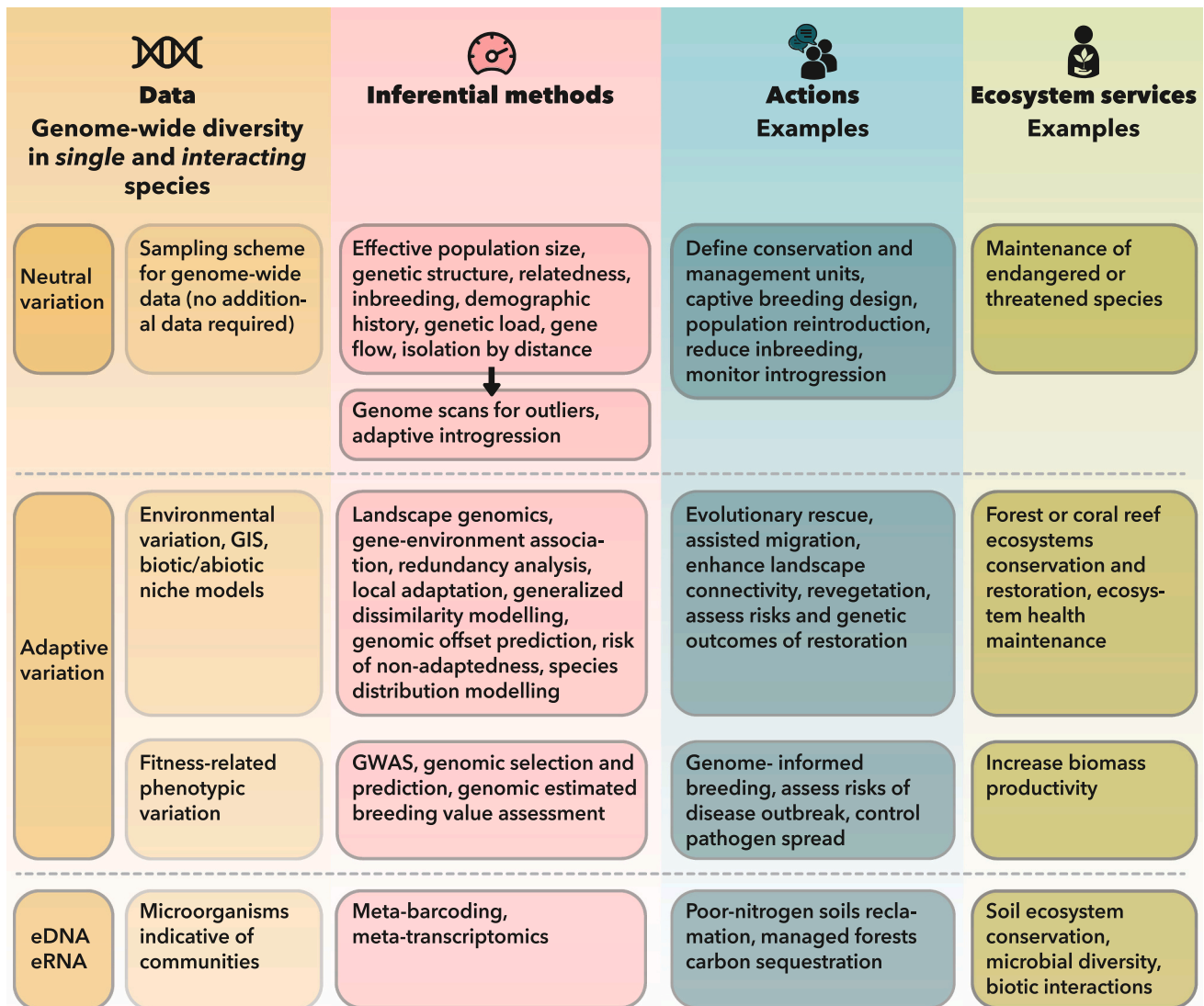


Fig. 3. Methodological framework on how to use genome-wide diversity in association with phenotypic or environmental data to guide management actions for biodiversity and ecosystem services. The column “Data” is divided into types of genomic diversity data (left) and complementary data (right). GWAS, genome-wide association study; eDNA: environmental DNA; eRNA: environmental RNA.

diversity knowledge to define population boundaries and conservation units that maximise evolutionary potential and improve population management (Funk et al., 2012; Moritz, 1994). Genome-wide data allow for powerful insights into neutral and adaptive evolutionary processes and their drivers in non-model species (Eklom and Galindo, 2011; Rajora, 2019). They promote the development of fast and effective methods and MAs to mitigate the impacts of decreasing genetic diversity on populations, species diversity, ES and climate change, as for example shown for the value of whales to sustain marine ES (Attard et al., 2018; Cook et al., 2020). The main ES MGs that benefit from genomic data on single species are listed in the following sections and include developing conservation strategies for threatened species (4.1.1), managing for sustainable productivity (4.1.2), facilitating adaptation to environmental change (4.1.3), and restoring species in degraded ecosystems (4.1.4).

4.1.1. Conservation of threatened species

Conserving endangered species is a major MG that pursues the ES of preserving genetic resources and products from rare species that can have significant functional roles in ecosystem processes (Dee et al., 2019). It involves specific MGs on securing the persistence of

populations and preventing genetic erosion. MAs generally aim at increasing the number of individuals through supplementation, for example from carefully designed captive breeding, in order to reduce inbreeding and thus to increase the diversity and adaptive potential of populations, or through assisted colonization into new habitats (Derry et al., 2019, Fig. 2, see also 4.2.2). Genomic applications that support these MAs typically involve the estimation of relatedness, inbreeding, effective population size and, occasionally, estimates of maladaptation or genomic load (Fig. 3, Arenas et al., 2021; Flesch et al., 2020; Leroy et al., 2018). A recent workflow on how to use genomics to guide conservation MAs (Rossetto et al., 2021) rests on well-established paradigms in conservation genetics (Willi et al., 2022).

One of these paradigms is that a severe reduction in population size is linked to reduced genetic diversity (Frankham et al., 2014). For example, in the case of the hihi (*Notiomystis cincta*), a threatened passerine bird endemic to New Zealand, a conservation programme starting in the 1980s used the sole remaining island population as a source for reintroduction to the mainland and other islands but failed to restore the species' adaptive potential (Brekke et al., 2011; de Villemerueil et al., 2019). Low genome-wide diversity was correlated with low adaptive potential of individuals (estimated from long-term

phenotypic trait and fitness data), which suggests genomic data can be used as a proxy for difficult to obtain long-term trait data (de Villemerueuil et al., 2019).

Another case of severe population reduction is that of the Iberian lynx (*Lynx pardinus*), which declined in the second half of the 20th century to only about 100 animals in two remaining subpopulations. A captive breeding program successfully minimised inbreeding in ex situ conservation and in the supplemented remnant populations (Kleinman-Ruiz et al., 2019). A new panel of 343 genome-wide markers selected for minimal redundancy in the lynx genome (Abascal et al., 2016) demonstrated the benefits of genomic markers, which outperformed microsatellites in four typical conservation applications (individual identification, parentage assignment, relatedness estimation, and admixture classification, Kleinman-Ruiz et al., 2017).

While threatened plant species have been underrepresented in past sequencing efforts (Exposito-Alonso et al., 2020), a recent surge in the use of genomic data studies opens possibilities for more efficient MAs in plant conservation (Lanes et al., 2018; Mamo et al., 2021; Tierney et al., 2020; van der Merwe et al., 2021; Wagner et al., 2021). For example, *Ipomoea cavalcantei*, a narrowly distributed endangered plant and a flagship species for tropical conservation, showed, unexpectedly, higher genome-wide genetic diversity and lower spatial genetic structure than *I. maurandioides*, a widespread species of least concern (Lanes et al., 2018). These results illustrate that genomic data are a useful complement to the IUCN Red List Criterion B (extent of occurrence) in conservation assessments (Garner et al., 2020).

4.1.2. Sustainable productivity

An important prerequisite for sustainable management of population productivity is the correct delimitation of genetically distinct populations with different demographic or adaptive histories to define conservation or management units (Fig. 2). For instance, genomic data is routinely used for this purpose in sustainable fisheries management (Benestan, 2020; Bernatchez et al., 2017). The high resolution of genomic data has made it possible to detect genetic structure in populations previously assumed to be panmictic (Koot et al., 2021; Pazmiño et al., 2019), to provide information about the directionality of gene flow between management areas (Barth et al., 2017), and to unveil mismatches between administrative and biological units (Benestan, 2020; Mejía-Ruiz et al., 2020; Mullins et al., 2018). These genomic insights allow optimisation of management areas for productivity while limiting the risk of overexploitation.

In many exploited species, the genomic underpinnings of biomass productivity traits (e.g., individual growth), phenotypic plasticity and sensitivity to environmental stressors remain poorly known. In forest trees, where genetic adaptation to the local population environment is common (Lind et al., 2018) breeding programs for biomass productivity and disease resistance have traditionally been based on phenotypic selection in pedigrees. SNPs associated with bud burst, drought resistance or wood properties have been identified in some species (Gailing et al., 2009; González-Martínez et al., 2006), but productivity-related traits are usually polygenic and may be shaped by negative selection (de Miguel et al., 2022). Genomics-informed breeding, or genomic selection, takes advantage of this polygenicity of traits allowing us to estimate the genomic estimated breeding value of each individual based on genome-wide markers only, exploiting their associations with numerous small-effect quantitative trait loci (Lebedev et al., 2020). In perennial species such as forest trees, genomic selection allows for an early selection of individuals before trait expression and can outperform pedigree-based selection while preserving genomic variation and adaptive potential (Pégaré et al., 2020).

Assisted gene flow or migration to spread adaptive alleles is an option to boost productivity when allochthonous provenances outperform local ones, and is currently proposed to attenuate the impacts of climate change (Aitken and Whitlock, 2013, see 4.1.3). The potential of this approach alongside genomic selection in a breeding program has been

suggested for Norway spruce (*Picea abies*) in Sweden, where growth and phenology traits are polygenic and strongly geographically determined (Milesi et al., 2019). A study in lodgepole pine (*Pinus contorta*) showed that alleles associated with climate variables can be used to predict tree heights in a long-term provenance trial, illustrating the potential of genomic data to inform management if phenotypic trials are not available (Mahony et al., 2020).

4.1.3. Facilitate adaptation to climate change

Climate change affects all levels of biological organisation, changing species' distributions, species interactions and population allele frequencies (Scheffers et al., 2016), which affects many ES of the Provisioning and of the Regulation and Maintenance Sections. Climate change effects on ES are mostly negative although variable across services (Bindoff et al., 2019; Pecl et al., 2017; Runting et al., 2017). Populations can respond to climate change by migration to track their climate optimum, persist locally thanks to phenotypic plasticity or genetic adaptation, or face demographic decline and increased extinction risk, the latter being exacerbated by loss of habitats (Aitken et al., 2008). Predicting species and population responses to climate change is key to inform MA for their persistence, especially if they lose suitable habitat or cannot track climate change through migration (Urban et al., 2016). These predictions have been improved with the inclusion of genetic structure information into species distribution models (Ikeda et al., 2017), and the identification of climate-adaptive genetic variants through landscape genomics approaches (Capblancq et al., 2020; Razgour et al., 2019; Rochat et al., 2021).

In European beech (*Fagus sylvatica*), a keystone species in temperate forests, genomic variants associated with extreme phenotypes for drought damage were identified in natural panmictic populations using a cost-efficient genome-wide association study (GWAS) on sample pools and then validated in a genotyping assay that effectively predicted damage phenotypes (Pfenninger et al., 2021). These results can inform future MAs to facilitate adaptation to climate change in these forests. In the bat species *Myotis crypticus* and *M. escalerai*, gene-environment association (GEA) methods identified over 30 potentially climate-adaptive variants (Fig. 3, Razgour et al., 2019). Ecological niche models that included these variants significantly reduced the geographic range loss predictions under future climate scenarios, and can inform MAs for evolutionary rescue of threatened cold-wet adapted populations through enhancing landscape connectivity and gene flow from hot-dry adapted ones (Razgour et al., 2019).

Another approach to assessing climate change response is the prediction of genomic offset, or risk of non-adaptedness (RONA), i.e., the estimated level of maladaptation of a population to new environmental conditions based on genomic and environmental data from different time points and/or locations (Rellstab et al., 2021). For instance, current and future RONA estimates of *Betula nana*, a keystone woody species of conservation concern in Britain (Borrell et al., 2020) identify priority areas for the conservation of local adaptations and adaptive diversity (see also 4.2.5) and propose assisted gene flow or migration strategies to maximise local adaptation under climate change. Similarly, SNPs for climatic maladaptation were identified in maritime pine (*Pinus pinaster*) and validated based on differential survival in a common garden trial in an extreme environment (Jaramillo-Correa et al., 2015). These examples illustrate the contribution of genomic applications to predicting natural population responses to climate change and inform MAs for adaptation and mitigation of effects. However, gene-targeted MAs, which are often based on the current adaptive state, should be applied with caution in order to preserve sufficient genetic diversity for future unknown threats (Derry et al., 2019; Kardos and Shafer, 2018).

4.1.4. Restore and renew diversity

Restoring terrestrial and aquatic ecosystems provides important ES including climate change mitigation and carbon sequestration (Bastin et al., 2019; Isabel et al., 2020, see also 4.2.6). Genomic diversity

knowledge obtained in keystone species can meaningfully inform MAs on the choice and sampling strategy of population provenances for restoration, leading to more successful establishment and persistence and greater resilience or restored populations (Breed et al., 2019; Gann et al., 2019; Rossetto et al., 2019).

Recent restoration MAs for terrestrial ecosystems document a shift from local provenancing to climate-adjusted provenancing (Prober et al., 2015), using landscape genomics methods (see 4.1.3) to inform seed sourcing and to assess the risks and successes of MAs (Supple et al., 2018). Generalised Dissimilarity Modelling which controls for isolation by distance when testing GEA (Fig. 3) revealed distinct patterns of spatial genomic diversity in five largely co-distributed *Acacia* species supporting provenance regions of different sizes and species-specific seed-sourcing strategies for restoration (Rossetto et al., 2020). In *Eucalyptus microcarpa* fragmented woodlands of South-eastern Australia, GEA supported climate-based seed sourcing as well as mixed seed sourcing to enhance genetic diversity in revegetation (Jordan et al., 2019, see 4.2.6). Genetic assessment of reforestation MAs revealed that revegetated sites captured a large proportion of overall genomic diversity (Jordan et al., 2016, 2019). *Eucalyptus melliodora* is another keystone tree species in many native ecosystems in Australia, some of which are critically endangered. A genomic study in this species showed that restoration projects could source seeds much more broadly (up to ~500 km) than current practice, consistent with recommendations based on phenotypic trait analyses (Supple et al., 2018). This strategy could increase the number of available provenances for restoration, and help enhance the adaptive potential in planted sites.

In the broader context of renewing biodiversity, genomic knowledge is important to monitor the consequences of assisted re-colonization of species into areas where they were previously depleted, and also of natural expansion of species into new areas (Berthouly-Salazar et al., 2013; Excoffier et al., 2009; McInerney et al., 2009; Mueller et al., 2022).

4.2. Interacting species genomic diversity for biodiversity and ES management

The provision of many ES depends on the complex interaction of species with each other and their environment (Keith et al., 2017; Moreno-Mateos et al., 2020; Pollock et al., 2020). Genomic applications play a key role in elucidating the evolutionary processes affecting communities and species interactions, evaluating their potential effects on biodiversity and ES and can thus inform ES management (Blasco-Costa et al., 2021; Schielzeth and Wolf, 2021; Whitham et al., 2006). The MGs that benefit from genomic information on interacting species include the management of invasives (4.2.1), of hybridization (4.2.2), of host-microbe interactions (4.2.3) and of microbial community diversity (4.2.4). Multi-species patterns of genomic diversity in communities also inform the delineation of conservation areas (4.2.5) and the restoration of communities (4.2.6).

4.2.1. Manage invasive species and their effects on species interactions

Invasive species are among the biggest threats to biodiversity and ecosystem stability (Simberloff, 2013). They interact with their competitors or hosts, may hybridise with related species (see also 4.2.2), often introduce parasites and pathogens, and may threaten biodiversity and many ES, e.g., material and food production, carbon storage, nutrient cycling, water and air purification (Hamelin and Roe, 2020; North et al., 2021). The process of invasion involves the stages of transport, introduction, establishment, and spread (Chown et al., 2015; Hamelin and Roe, 2020). Genomic applications can inform MAs on each of these stages: metagenomic approaches (eDNA or metabarcoding, Fig. 3) are appropriate to detect potentially invasive species, assess invasion risk and inform MAs on prevention strategies in early stages whereas population genomic approaches are suitable to assess the origins, the risks and the drivers of invasion and to monitor its progression so as to inform MAs to limit the spread of invaders and their negative

impact on native species, their associated communities and ES (Bouteiller et al., 2019; Chown et al., 2015; Hamelin and Roe, 2020; North et al., 2021).

In black locust (*Robinia pseudoacacia*), a North American native species that invaded Europe in the 19th century, SNP data allowed to trace the origin of invasion to a few populations from the northeastern part of the US native range and assign invasion success in Europe to higher clonality (Bouteiller et al., 2019). In the shrub Scotch broom (*Cytisus scoparius*) in Denmark, a genomic marker study confirmed the invasion by a non-native gene pool and genetic swamping of native vulnerable heathland populations of the same species but the authors cautioned against negative side-effects (e.g., unintended seed dispersal) by removal of the invasive phenotype (Rostgaard Nielsen et al., 2016). In some cases removal of genetically identified migrants could minimize such risks.

The raccoon dog (*Nyctereutes procyonoides*) from the *Canidae* family is of East-Asian origin and introduced in Europe for fur trade. It is a host and potential vector for a range of zoonotic diseases including echinococcosis, trichinellosis, rabies and SARS-CoV-2 (Freuling et al., 2020). Genomic information on the origin and spread of invasive populations (see Nørgaard et al., 2017, for an example in Denmark) and marker development from the recently available full genome (Chueca et al., 2021) constitute valuable resources to monitor and control invasive populations and possible associated infectious diseases.

Genome-wide studies also have the power to pinpoint genes or molecular processes that help understanding the success of an invasive species and develop countermeasures. In the case of the highly invasive house mouse (*Mus musculus*), island populations in California and in the Galápagos lacked rodenticide resistance alleles, which represents an option for population control or eradication (Morgan et al., 2018). In the case of two sister pathogenic tree fungi, introgression from the invasive North American *Heterobasidion irregulare* into the native European *H. annosum* increased invasiveness of the latter, suggesting adaptive introgression (Sillo et al., 2021, see also 4.2.2). Altogether, these studies demonstrate the usefulness of genomic approaches to elucidate and monitor invasion processes and inform MAs for the management of invasives.

4.2.2. Harness hybridization

Hybridization is a common evolutionary process that may impact all processes of divergence along the speciation continuum (Abbott et al., 2013). Introgression of genes following hybridization can either (i) compromise species survival and integrity by disrupting coadapted gene complexes (Allendorf et al., 2001; Rhymer and Simberloff, 1996), or (ii) increase the adaptive potential of populations, by enhancing diversity and creating novel genetic combinations (Becker et al., 2013; Hamilton and Miller, 2016; Hoffmann and Sgrò, 2011; Pfennig et al., 2016; Whiteley et al., 2015). Detecting hybrids and characterising introgression and its effects on adaptation is thus directly relevant for conservation and natural resource management (Flanagan et al., 2018; Quilodrán et al., 2020). Genomic diversity knowledge in hybrid systems allows to design strategies to monitor hybridization and its effects and as a result, hybridization is being increasingly harnessed as a management tool for genetic rescue or to enhance adaptation or adaptive potential (Chan, 2018; Hamilton and Miller, 2016; Moran et al., 2021; Strait et al., 2021). In this context, the possibility of conserving hybrids should be examined and integrated in novel conservation policies that allow to consider species not as fixed entities but as evolving lineages (Chan et al., 2019; Donfrancesco and Luque-Lora, 2021; Draper et al., 2021).

A widely documented case of the use of hybridization for genetic rescue from an imminent threat of extinction is that of the Florida panther (*Puma concolor coryi*). Release of pumas from the Texas subspecies (*P. c. stanleyana*) increased survival, fitness and heterozygosity and reduced inbreeding depression in the Florida population (see also 4.1.1), although this MA also illustrated the need of managing infectious disease risks in genetic rescue (Johnson et al., 2010). More generally,

understanding the phenotypic effects of introgression, developing cost-effective genotyping tools applicable across a wide range of sample provenances, DNA quantities and qualities is crucial for large-scale monitoring of hybridization and its associated risks, as shown in an assessment of hybridization between wolves (*Canis lupus*) and domestic dogs (Harmoinen et al., 2021).

In marine ecosystems, coral phylogenies bear a legacy of hybridization, suggesting that introgression promoted resilience to environmental changes, e.g., in the genera *Porites*, *Pocillopora* and *Acropora* (Forsman et al., 2017; Willis et al., 2006). For example, genome sequencing in five *Acropora* corals identified a phylogeny shaped by adaptive introgression and climate change (Mao et al., 2018). Recent studies confirmed the past introgression events among more than a hundred coral species, some of them also revealing substantial ecological differentiation despite ancient morphological stasis (Bongaerts et al., 2021a; Hobbs et al., 2021). These studies support hybridization as a promising tool for adaptive management in coral reef restoration (Chan et al., 2018, 2019; Rinkevich, 2020).

Hybridization has also shaped the genomes of numerous other animal or plant taxa (Marques et al., 2019; Suarez-Gonzalez et al., 2018). In the genus *Quercus* (oaks), introgression has led to the transfer of genetic adaptations between species (Cannon and Petit, 2020; Leroy et al., 2020), suggesting its usefulness in MAs such as assisted gene flow, migration or genetic rescue in the context of adapting forests to climate change, or to disturbed or urban environments (previously developed in 4.1.2, 4.1.3 and 4.1.4, Cannon and Petit, 2020; Hamilton and Miller, 2016; Leroy et al., 2020). Knowledge on gene flow between populations is essential to design such MAs since contact between long-isolated populations might cause outbreeding depression due to incompatibilities in adaptive differences (Aitken and Whitlock, 2013).

4.2.3. Manage host-microorganism interactions

Global change is associated with deregulation of interactions between host species and their interacting microorganisms, which is projected to disrupt host-symbiont interactions and to increase the frequency of epidemic pest attacks (Bartoli et al., 2016; Mohan et al., 2014). GWAS can address the coevolution of hosts and their associated organisms, and, in the case of pathogens, reveal the genetic basis of host resistance (La Mantia et al., 2013). This is useful to assess the risks of disease outbreaks and for MAs to protect hosts from pathogens, thus contributing to ES by maintaining ecosystem health.

In cetaceans, for example, GWAS revealed the genetic bases of adaptation to harmful algal blooms and of resistance to a lethal virus (Batley et al., 2019; Cammen et al., 2015), potentially useful in vaccine development (Batley et al., 2019). In plants, provenance and progeny trials (see 4.1.2) represent opportunities to study interactions between host genotypes and associated organisms. In trees of the genus *Populus*, genes associated with defence chemistry, phenology, growth and insect community composition have been identified (Barker et al., 2019; DeWoody et al., 2013). These co-evolutionary interactions between plant genotypes and associated communities can be harnessed to foster plant health, to maintain or increase biodiversity, or to protect endangered species within their environment. It has also been suggested that genomic information on interactions between host plants and their symbionts, in particular arbuscular mycorrhizal fungi, can be used to enhance those beneficial associations and restoration success (Aavik et al., 2021).

A promising approach to improve risk assessment for pathogen outbreaks is to examine genomic signatures of host response and pest genetic variability in parallel (Bartoli and Roux, 2017; Karasov et al., 2014). This approach can contribute to monitoring the risks or to prevent pathogen spillover from one host to another, as has been shown for an important fungal pathogen at risk of spillover from cultivated apple to the Asian wild apple *Malus sieversii* (Feurtey et al., 2020). If the risk of pathogen spillover to an endangered species is high, discontinuation of host cultivation could be an adapted MA. Similarly, genomic assessment

of disease spillover risk could be applied to aquaculture and wild fish populations, as a complement to pathogen monitoring (Bouwmeester et al., 2021). Target organisms are a priori at higher risk in the case of spillover of new, non co-evolutionary pathogen attacks. In such systems, it is possible to identify genomic regions responsible for so-called exapted, i.e., non co-evolutionary host resistant phenotypes, that would be due to the presence of genes providing broad-spectrum resistance, as has been shown in the oak species *Quercus robur* (Bartholomé et al., 2020). Although this requires both field work and substantial genomic resources (e.g. mapping populations and a reference genome), rapid progress in non-model species paves the way to more practical applications in the near future (Storfer et al., 2021).

4.2.4. Conserve and utilise microbial communities in water, soils and sediments

Numerous ES of the Provisioning Section such as agricultural or material production and the Regulation and Maintenance Section such as water quality, reduction of contamination, or nutrient cycling are mediated by microorganisms. In terrestrial and marine environments, microorganisms regulate, balance or otherwise affect inter- and intra-specific interactions (Freimoser et al., 2016; Jiao et al., 2014; Marco and Abram, 2019). DNA metabarcoding, metagenomics and metatranscriptomics have been called 'thermometers for biodiversity' as they rapidly provide large data sets on inter- and intraspecific diversity of microorganisms and small organisms from a variety of taxonomic and functional groups based on environmental DNA (eDNA) from environmental samples (Breed et al., 2019; Saccò et al., 2022; Wilson et al., 2019). These tools can be applied simply and systematically on large geographical scales, their efficiency in detecting species depending on taxonomic groups, sampling conditions and available reference databases (Hua et al., 2015; Ji et al., 2013; Watts et al., 2019; Wilson et al., 2019).

In forests, wood decomposition by microorganisms, in particular by saprophytic fungi, is crucial for ES such as nutrient recycling, carbon sequestration, soil formation, habitats creation and the preservation of the diversity of organisms living in dead wood (Tedersoo et al., 2016). DNA metabarcoding of forest soils showed the impact of distinct keystone forest tree species, edaphic variables and past forest management on microorganisms community structures (Behnke-Borowczyk et al., 2021; Jamy et al., 2020; Tedersoo et al., 2016). This knowledge can inform forest management on which tree species are most appropriate to maximise soil functions such as carbon sequestration and nitrogen storage and to preserve soil microorganism diversity and their derived ES (Fig. 2). For example, shotgun metagenomic sequencing revealed that soils under *Prunus serotina* exhibited functions that indicate a rapid nitrogen cycle and a high inorganic nitrogen availability (Kelly et al., 2021), suggesting that *P. serotina* can be used for soil reclamation in nitrogen-poor soil conditions (e.g. in coal mine spoil heaps) to restore post-industrial ecosystems (see also 4.2.6). More generally, metagenomics and metatranscriptomics can inform on the response of microorganism communities to environmental change and identify mutualistic endophytic and rhizosphere plant-microbial associations, which opens possibilities to harness these microbial functions through MAs (changing plant cover, inoculation) to support desired responses (Hamilton et al., 2016; Jansson and Hofmockel, 2020).

eDNA approaches are also increasingly applied in aquatic environments (Pawlowski et al., 2018; Saccò et al., 2022; Wang et al., 2021). For example, functional metagenomics can refine microbial community profiles associated with specific water masses at different depths that support different ES (Keuter et al., 2015; Lam et al., 2015).

4.2.5. Delineate areas for conservation and ES

Delineating priority areas for biodiversity conservation and ES is a common challenge for managers (Hermoso et al., 2018; Jung et al., 2021a; Mokany et al., 2014; Sala et al., 2021; Weeks and Adams, 2018). Traditional approaches for conservation prioritization identified

hotspots based on species richness and endemism (Mittermeier et al., 2005; Myers et al., 2000). Recent approaches use multiple criteria to optimise the spatial representation and conservation of multiple biodiversity levels or ecosystem properties, while also minimising socio-economic limitations (Carvalho et al., 2016, 2017; Jung et al., 2021b; Moilanen et al., 2009; Morán-Ordóñez et al., 2018; Pollock et al., 2020). Genomic applications can facilitate spatial prioritization through informing on drivers and features of biodiversity representation and persistence (4.2.4) and on adaptive population management (Andrello et al., 2022; Hohenlohe et al., 2021; Nielsen et al., 2022), thus contributing to ecosystem resilience and regulation (Des Roches et al., 2021; Raffard et al., 2019, see also 4.1). When combined with spatially explicit measures of ES supply, demand and flow, genomics-informed conservation prioritization can help resolve trade-offs between different management objectives for biodiversity conservation and different provisioning and/or maintenance and regulation ES (Hermoso et al., 2018; Jung et al., 2021a; Law et al., 2021; Pereira et al., 2020; Sala et al., 2021; Villarreal-Rosas et al., 2020), thus maximising benefits of biodiversity and ES.

The body of research on genetic diversity across diverse species and evolutionary timescales suggests that multi-species conservation objectives are necessary to delineate protected-area networks that preserve evolutionary processes at the species and community levels (Carvalho et al., 2017; Nielsen et al., 2017). Genomic data provide such metrics and enable the robust delineation of conservation areas that can be adjusted to desired MGs with regard to population adaptation or to maximise multispecies evolutionary potential (Phair et al., 2021; Xuereb et al., 2021). A study on six freshwater fish species suggested maximising the representation of individual alleles (Paz-Vinas et al., 2018) while another on three amphibian species recommended maximising the representation of both neutral and adaptive allele clusters (Hanson et al., 2020). In aquatic ecosystems multispecies information from metabarcoding is increasingly applied in spatial planning (Bani et al., 2020; Pawlowski et al., 2018). Although still rare, the application of genomic multi-species assessments for protected area delineation are increasingly relevant for conservation planning and climate-adaptive management of communities (Gaitán-Espitia and Hobday, 2021).

4.2.6. Restore communities, habitats and ecosystems

The large-scale restoration of converted or degraded ecosystems is primordial to mitigate climate change and limit species extinction world-wide (Rey Benayas et al., 2009; Strassburg et al., 2020; Suding et al., 2015). Restoration success will strongly depend on defining specific, pertinent and achievable MGs (see 2.2, Coleman et al., 2020; Coleman and Bragg, 2021). These will aim to restore the biodiversity of a historical or extant reference state to renew forfeited ES (Breed et al., 2019; Suding et al., 2015), or, alternatively, to reinforce or redefine the community for biodiversity conservation and ES provisioning under future conditions (Coleman et al., 2020; Kleypas et al., 2021).

Restoration of habitats, communities or ecosystems first depends on the restoration success of keystone species (see 4.1.4). Genomic applications in keystone and associated species allow to select provenances adapted to the current or future predicted climate, to assess the risks associated to their use in restoration in terrestrial or aquatic environments, and to monitor genetic diversity in the restored populations (4.1.4, Breed et al., 2019; Coleman et al., 2020; Rossetto et al., 2019; Wood et al., 2020). A scientifically supported strategy for restoration of resilient communities is regional admixture provenancing based on mixing seeds of a locally adapted provenance with that of a few surrounding provenances which contributes to increasing the diversity for future adaptation, as implemented jointly for multiple species in the restoration of European mesic grasslands (Bucharova et al., 2019). In this approach, provenance regions are defined based on the abiotic environment and are the same for all species (Bucharova et al., 2019). Multispecies regional admixture provenancing could benefit from species-specific genomics-based delineation (Rossetto et al., 2020) to

facilitate reaching a compromise between current adaptation and the need for future adaptive potential of restored communities (Bucharova et al., 2019). A study that combined genomic, phenotypic and environmental data concluded that local provenances were the most appropriate to restore moderately disturbed sites, whereas provenance admixture was found to be most effective for the restoration of highly degraded sites (Carvalho et al., 2021; Rico, 2021). Monitoring the genetic outcomes of restoration strategies allows management practices to evolve as knowledge accumulates (Hodgins and Moore, 2016).

In marine ecosystems, the use of genetics has been identified as a priority in reef restoration (Kleypas et al., 2021; Vardi et al., 2021), where MAs such as assisted migration of multiple species may create novel species assemblages (sensu Rinkevich, 2015) and dynamics, and in effect, lead to assisted translocation of communities (Rinkevich, 2021). The recent development of 'reefscape genomics' approaches that combine genomic data with state of the art spatial mapping and mass phenotyping paves the way for fine-scale landscape genomic approaches on coral reefs and other marine ecosystems, facilitating the characterization of evolutionary processes that provide guidance and monitoring tools for coral reef restoration (Bongaerts et al., 2021b).

Metagenomic and metatranscriptomic applications can monitor the species composition, the desired species interactions and the metabolic pathways necessary to deliver the targeted ES in restored ecosystems (Breed et al., 2019; Cordier et al., 2021). New biotechnology techniques, in particular the CRISPR-Cas9 system (Hsu et al., 2014), bring the possibility to manipulate and edit genetic material in a rapid fashion. While sometimes controversial, such biotechnological tools can tackle urgent conservation and ES challenges by introducing precisely the desired traits into an original genetic background (Breed et al., 2019; Segelbacher et al., 2022). Key restoration species can be targeted with fitness-improving gene edits while pests can be controlled with suppression gene edits that cause infertility or lethality (Breed et al., 2019). Another biotechnology application is chimerism, the assembling of entities that possess cells of two or more conspecifics, which may help to accelerate adaptation of corals in restoration (Rinkevich, 2021). However, before application of biotechnology for restoration, a careful risk assessment on a case-by-case basis is needed, including technical, ethical and political aspects (Breed et al., 2019; Segelbacher et al., 2022).

5. Discussion

We have identified through a keyword search in the scientific literature that there is a gap in recognizing, addressing and discussing the use of genomics for biodiversity conservation and management of ecosystem services (ES). Further, examining the scientific literature on specific genomic applications pertaining to specific management goals, we found that there was also an application gap. Indeed, we show with case studies that: Genome-wide genetic marker approaches are mostly limited to keystone or flagship species such as iconic animals (e.g., the hihi, bat species), top predators (e.g., the Iberian lynx, the Florida panther) or habitat-shaping and economically important tree species (e.g., pines, spruces, oaks). Although approaches on more modest numbers of genetic markers are more common and remain useful especially to capture neutral genetic variation (Fig. 3), genomic approaches are not yet widely applied, i.e., mainstreamed into biodiversity conservation and ES management. The outlook for such mainstreaming is favorable: we are at the beginning of an exponential stage of data gathering on whole genomes of species and genomic variation across populations and, additionally, we are increasingly accessing genomic information from historical or ancient DNA samples for a temporal, holistic insight into eco-evolutionary processes (Jensen et al., 2022). We summarise below our findings on genomic applications for natural resource management, we discuss the ambitious scientific and management goals they allow to tackle and the policy and management contexts and developments that will enable their most effective use.

5.1. Genomics applications allow to tackle ambitious management goals

We showed that genomics can significantly improve the design of management actions to meet specific management goals of interest to natural resources managers. These include goals on biodiversity conservation and restoration as well as multifaceted goals on sustainable productivity and provision of ES under environmental changes and anthropogenic stressors. Genomic applications help to solve trade-offs between different management objectives, and inform decision making to maximise the long-term sustainable provision of ES (Hermoso et al., 2018; Jung et al., 2021a; Law et al., 2021; Pereira et al., 2020; Sala et al., 2021; Villarreal-Rosas et al., 2020). Usually, such goals are intrinsically interconnected. We chose to organise them separately on purpose to visualise and exemplify possible management options unambiguously to ecosystem managers. We deliberately included several application examples in this review to illustrate the power of genomic information, including functional genetic and potentially adaptive variation, in species and communities. Beyond approaches that focus on single species, promising novel applications for genomics in biodiversity and ES management clearly lie in using its power to exploit species interactions. Introgression of adaptive variation from closely related populations or species can enhance the resilience of populations after only a few generations of natural selection, while preserving the adaptive potential of the recipient population (Hamilton and Miller, 2016; Leroy et al., 2020). Managing the co-evolutionary diversity of species interactions with their symbionts or key pathogens can support ecosystem health for the sustainable provision of ES (Aavik et al., 2021; Feurtey et al., 2020). Finally, managing microbial function in terrestrial and marine ecosystems has the power to increase crucial ecosystem functions such as carbon storage (Jansson and Hofmøckel, 2020; Pawłowski et al., 2018; Saccò et al., 2022).

5.2. Genomics applications or alternative approaches: how to choose?

It should be pointed out that the necessary evolution-based management actions do not always require molecular genetic or genomic data (Hoban et al., 2020). A careful examination of the management problem and available resources will help to identify the most appropriate data strategy, for example, (1) to use proxies such as census population size to assess effective population size (Hoban et al., 2020; Hoban et al., 2021b), (2) to use phenotypes to assess short-term responses to selection based on quantitative genetics (Alexandre et al., 2020) or (3) to use an effective strategy to obtain the most appropriate genetic or genomic data in pertinent species or communities (see 2.2, Angeloni et al., 2012; Blasco-Costa et al., 2021; Flanagan et al., 2018; Schielzeth and Wolf, 2021). It should also be stressed again that it is precarious to focus on current genetic adaptations alone to foster the future persistence and resilience of populations. This is because 1) even if major effect loci can be found for a trait of interest in a particular population, promoting them in another environment can have neutral or even negative effects because complex adaptive traits are highly polygenic and thus phenotypes depend on a given genomic background which can respond to different environments in different ways due to genotype by environment interactions (Lind et al., 2018), and 2) there is uncertainty as to what future environmental conditions will be. In the case of MAs that involve moving genetic materials (individuals, populations, communities) or confronting them with new environments through environmental change, the best assurance for future adaptability is to preserve and foster high genetic diversity (Derry et al., 2019; Kardos and Shafer, 2018).

Epigenetic variation may also offer applications to the benefit of ES management. Transgenerational epigenetic and novel epigenetic landscapes may help predict adaptive responses through their effects on phenotypes and thus the fitness of organisms (Jeremias et al., 2018). The dynamic epigenetic system, in interaction with the environment, can thus direct genetically determined natural selection (Manjrekar, 2017).

As a consequence, epigenetic processes can support fast intraspecific adaptation, impacting ecosystem services and functions (McCaw et al., 2020; Rey et al., 2020). Although epigenetic variation and processes appear to strongly vary across species with regard to their frequency and type of responses to climate change (McCaw et al., 2020), they can collectively impact important ES and their study is just beginning in non-model species.

5.3. Genomic applications in the natural resource policy context

Adopting effective biodiversity conservation and management for ES is urgent and necessary in the current biodiversity crisis, and genetic and genomic methods and data are ready to be implemented to support the most effective management as we show in this paper (see also Hoban et al., 2020; Hoban et al., 2021a; Laikre et al., 2020). In this context, it is especially important that the CBD post-2020 Global Biodiversity Framework adopt a strong goal for the conservation of genetic diversity, and genetic diversity indicators to monitor progress towards achieving this goal (Hoban et al., 2020; Hoban et al., 2021a). Genetic and genomic approaches are also crucial to improve management for the implementation of policies that are already in place, for biodiversity conservation and provision of ES as well as for human well-being, such as the UN 2030 sustainable development goals, and the EU Biodiversity strategy for 2030. For example, genomics can help decide which species and provenances are the most suitable for major ongoing tree planting initiatives, such as the ‘3 Billion Trees Pledge’ committed by the EU biodiversity strategy for 2030 under the EU Green deal, and its North American counterparts, the ‘1 trillion tree initiative’ in the USA and the ‘2 billion trees commitment’ in Canada. Genomic applications will also support a faster implementation of sustainable fishing practices regulated by the EU Common fisheries policy and the Marine Strategy Framework Directive. Long-term natural resource planning and policy requires genetic diversity and gene flow information in increasing numbers of species to reach the best management decisions without compromising the resilience and adaptive potential of ecosystems (G-BIKE, 2020). Novel developments and adaptations of the policy framework will be necessary to allow for ambitious MGs to adapt natural resources to future needs. For example, legal recognition of hybrids in conservation and natural resource policies would make a significant step forward to enhance such MGs, recognizing that species are not fixed but evolving entities (Draper et al., 2021; Fitzpatrick et al., 2015). Other ambitious policy developments that genomic data can support through proposing consensus methods concern the taxonomic delimitation of closely related species in species complexes (Coates et al., 2018) and the conservation of adaptive potential (Funk et al., 2019).

5.4. Genomics applications in natural resource management in practice

The scientific community is increasingly well organised, in conjunction with natural resource managers, to use the most powerful scientific knowledge to promote and achieve ambitious goals for biodiversity in policy and practice, e.g., through collaborative instruments such as the EU COST Action G-BIKE (Genomic Biodiversity Knowledge for Resilient Ecosystems, G-BIKE, 2019) or the Coalition for Conservation Genetics that federates four eminent organizations (Kershaw et al., 2022). Scientists increasingly recognize the power of genome-wide data for monitoring and managing genetic diversity (e.g., Meuwissen et al., 2020), with the great promise of mitigating the ever intensifying environmental change. At the same time, natural resource managers are increasingly aware of the benefits provided by genomic monitoring tools, and teaming up with geneticists for timely interventions and optimising ES. There remains a need to enhance standardisation and simplification of genomic data acquisition and analysis workflows to reduce the cost, increase the speed and facilitate the practical deployment of genomics in MAs (Rossetto et al., 2021; von Thaden et al., 2020). Synergies between scientists and ES managers need

to be increasingly fostered not only at international (Kershaw et al., 2022) but also national and local levels to bridge the science-ES management application gap. Ambitious goals for biodiversity conservation, its sustainable use and provision of ES can be achieved by merging the high level of expertise required to analyse the genomic data and the expertise of real-world ES management using appropriate workflows, deploying genomics training to ES managers, and incorporating indigenous and local knowledge into science-informed MAs (e.g., Díaz et al., 2020). In COST Action G-BIKE we follow this rationale, and in this work in particular, we prepared a “Brief for nature managers” (Supplementary material S2) that summarizes our main findings and provides application examples targeted to biodiversity and ES managers. The brief will be made available on the G-BIKE website (<https://g-bikegenetics.eu/>) in a user-friendly layout with illustrations and translated to several languages for dissemination. Another example framework for science-informed biodiversity and conservation actions on the ground is the Biodiversity and Ecosystem Services Network (BES-Net) that builds capacity and commitment for biodiversity action across the world by translating the latest IPBES products into action, but BES-Net still lacks the implementation of genomics. Governments and natural resource managers need to embrace the huge potential of genomics for ES, particularly in this time of rapid changes in our ecosystems as a result of anthropogenic effects.

CRediT authorship contribution statement

Conceptualization: MH, PGG, JAMR, SBC, JG, BR, PR, TG, BJM, ST, AVa, AVe

Data curation: MH, TG, PGG

Formal analysis: MH, TG, PGG

Funding acquisition: SH, CV

Investigation: MH, PGG, SBC, JG, BR, PR, TG, JAMR, ST

Methodology: PGG, MH, SBC, JG, BR, PR, TG, JAMR, ST

Project administration: CV

Resources: CV

Visualisation: JMIB, PGG, MH, JG, ST, BR

Roles/Writing - original draft: MH, PGG, SBC, JG, BR, PR, TG, JAMR, ST, AVa, SCGM, IP, AVe

Writing - review & editing: MH, PGG, SBC, JG, BR, PR, TA, IA, JMIB, HC, RG, SCGM, TG, SH, AK, BJM, IP, JAMR, ST, AVa, AVe, CV

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

Data will be made available on request.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.biocon.2022.109883>.

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