

1 The application gap: genomics for 2 biodiversity and ecosystem service 3 management

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47 **Highlights**

48

- 49 ● Genomic knowledge can benefit biodiversity and ecosystem services (ES) management
- 50 ● Genomics benefits are underachieved: there is an application gap in ES management
- 51 ● We propose a framework for genomics-informed biodiversity and ES management actions
- 52 ● Actions tackle conservation, adaptation, productivity, invasives, restoration
- 53 ● Policy developments and scientists-managers synergies are needed to bridge the gap

54

55 **Keywords**

56 Genomics, sustainable ecosystem services, biodiversity conservation, management goals,
57 management actions, evolutionary processes

58

59

60 Abstract

61

62 The conservation of biodiversity from the genetic to the community levels is fundamental for the
63 continual provision of ecosystem services (ES), the benefits that ecosystems provide to people.
64 Genetic and genomic diversity enhance the resilience of populations and communities that underpin
65 the provision of ecosystem functions and services. We show that genomics applications are mostly
66 limited to flagship species and that their benefits for biodiversity conservation and ES management
67 are underachieved. We propose a framework on how genomics applications can guide management
68 for biodiversity conservation and sustainable ES to bridge this genomics-ES management 'application
69 gap'. We review how genomic knowledge in single species (relatedness, potentially adaptive variants)
70 or in interacting species (host-microorganism coevolution, hybridization) can guide effective
71 management actions. These include population supplementation, assisted migration or hybridization
72 to promote climate-adapted variants or adaptive potential, control of invasives, delimitation of
73 conservation or management areas, provenancing strategies for restoration, managing microbial
74 function and solving conservation and ES trade-offs. Genomics-informed management actions for
75 improved conservation and ES outcomes are supported through synergies between scientists and ES
76 managers at local, regional and international levels, through the development of standardized genomic
77 workflows, training to ES managers and incorporation of local information. Such actions facilitate the
78 implementation of biodiversity conservation and ES policies such as the UN 2030 sustainable
79 development goals and the EU Biodiversity strategy for 2030, and support the inclusion of ambitious
80 biodiversity conservation goals in the development of new policies such as the CBD post-2020 Global
81 Biodiversity Framework or conservation policies on hybrids.

82

83 A. Introduction

84 Managers of terrestrial or aquatic ecosystems increasingly use scientific evidence to design strategies
85 for biodiversity conservation, its sustainable use and the sustainable provision of ecosystem services
86 (Addison et al., 2017; Bland et al., 2017; Keith et al., 2013; Milner-Gulland and Rowcliffe, 2007;
87 Perrings et al., 2011). Ecosystem services (ES) are the benefits that ecosystems provide to people
88 (Haines-Young and Potschin, 2018). Sustainable ES and human well-being critically rely on
89 biodiversity, which encompasses the diversity of ecosystems, species, and genes (Bennett et al.,
90 2015; Díaz et al., 2018; Reid et al., 2005). Biodiversity drives ES through sustaining ecosystem
91 functions and enabling the resilience of populations, species and communities (Breed et al., 2019;
92 Mace et al., 2012; Stange et al., 2021). As global assessments document alarming rates of
93 degradation of biodiversity, ES and the climate (CBD, 2020; Fao and Unep, 2020; IPBES, 2019; IPCC,
94 2020; WWF, 2020), there is an increasing urgency and necessity to preserve and restore life-
95 sustaining biodiversity for ES management (Breed et al., 2019; Keith et al., 2013; Mace et al., 2012;
96 Oliver et al., 2015; Stange et al., 2021).

97

98 Ecosystem managers have given different levels of attention to biodiversity among and within species.
99 The diversity of species, their functions and interactions are regularly considered (Barbaro et al., 2017;
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100 Brockerhoff et al., 2017; Cadotte et al., 2011; Dee et al., 2019; Lavorel et al., 2013), but the underlying
101 genetic diversity within species is less conspicuous and remains often overlooked (Hoban et al.,
102 2021b; Laikre et al., 2020, 2010). Genomic diversity, i.e. genetic diversity at the genome-wide level, is
103 composed of DNA variants that are mostly neutral to natural selection, and of variants that can respond
104 to selection, affecting individual fitness and population adaptation. Genomic diversity is responsible
105 for the level of adaptation of populations to their current environment, and for their adaptive potential
106 (Derry et al., 2019; Hoffmann et al., 2017) which enables them to adapt to environmental change and
107 increases their resilience to anthropogenic risks (Hoffmann and Sgrò, 2011; Hughes and Stachowicz,
108 2004; Sgrò et al., 2011; Wernberg et al., 2018). The natural resource manager can harness this
109 genetic diversity information for an evolutionary management of populations, with relatively fast
110 effects, in just one or a few generations, e.g., slowing down genetic erosion or producing a shift in
111 adaptive allele frequencies (Hairston et al., 2005; Rudman et al., 2017). Recent reviews have
112 highlighted the relevance and application potential of genomics for biodiversity, ecosystems and
113 people (Breed et al., 2019; Stange et al., 2021). However, despite available scientific knowledge,
114 methods and guidance, the integration of genetic and genomic information into international policy on
115 biodiversity conservation and sustainable management is progressing slowly (Arlettaz et al., 2010;
116 Dubois et al., 2020; Shafer et al., 2015), notably with regard to the post-2020 global biodiversity
117 framework of the Convention on Biological Diversity (Hoban et al., 2021a,b; Laikre et al., 2020) and
118 the 2030 UN sustainable development goals (Huddart et al., 2022; Mondejar et al., 2021).

119
120 In this paper we focus on genomic variation and its applications to facilitate biodiversity conservation
121 and management for the sustainable provision of ES. Using a literature keyword search and the review
122 of papers relating to specific ES management goals, we illustrate how genomic applications appear to
123 have poor representation in the ES literature and how their use is still largely focused on a few flagship
124 species. Consequently, benefits from genomics are underachieved, a reality we can qualify as a
125 **genomics-management ‘application gap’** (see also (Taylor et al., 2017)). We illustrate solutions to
126 bridge this gap which extends beyond the earlier defined conservation genetics gap and its proposed
127 solutions (Hoban et al., 2013a; Holderegger et al., 2019). We show how genomic data captures
128 relevant conservation and management information in single and in interacting species (e.g.,
129 inbreeding, population structure, adaptive genetic variation, symbiotic interactions, co-evolutionary
130 history) and how this information is actually or potentially used to support management actions to
131 effectively attain ES-related management goals in a broad range of ecosystems.

132
133 Our paper comprises four sections: 1) A section on the concepts and our proposed framework relevant
134 to genomic applications in natural and weakly to moderately managed ecosystems; 2) a Methods
135 section that describes our approach of reviewing the literature; 3) a core section that addresses the
136 application gap and illustrates with case studies how genomics can facilitate conserving biodiversity
137 and achieving a large range of species-level and community-level management goals for ES; and 4)
138 a Discussion section that summarises our findings on genomics for biodiversity conservation and ES
139 management and discusses their implications for improved research and biodiversity management in
140 an international conservation context.

141 **B. Concepts and framework for sustainable genomics-informed**
142 **biodiversity conservation and ecosystem service management**

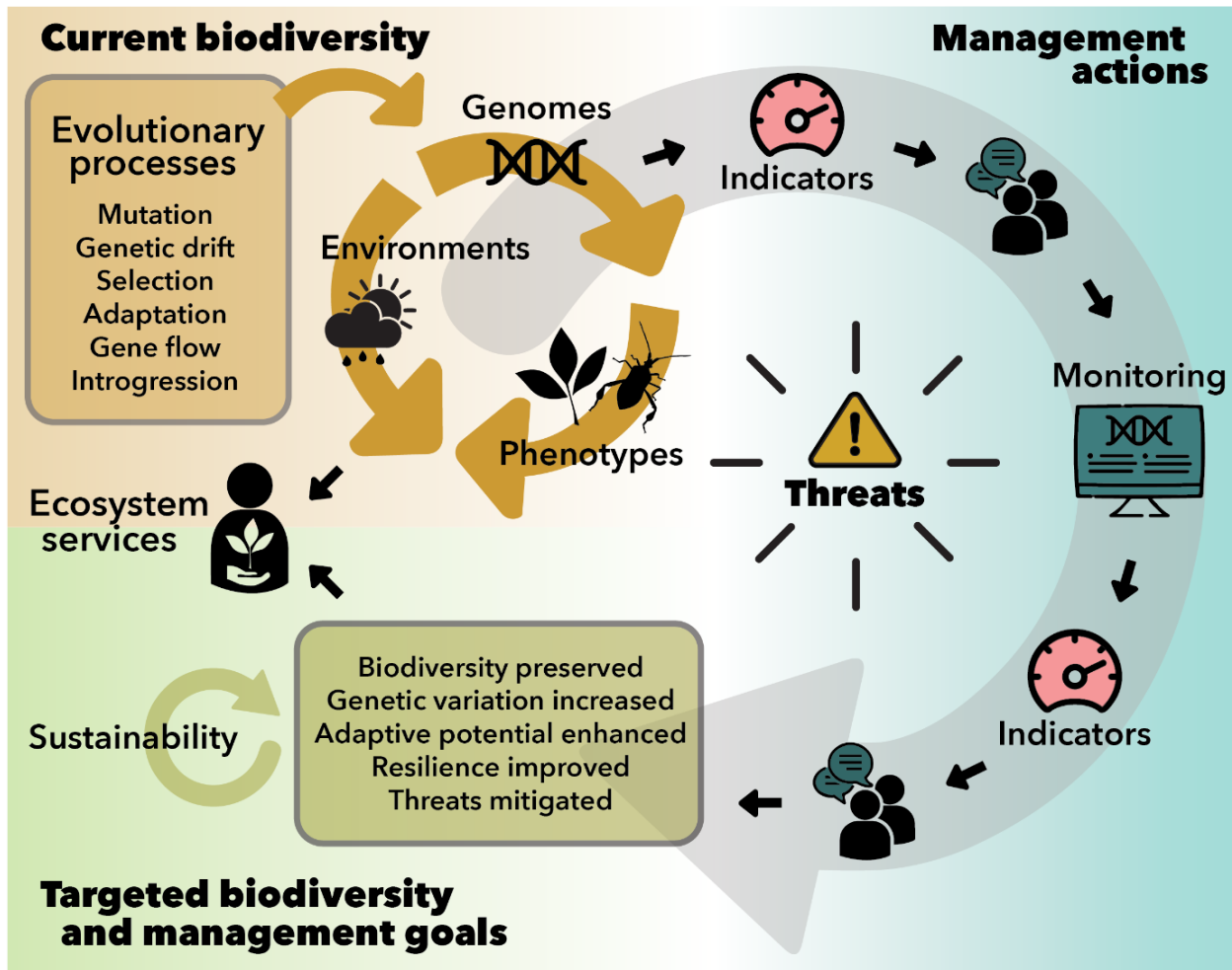
143 **B1. Ecosystem services and a suggested framework for their sustainable management**

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

157
158 We propose a conceptual framework for effective and sustainable genomics-informed biodiversity
159 conservation and management of ES as detailed in Fig.1. The ecosystem manager first has to define
160 a management goal that aims to maximise one or multiple ES (Villarreal-Rosas et al., 2020), while
161 also preserving the ecosystem with a high level of biodiversity for future needs under uncertainty (Grêt-
162 Regamey et al., 2013; Hamel and Bryant, 2017). To establish a management plan, they must identify
163 ecosystem biodiversity reference points in time, such as i) the current biodiversity in the ecosystem
164 before management actions are applied, and ii) the biodiversity at a specific future time point in which
165 the targeted management goal will be achieved (Fig. 1). Indicators based on species diversity,
166 genomic, phenotypic and environmental diversity can be used to measure the biodiversity status and
167 eco-evolutionary processes of the ecosystem and the ES it provides. This is useful to understand and
168 predict effects of potential threats to biodiversity and the ES (Keith et al., 2013), to provide insights
169 into the mitigation of these threats, and thus to contribute to designing management actions to achieve
170 the management goal (Fig. 1). Monitoring the change in these ecological and evolutionary indicators
171 and adjusting management action as necessary is key for successful biodiversity conservation and
172 sustainable ES management (Hoban et al., 2020). Collaboration between managers and scientists is
173 highly relevant in this process, to exchange information, samples and methods.

174

Figure 1



175

176 **Figure 1 Framework to reduce the application gap of genomics in biodiversity conservation**
177 **and ecosystem service management.** Current biodiversity and ecosystem services (ES) are
178 affected by evolutionary processes that modulate genomic diversity. Managers can use indicators
179 based on genomic, phenotypic and environmental diversity to assess and understand this current state
180 of an ecosystem and to inform which management actions lead to the targeted management goals.
181 Collaboration between managers and scientists is highly relevant in this process, to exchange
182 information, samples and methods. Threats can affect all stages of the ecosystem and its
183 management, but monitoring and adjustment of management actions will make it possible to achieve
184 the management goals in which the targeted biodiversity can sustainably provide ecosystem services.
185 The colour codes used are the same in figs. 1, 2 and 3, i.e. orange for genomic and other data, blue
186 for management actions and green for management goals.

187

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188 **B2. Evolutionary processes and the added value of genomics for biodiversity**
189 **conservation and ES management**

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

195
196 High-throughput sequencing technologies have made it possible to study evolutionary processes at
197 the genomic level in model and in non-model organisms (Ekblom and Galindo, 2011; Formenti et al.,
198 2022; Rajora, 2019). The main advance compared to previous technologies is a 100-10,000 fold
199 increase in the number of genetic markers assessed (e.g., single nucleotide polymorphisms, SNPs)
200 which allows for more accurate estimation of evolutionary parameters and removes biases due to
201 uneven genome sampling (Peterson et al., 2012). Intra-specific genomic data informs on the level of
202 population genetic diversity (e.g., the risk of loss of genetic diversity through genetic drift), on the
203 relatedness among individuals and substructure of populations, on their connectivity through gene
204 flow, and on past demographic history including events such as population genetic bottlenecks or
205 expansions (Gaut et al., 2018). In addition, the increased quantity and density of markers allow the
206 detection of genomic regions or genes potentially involved in adaptive genetic variation, for example,
207 based on molecular signatures of selection (Nielsen, 2005; Pritchard et al., 2010) or their association
208 with relevant phenotypes or putative environmental drivers of selection (Flood and Hancock, 2017;
209 Rellstab et al., 2015).

210
211 The provision of sustainable ES depends on the persistence and continued performance of the species
212 that provide the ES ('ES species'), which relies on the sustainability and adaptive evolution of
213 biodiversity at all levels, as well as the ecosystem's stability (Hairston et al., 2005). Keystone species
214 are species that exert very large effects on other associated species in a community (Paine, 1995).
215 Their adaptive potential is therefore particularly important to consider for management alongside that
216 of the co-occurring ES species. A cost-effective genomics-informed ES management requires the
217 identification of keystone and ES species and populations, and a suitable study design, sampling
218 strategy and choice of genomic markers to inform on evolutionary processes within species and, in
219 some cases, in communities of co-occurring and/or interacting species (Angeloni et al., 2012; Blasco-
220 Costa et al., 2021; Flanagan et al., 2018; Hoban et al., 2013b; Schielzeth and Wolf, 2021; Whitham et
221 al., 2006).

Figure 2



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223
224
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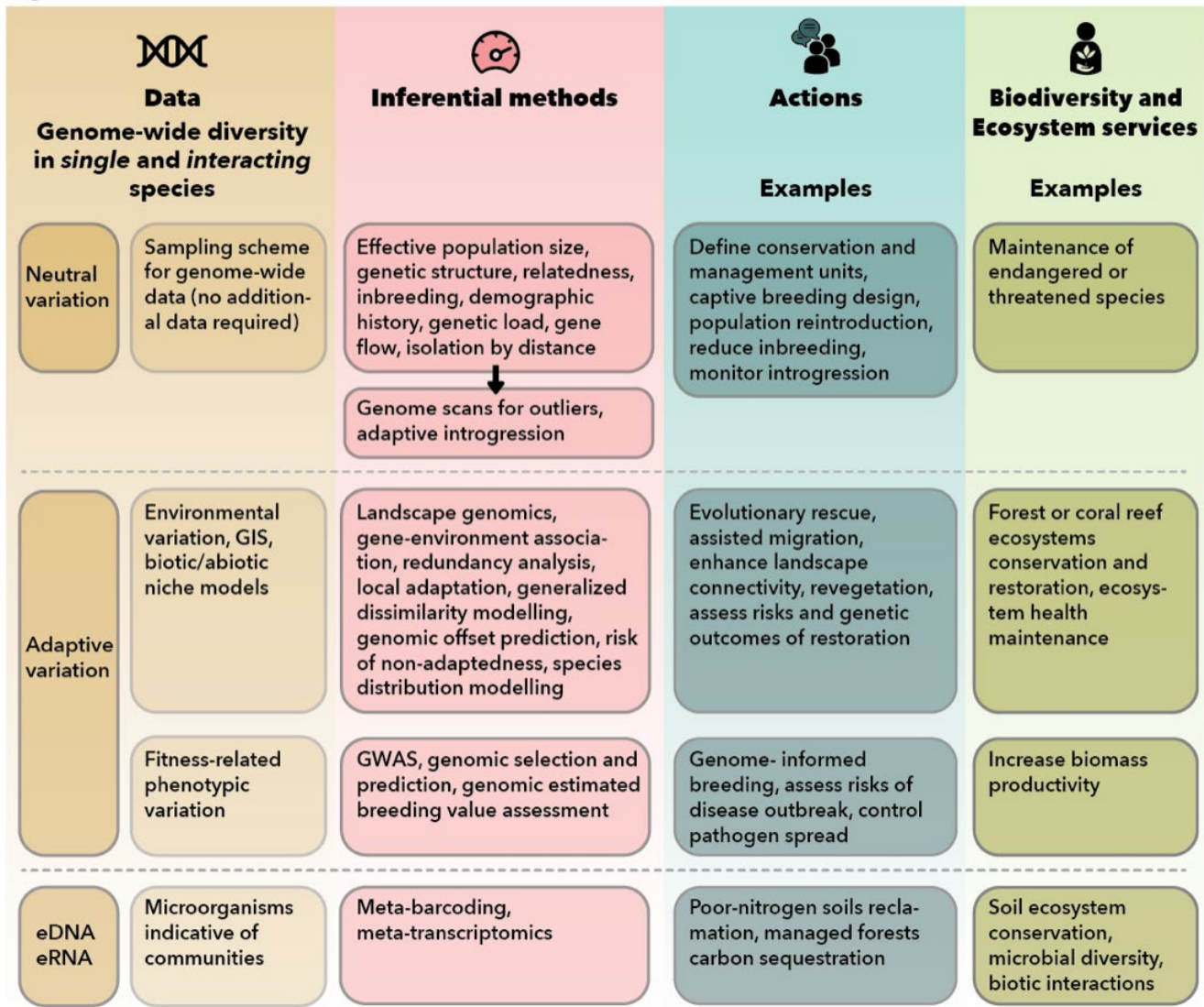
Figure 2 The value of genomic diversity knowledge for biodiversity and ecosystem services management goals and associated management actions. Management actions can be connected to multiple management goals (see text).

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226 C. Methods

227 To identify the best strategy to select the literature to review for this paper, we first evaluated the
228 potential of a systematic literature extraction. We conducted a terminology research on Pubmed
229 Central (www.ncbi.nlm.nih.gov/pmc/) to systematically and quantitatively examine the links between
230 the keywords 'genom' (contained in genome, genomic, genomics), 'biodiversity' and 'ecosystem
231 service' in the scientific literature. In over 6,000 papers that contained at least two of the keywords in
232 the full text, only nine mentioned 'genom' and 'ecosystem service' simultaneously in the abstract,
233 although both keywords co-occurred hundreds of times with 'biodiversity' (details in Supplementary
234 material S1). Studies on genomic applications that are relevant for ES management thus appear to
235 lack visibility in the scientific literature, or match poorly the terminology of ES (details on terminology
236 match with CICES V5.1 ES Sections and Classes in Supplementary material S1). The keyword search
237 suggested limited power for a systematic literature extraction; we thus defined our literature search in
238 consultation with natural resource managers. Based on our framework (Fig. 1), we developed a list of
239 management goals (MGs) in ecosystems that derive from natural biodiversity (Fig. 2). We selected
240 review papers and case studies pertaining to each MG, structured into the categories 'Single species
241 genomic diversity' or 'Interacting species genomic diversity' to illustrate how management actions
242 (MAs, in **bold** in the text) for these MGs benefit from genomic data on a single species, or on multiple
243 interacting species (Fig. 2). We are conscious that some MGs are overlapping (Fig. 2) but list them
244 separately on purpose to enhance their accessibility to natural resource managers. When possible,
245 we preferred case studies that implemented genomics-informed MAs over those that only suggested
246 them. Given the wide scope of MGs, we did not aim to cover the literature on genomics and ES
247 management exhaustively. The main workflows that link genomic and other data to MAs are
248 summarised in Fig. 3.

Figure 3



249
250
251
252
253
254

Figure 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.

255

D. Genomic applications to support biodiversity and ES management

256

D1. Single species genomic diversity for biodiversity and ES management

257

258 Ecosystem managers have long recognized the importance of genetic diversity knowledge to define **Heuertz, Myriam et al 2022**. The application gap: Genomics for biodiversity and ecosystem service management. *Biological Conservation* 2023 ;Volum 278. [10.1016/j.biocon.2022.109883](https://doi.org/10.1016/j.biocon.2022.109883)
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259 population boundaries and conservation units that maximise evolutionary potential and improve
260 population management (Funk et al., 2012; Moritz, 1994). Genome-wide data allow for powerful
261 insights into neutral and adaptive evolutionary processes and their drivers in non-model species
262 (Ekblom and Galindo, 2011; Rajora, 2019). They promote the development of fast and effective
263 methods and MAs to mitigate the impacts of decreasing genetic diversity on populations, species
264 diversity, ES and climate change, as for example shown for the value of whales to sustain marine ES
265 (Attard et al., 2018; Cook et al., 2020). The main ES MGs that benefit from genomic data on single
266 species are listed in the following sections and include developing conservation strategies for
267 threatened species (D1.1), managing for sustainable productivity (D1.2), facilitating adaptation to
268 environmental change (D1.3), and restoring species in degraded ecosystems (D1.4).

269 **D1.1 Conservation of threatened species**

270 Conserving endangered species is a major MG that pursues the ES of preserving genetic resources
271 and products from rare species that can have significant functional roles in ecosystem processes (Dee
272 et al., 2019). It involves specific MGs on securing the persistence of populations and preventing
273 genetic erosion. MAs generally aim at increasing the number of individuals through **supplementation**,
274 for example from carefully **designed captive breeding**, in order to **reduce inbreeding** and thus to
275 increase the diversity and adaptive potential of populations, or through **assisted colonisation** into
276 new habitats (Derry et al., 2019, Fig. 2, see also D2.2). Genomic applications that support these MAs
277 typically involve the estimation of relatedness, inbreeding, effective population size and, occasionally,
278 estimates of maladaptation or genomic load (Fig. 3, Arenas et al., 2021; Flesch et al., 2020; Leroy et
279 al., 2018). A recent workflow on how to use genomics to guide conservation MAs (Rossetto et al.,
280 2021) rests on well-established paradigms in conservation genetics (Willi et al., 2022).

281
282 One of these paradigms is that a severe reduction in population size is linked to reduced genetic
283 diversity (Frankham et al., 2014). For example, in the case of the hihi (*Notiomystis cincta*), a threatened
284 passerine bird endemic to New Zealand, a conservation programme starting in the 1980s used the
285 sole remaining island population as a source for reintroduction to the mainland and other islands but
286 failed to restore the species' adaptive potential (Brekke et al., 2011; de Villemereuil et al., 2019). Low
287 genome-wide diversity was correlated with low adaptive potential of individuals (estimated from long-
288 term phenotypic trait and fitness data), which suggests genomic data can be used as a proxy for
289 difficult to obtain long-term trait data (de Villemereuil et al., 2019).

290
291 Another case of severe population reduction is that of the Iberian lynx (*Lynx pardinus*), which declined
292 in the second half of the 20th century to only about 100 animals in two remaining subpopulations. A
293 captive breeding program successfully minimised inbreeding in *ex situ* conservation and in the
294 supplemented remnant populations (Kleinman-Ruiz et al., 2019). A new panel of 343 genome-wide
295 markers selected for minimal redundancy in the lynx genome (Abascal et al., 2016) demonstrated the
296 benefits of genomic markers, which outperformed microsatellites in four typical conservation
297 applications (individual identification, parentage assignment, relatedness estimation, and admixture
298 classification, Kleinman-Ruiz et al., 2017).

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299

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

309

310 **D1.2 Sustainable productivity**

311 An important prerequisite for sustainable management of population productivity is the correct
312 delimitation of genetically distinct populations with different demographic or adaptive histories to
313 **define conservation or management units** (Fig. 2). For instance, genomic data is routinely used for
314 this purpose in sustainable fisheries management (Benestan, 2020; Bernatchez et al., 2017). The high
315 resolution of genomic data has made it possible to detect genetic structure in populations previously
316 assumed to be panmictic (Koot et al., 2021; Pazmiño et al., 2019), to provide information about the
317 directionality of gene flow between management areas (Barth et al., 2017), and to unveil mismatches
318 between administrative and biological units (Benestan, 2020; Mejía-Ruíz et al., 2020; Mullins et al.,
319 2018). These genomic insights allow optimisation of management areas for productivity while limiting
320 the risk of overexploitation.

321 In many exploited species, the genomic underpinnings of biomass productivity traits (e.g., individual
322 growth), phenotypic plasticity and sensitivity to environmental stressors remain poorly known. In forest
323 trees, where genetic adaptation to the local population environment is common (Lind et al., 2018)
324 **breeding programs for biomass productivity** and disease resistance have traditionally been based
325 on phenotypic selection in pedigrees. SNPs associated with bud burst, drought resistance or wood
326 properties have been identified in some species (Gailing et al., 2009; González-Martínez et al., 2006),
327 but productivity-related traits are usually polygenic and may be shaped by negative selection (de
328 Miguel et al., 2022). **Genomics-informed breeding**, or genomic selection, takes advantage of this
329 polygenicity of traits allowing us to estimate the genomic estimated breeding value of each individual
330 based on genome-wide markers only, exploiting their associations with numerous small-effect
331 quantitative trait loci (Lebedev et al., 2020). In perennial species such as forest trees, genomic
332 selection allows for an early selection of individuals before trait expression and can outperform
333 pedigree-based selection while preserving genomic variation and adaptive potential (Pégard et al.,
334 2020).

335 **Assisted gene flow or migration** to spread adaptive alleles is an option to boost productivity when
336 allochthonous provenances outperform local ones, and is currently proposed to attenuate the impacts

337 of climate change (Aitken and Whitlock, 2013, see D1.3). The potential of this approach alongside
338 genomic selection in a breeding program has been suggested for Norway spruce (*Picea abies*) in
339 Sweden, where growth and phenology traits are polygenic and strongly geographically determined
340 (Milesi et al., 2019). A study in lodgepole pine (*Pinus contorta*) showed that alleles associated with
341 climate variables can be used to predict tree heights in a long-term provenance trial, illustrating the
342 potential of genomic data to inform management if phenotypic trials are not available (Mahony et al.,
343 2020).

344

345 **D1.3 Facilitate adaptation to climate change**

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

359 In European beech (*Fagus sylvatica*), a keystone species in temperate forests, genomic variants
360 associated with extreme phenotypes for drought damage were identified in natural panmictic
361 populations using a cost-efficient genome-wide association study (GWAS) on sample pools and then
362 validated in a genotyping assay that effectively predicted damage phenotypes (Pfenninger et al.,
363 2021). These results can inform future MAs to facilitate adaptation to climate change in these forests.
364 In the bat species *Myotis crypticus* and *M. escalerai*, gene-environment association (GEA) methods
365 identified over 30 potentially climate-adaptive variants (Fig. 3, Razgour et al., 2019). Ecological niche
366 models that included these variants significantly reduced the geographic range loss predictions under
367 future climate scenarios, and can inform MAs for **evolutionary rescue** of threatened cold-wet adapted
368 populations through **enhancing landscape connectivity** and gene flow from hot-dry adapted ones
369 (Razgour et al., 2019).

370 Another approach to assessing climate change response is the prediction of genomic offset, or **risk**
371 **of non-adaptedness** (RONA), i.e., the estimated level of maladaptation of a population to new
372 environmental conditions based on genomic and environmental data from different time points and/or
373 locations (Rellstab et al., 2021). For instance, current and future RONA estimates of *Betula nana*, a
374 keystone woody species of conservation concern in Britain (Borrell et al., 2020) identify priority areas

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375 for the conservation of local adaptations and adaptive diversity (see also D2.5) and propose **assisted**
376 **gene flow** or **migration** strategies to maximise local adaptation under climate change. Similarly, SNPs
377 for climatic maladaptation were identified in maritime pine (*Pinus pinaster*) and validated based on
378 differential survival in a common garden trial in an extreme environment (Jaramillo-Correa et al., 2015).
379 These examples illustrate the contribution of genomic applications to predicting natural population
380 responses to climate change and inform MAs for adaptation and mitigation of effects. However, gene-
381 targeted MAs, which are often based on the current adaptive state, should be applied with caution in
382 order to preserve sufficient genetic diversity for future unknown threats (Derry et al., 2019; Kardos and
383 Shafer, 2018).

384 **D1.4 Restore and renew diversity**

385 Restoring terrestrial and aquatic ecosystems provides important ES including climate change
386 mitigation and carbon sequestration (Bastin et al., 2019; Isabel et al., 2020, see also D2.6). Genomic
387 diversity knowledge obtained in keystone species can meaningfully inform MAs on the choice and
388 sampling strategy of population provenances for restoration, leading to more successful establishment
389 and persistence and greater resilience or restored populations (Breed et al., 2019; Gann et al., 2019;
390 Rossetto et al., 2019).

391 Recent restoration MAs for terrestrial ecosystems document a shift from local provenancing to
392 **climate-adjusted provenancing** (Prober et al., 2015), using landscape genomics methods (see D1.3)
393 to inform seed sourcing and to **assess the risks and successes of MAs** (Supple et al., 2018).
394 Generalised Dissimilarity Modelling which controls for isolation by distance when testing GEA (Fig. 3)
395 revealed distinct patterns of spatial genomic diversity in five largely co-distributed *Acacia* species
396 supporting provenance regions of different sizes and species-specific seed-sourcing strategies for
397 restoration (Rossetto et al., 2020). In *Eucalyptus microcarpa* fragmented woodlands of South-eastern
398 Australia, GEA supported climate-based seed sourcing as well as mixed seed sourcing to enhance
399 genetic diversity in revegetation (Jordan et al., 2019, see D2.6). Genetic assessment of **reforestation**
400 MAs revealed that revegetated sites captured a large proportion of overall genomic diversity (Jordan
401 et al., 2019, 2016). *Eucalyptus melliodora* is another keystone tree species in many native ecosystems
402 in Australia, some of which are critically endangered. A genomic study in this species showed that
403 restoration projects could source seeds much more broadly (up to ~500 km) than current practice,
404 consistent with recommendations based on phenotypic trait analyses (Supple et al., 2018). This
405 strategy could increase the number of available provenances for restoration, and help enhance the
406 adaptive potential in planted sites.

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

411

412 **D2. Interacting species genomic diversity for biodiversity and ES management**

413 The provision of many ES depends on the complex interaction of species with each other and their
414 environment (Keith et al., 2017; Moreno-Mateos et al., 2020; Pollock et al., 2020). Genomic
415 applications play a key role in elucidating the evolutionary processes affecting communities and
416 species interactions, evaluating their potential effects on biodiversity and ES and can thus inform ES
417 management (Blasco-Costa et al., 2021; Schielzeth and Wolf, 2021; Whitham et al., 2006). The MGs
418 that benefit from genomic information on interacting species include the management of invasives
419 (D2.1), of hybridization (D2.2), of host-microbe interactions (D2.3) and of microbial community diversity
420 (D2.4). Multi-species patterns of genomic diversity in communities also inform the delineation of
421 conservation areas (D2.5) and the restoration of communities (D2.6).

422

423 **D2.1 Manage invasive species and their effects on species interactions**

424 Invasive species are among the biggest threats to biodiversity and ecosystem stability (Simberloff,
425 2013). They interact with their competitors or hosts, may hybridise with related species (see also D2.2),
426 often introduce parasites and pathogens, and may threaten biodiversity and many ES, e.g., material
427 and food production, carbon storage, nutrient cycling, water and air purification (Hamelin and Roe,
428 2020; North et al., 2021). The process of invasion involves the stages of transport, introduction,
429 establishment, and spread (Chown et al., 2015; Hamelin and Roe, 2020). Genomic applications can
430 inform MAs on each of these stages: metagenomic approaches (eDNA or metabarcoding, Fig. 3) are
431 appropriate to detect potentially invasive species, assess invasion risk and inform MAs on **prevention**
432 **strategies** in early stages whereas population genomic approaches are suitable to assess the origins,
433 the risks and the drivers of invasion and to monitor its progression so as to inform MAs to **limit the**
434 **spread of invaders** and their **negative impact on native species**, their associated communities and
435 ES (Bouteiller et al., 2019; Chown et al., 2015; Hamelin and Roe, 2020; North et al., 2021).

436 In black locust (*Robinia pseudoacacia*), a North American native species that invaded Europe in the
437 19th century, SNP data allowed to trace the origin of invasion to a few populations from the
438 northeastern part of the US native range and assign invasion success in Europe to higher clonality
439 (Bouteiller et al., 2019). In the shrub Scotch broom (*Cytisus scoparius*) in Denmark, a genomic marker
440 study confirmed the invasion by a non-native gene pool and genetic swamping of native vulnerable
441 heathland populations of the same species but the authors cautioned against negative side-effects
442 (e.g., unintended seed dispersal) by removal of the invasive phenotype (Rostgaard Nielsen et al.,
443 2016). In some cases removal of genetically identified migrants could minimise such risks.

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

451 Genome-wide studies also have the power to pinpoint genes or molecular processes that help
452 understanding the success of an invasive species and develop countermeasures. In the case of the
453 highly invasive house mouse (*Mus musculus*), island populations in California and in the Galápagos
454 lacked rodenticide resistance alleles, which represents an option for **population control or**
455 **eradication** (Morgan et al., 2018). In the case of two sister pathogenic tree fungi, introgression from
456 the invasive North American *Heterobasidion irregulare* into the native European *H. annosum* increased
457 invasiveness of the latter, suggesting adaptive introgression (Sillo et al., 2021, see also D2.2).
458 Altogether, these studies demonstrate the usefulness of genomic approaches to elucidate and monitor
459 invasion processes and inform MAs for the management of invasives.

460

461 **D2.2 Harness hybridization**

462 Hybridization is a common evolutionary process that may impact all processes of divergence along
463 the speciation continuum (Abbott et al., 2013). Introgression of genes following hybridization can either
464 (i) compromise species survival and integrity by disrupting coadapted gene complexes (Allendorf et
465 al., 2001; Rhymer and Simberloff, 1996), or (ii) increase the adaptive potential of populations, by
466 enhancing diversity and creating novel genetic combinations (Becker et al., 2013; Hamilton and Miller,
467 2016; Hoffmann and Sgrò, 2011; Pfennig et al., 2016; Whiteley et al., 2015). Detecting hybrids and
468 characterising introgression and its effects on adaptation is thus directly relevant for conservation and
469 natural resource management (Flanagan et al., 2018; Quilodrán et al., 2020). Genomic diversity
470 knowledge in hybrid systems allows to design strategies to **monitor hybridization** and its effects and
471 as a result, **hybridization** is being increasingly **harnessed** as a management tool **for genetic rescue**
472 or to **enhance adaptation or adaptive potential** (Chan, 2018; Hamilton and Miller, 2016; Moran et
473 al., 2021; Strait et al., 2021). In this context, the possibility of conserving hybrids should be examined
474 and integrated in novel conservation policies that allow to consider species not as fixed entities but as
475 evolving lineages (Chan et al., 2019; Donfrancesco and Luque-Lora, 2021; Draper et al., 2021).

476 A widely documented case of the use of hybridization for genetic rescue from an imminent threat of
477 extinction is that of the Florida panther (*Puma concolor coryi*). Release of pumas from the Texas
478 subspecies (*P. c. stanleyana*) increased survival, fitness and heterozygosity and reduced inbreeding
479 depression in the Florida population (see also D1.1), although this MA also illustrated the need of
480 **managing infectious disease risks in genetic rescue** (Johnson et al., 2010). More generally,
481 understanding the phenotypic effects of introgression, developing cost-effective genotyping tools
482 applicable across a wide range of sample provenances, DNA quantities and qualities is crucial for
483 large-scale monitoring of hybridization and its associated risks, as shown in an assessment of
484 hybridization between wolves (*Canis lupus*) and domestic dogs (Harmoinen et al., 2021).

485 In marine ecosystems, coral phylogenies bear a legacy of hybridization, suggesting that introgression
486 promoted resilience to environmental changes, e.g., in the genera *Porites*, *Pocillopora* and *Acropora*

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487 (Forsman et al., 2017; Willis et al., 2006). For example, genome sequencing in five *Acropora* corals
488 identified a phylogeny shaped by adaptive introgression and climate change (Mao et al., 2018). Recent
489 studies confirmed the past introgression events among more than a hundred coral species, some of
490 them also revealing substantial ecological differentiation despite ancient morphological stasis
491 (Bongaerts et al., 2021a; Hobbs et al., 2021). These studies support hybridization as a promising tool
492 for adaptive management in coral reef restoration (Chan et al., 2019, 2018; Rinkevich, 2020).

493 Hybridization has also shaped the genomes of numerous other animal or plant taxa (Marques et al.,
494 2019; Suarez-Gonzalez et al., 2018). In the genus *Quercus* (oaks), introgression has led to the transfer
495 of genetic adaptations between species (Cannon and Petit, 2020; Leroy et al., 2020), suggesting its
496 usefulness in MAs such as assisted gene flow, migration or genetic rescue in the context of adapting
497 forests to climate change, or to disturbed or urban environments (previously developed in D1.2, D1.3
498 and D1.4, Cannon and Petit, 2020; Hamilton and Miller, 2016; Leroy et al., 2020). Knowledge on gene
499 flow between populations is essential to design such MAs since contact between long-isolated
500 populations might cause outbreeding depression due to incompatibilities in adaptive differences
501 (Aitken and Whitlock, 2013).

502

503 **D2.3 Manage host-microorganism interactions**

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

511 In cetaceans, for example, GWAS revealed the genetic bases of adaptation to harmful algal blooms
512 and of resistance to a lethal virus (Batley et al., 2019; Cammen et al., 2015), potentially useful in
513 vaccine development (Batley et al., 2019). In plants, provenance and progeny trials (see D1.2)
514 represent opportunities to study interactions between host genotypes and associated organisms. In
515 trees of the genus *Populus*, genes associated with defence chemistry, phenology, growth and insect
516 community composition have been identified (Barker et al., 2019; DeWoody et al., 2013). These co-
517 evolutionary interactions between plant genotypes and associated communities can be harnessed to
518 foster plant health, to maintain or increase biodiversity, or to protect endangered species within their
519 environment. It has also been suggested that genomic information on interactions between host plants
520 and their symbionts, in particular arbuscular mycorrhizal fungi, can be used to **enhance** those
521 **beneficial associations** and restoration success (Aavik et al., 2021).

522 A promising approach to improve risk assessment for pathogen outbreaks is to examine genomic
523 signatures of host response and pest genetic variability in parallel (Bartoli and Roux, 2017; Karasov

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524 et al., 2014). This approach can contribute to monitoring the risks or to **prevent pathogen spillover**
525 from one host to another, as has been shown for an important fungal pathogen at risk of spillover from
526 cultivated apple to the Asian wild apple *Malus sieversii* (Feurtey et al., 2020). If the risk of pathogen
527 spillover to an endangered species is high, **discontinuation of host cultivation** could be an adapted
528 MA. Similarly, genomic assessment of disease spillover risk could be applied to aquaculture and wild
529 fish populations, as a complement to pathogen monitoring (Bouwmeester et al., 2021). Target
530 organisms are *a priori* at higher risk in the case of spillover of new, non co-evolutionary pathogen
531 attacks. In such systems, it is possible to identify genomic regions responsible for so-called exapted,
532 i.e., non co-evolutionary host resistant phenotypes, that would be due to the presence of genes
533 providing broad-spectrum resistance, as has been shown in the oak species *Quercus robur*
534 (Bartholomé et al., 2020). Although this requires both field work and substantial genomic resources
535 (e.g. mapping populations and a reference genome), rapid progress in non-model species paves the
536 way to more practical applications in the near future (Storfer et al., 2021).

537

538 **D2.4 Conserve and utilise microbial communities in water, soils and sediments**

539 Numerous ES of the Provisioning Section such as agricultural or material production and the
540 Regulation and Maintenance Section such as water quality, reduction of contamination, or nutrient
541 cycling are mediated by microorganisms. In terrestrial and marine environments, microorganisms
542 regulate, balance or otherwise affect inter- and intraspecific interactions (Freimoser et al., 2016; Jiao
543 et al., 2014; Marco and Abram, 2019). DNA metabarcoding, metagenomics and metatranscriptomics
544 have been called ‘thermometers for biodiversity’ as they rapidly provide large data sets on inter- and
545 intraspecific diversity of microorganisms and small organisms from a variety of taxonomic and
546 functional groups based on environmental DNA (eDNA) from environmental samples (Breed et al.,
547 2019; Saccò et al., 2022; Wilson et al., 2019). These tools can be applied simply and systematically
548 on large geographical scales, their efficiency in detecting species depending on taxonomic groups,
549 sampling conditions and available reference databases (Hua et al., 2015; Ji et al., 2013; Watts et al.,
550 2019; Wilson et al., 2019).

551 In forests, wood decomposition by microorganisms, in particular by saprophytic fungi, is crucial for ES
552 such as nutrient recycling, carbon sequestration, soil formation, habitats creation and the preservation
553 of the diversity of organisms living in dead wood (Tedersoo et al., 2016). DNA metabarcoding of forest
554 soils showed the impact of distinct keystone forest tree species, edaphic variables and past forest
555 management on microorganisms community structures (Behnke-Borowczyk et al., 2021; Jamy et al.,
556 2020; Tedersoo et al., 2016). This knowledge can inform forest management on which tree species
557 are most appropriate to **maximise soil** functions such as **carbon sequestration and nitrogen**
558 **storage** and to preserve soil microorganism diversity and their derived ES (Fig. 2). For example,
559 shotgun metagenomic sequencing revealed that soils under *Prunus serotina* exhibited functions that
560 indicate a rapid nitrogen cycle and a high inorganic nitrogen availability (Kelly et al., 2021), suggesting
561 that *P. serotina* can be used for **soil reclamation** in nitrogen-poor soil conditions (e.g. in coal mine

562 spoil heaps) to **restore post-industrial ecosystems** (see also D2.6). More generally, metagenomics
563 and metatranscriptomics can inform on the response of microorganism communities to environmental
564 change and identify mutualistic endophytic and rhizosphere plant-microbial associations, which opens
565 possibilities to harness these microbial functions through MAs (changing plant cover, inoculation) to
566 support desired responses (Hamilton et al., 2016; Jansson and Hofmockel, 2020).

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

571

572 **C2.5 Delineate areas for conservation and ES**

573 Delineating priority areas for biodiversity conservation and ES is a common challenge for managers
574 (Hermoso et al., 2018; M. Jung et al., 2021; Mokany et al., 2014; Sala et al., 2021; Weeks and Adams,
575 2018). Traditional approaches for conservation prioritisation identified hotspots based on species
576 richness and endemism (Mittermeier et al., 2005; Myers et al., 2000). Recent approaches use multiple
577 criteria to optimise the spatial representation and conservation of multiple biodiversity levels or
578 ecosystem properties, while also minimising socio-economic limitations (Carvalho et al., 2017, 2016;
579 V. Jung et al., 2021; Moilanen et al., 2009; Morán-Ordóñez et al., 2018; Pollock et al., 2020). Genomic
580 applications can facilitate **spatial prioritisation** through informing on drivers and features of
581 biodiversity representation and persistence (D2.4) and on adaptive population management (Andrello
582 et al., 2022; Hohenlohe et al., 2021; Nielsen et al., 2022), thus contributing to ecosystem resilience
583 and regulation (Des Roches et al., 2021; Raffard et al., 2019, see also D1). When combined with
584 spatially explicit measures of ES supply, demand and flow, genomics-informed conservation
585 **prioritisation** can help resolve trade-offs between different management objectives for biodiversity
586 conservation and different provisioning and/or maintenance and regulation ES (Hermoso et al., 2018;
587 M. Jung et al., 2021; Law et al., 2021; Pereira et al., 2020; Sala et al., 2021; Villarreal-Rosas et al.,
588 2020), thus **maximising benefits of biodiversity and ES**.

589 The body of research on genetic diversity across diverse species and evolutionary timescales
590 suggests that multi-species conservation objectives are necessary to delineate protected-area
591 networks that preserve evolutionary processes at the species and community levels (Carvalho et al.,
592 2017; Nielsen et al., 2017). Genomic data provide such metrics and enable the robust **delineation of**
593 **conservation areas** that can be adjusted to desired MGs with regard to population adaptation or **to**
594 **maximise multispecies evolutionary potential** (Phair et al., 2021; Xuereb et al., 2021). A study on
595 six freshwater fish species suggested maximising the representation of individual alleles (Paz-Vinas
596 et al., 2018) while another on three amphibian species recommended maximising the representation
597 of both neutral and adaptive allele clusters (Hanson et al., 2020). In aquatic ecosystems multispecies
598 information from metabarcoding is increasingly applied in spatial planning (Bani et al., 2020;
599 Pawlowski et al., 2018). Although still rare, the application of genomic multi-species assessments for
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600 protected area delineation are increasingly relevant for conservation planning and climate-adaptive
601 management of communities (Gaitán-Espitia and Hobday, 2021).

602

603 **D2.6 Restore communities, habitats and ecosystems**

604 The large-scale restoration of converted or degraded ecosystems is primordial to mitigate climate
605 change and limit species extinction world-wide (Rey Benayas et al., 2009; Strassburg et al., 2020;
606 Suding et al., 2015). Restoration success will strongly depend on defining specific, pertinent and
607 achievable MGs (see B2, Coleman et al., 2020; Coleman and Bragg, 2021). These will aim to restore
608 the biodiversity of a historical or extant reference state to renew forfeited ES (Breed et al., 2019; Suding
609 et al., 2015), or, alternatively, to reinforce or redefine the community for biodiversity conservation and
610 ES provisioning under future conditions (Coleman et al., 2020; Kleypas et al., 2021).

611 Restoration of habitats, communities or ecosystems first depends on the restoration success of
612 keystone species (see D1.4). Genomic applications in keystone and associated species allow to
613 **select provenances adapted to the current or future predicted climate**, to assess the risks
614 associated to their use in restoration in terrestrial or aquatic environments, and to monitor genetic
615 diversity in the restored populations (D1.4, Breed et al., 2019; Coleman et al., 2020; Rossetto et al.,
616 2019; Wood et al., 2020). A scientifically supported strategy for restoration of resilient communities is
617 **regional admixture provenancing** based on mixing seeds of a locally adapted provenance with that
618 of a few surrounding provenances which contributes to increasing the diversity for future adaptation,
619 as implemented jointly for multiple species in the restoration of European mesic grasslands
620 (Bucharova et al., 2019). In this approach, provenance regions are defined based on the abiotic
621 environment and are the same for all species (Bucharova et al., 2019). **Multispecies regional**
622 **admixture provenancing** could benefit from species-specific genomics-based delineation (Rossetto
623 et al., 2020) to facilitate reaching a compromise between current adaptation and the need for future
624 adaptive potential of restored communities (Bucharova et al., 2019). A study that combined genomic,
625 phenotypic and environmental data concluded that local provenances were the most appropriate to
626 restore moderately disturbed sites, whereas provenance admixture was found to be most effective for
627 the restoration of highly degraded sites (Carvalho et al., 2021; Rico, 2021). **Monitoring** the genetic
628 **outcomes** of restoration strategies allows management practices to evolve as knowledge
629 accumulates (Hodgins and Moore, 2016).

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

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

651

652 **E. Discussion**

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

670

671 **E1. Genomics applications allow to tackle ambitious management goals**

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

692

693 **E2. Genomics applications or alternative approaches: how to choose?**

694 It should be pointed out that the necessary evolution-based management actions do not always require
695 molecular genetic or genomic data (Hoban et al., 2020). A careful examination of the management
696 problem and available resources will help to identify the most appropriate data strategy, for example,
697 (1) to use proxies such as census population size to assess effective population size (Hoban et al.,
698 2020; Hoban et al., 2021b), (2) to use phenotypes to assess short-term responses to selection based
699 on quantitative genetics (Alexandre et al., 2020) or (3) to use an effective strategy to obtain the most
700 appropriate genetic or genomic data in pertinent species or communities (see B2, Angeloni et al.,
701 2012; Blasco-Costa et al., 2021; Flanagan et al., 2018; Schielzeth and Wolf, 2021). It should also be
702 stressed again that it is precarious to focus on current genetic adaptations alone to foster the future
703 persistence and resilience of populations. This is because 1) even if major effect loci can be found for
704 a trait of interest in a particular population, promoting them in another environment can have neutral
705 or even negative effects because complex adaptive traits are highly polygenic and thus phenotypes
706 depend on a given genomic background which can respond to different environments in different ways
707 due to genotype by environment interactions (Lind et al., 2018), and 2) there is uncertainty as to what
708 future environmental conditions will be. In the case of MAs that involve moving genetic materials
709 (individuals, populations, communities) or confronting them with new environments through
710 environmental change, the best assurance for future adaptability is to preserve and foster high genetic
711 diversity (Derry et al., 2019; Kardos and Shafer, 2018).

712 Epigenetic variation may also offer applications to the benefit of ES management. Transgenerational

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713 epigenetic and novel epigenetic landscapes may help predict adaptive responses through their effects
714 on phenotypes and thus the fitness of organisms (Jeremias et al., 2018). The dynamic epigenetic
715 system, in interaction with the environment, can thus direct genetically determined natural selection
716 (Manjrekar, 2017). As a consequence, epigenetic processes can support fast intraspecific adaptation,
717 impacting ecosystem services and functions (McCaw et al., 2020; Rey et al., 2020). Although
718 epigenetic variation and processes appear to strongly vary across species with regard to their
719 frequency and type of responses to climate change (McCaw et al., 2020), they can collectively impact
720 important ES and their study is just beginning in non-model species.

721

722 **E3. Genomic applications in the natural resource policy context**

723 Adopting effective biodiversity conservation and management for ES is urgent and necessary in the
724 current biodiversity crisis, and genetic and genomic methods and data are ready to be implemented
725 to support the most effective management as we show in this paper (see also Hoban et al., 2020;
726 Hoban et al., 2021a; Laikre et al., 2020). In this context, it is especially important that the CBD post-
727 2020 Global Biodiversity Framework adopt a strong goal for the conservation of genetic diversity, and
728 genetic diversity indicators to monitor progress towards achieving this goal (Hoban et al., 2020; Hoban
729 et al., 2021a). Genetic and genomic approaches are also crucial to improve management for the
730 implementation of policies that are already in place, for biodiversity conservation and provision of ES
731 as well as for human well-being, such as the UN 2030 sustainable development goals, and the EU
732 Biodiversity strategy for 2030. For example, genomics can help decide which species and
733 provenances are the most suitable for major ongoing tree planting initiatives, such as the '3 Billion
734 Trees Pledge' committed by the EU biodiversity strategy for 2030 under the EU Green deal, and its
735 North American counterparts, the '1 trillion tree initiative' in the USA and the '2 billion trees
736 commitment' in Canada. Genomic applications will also support a faster implementation of sustainable
737 fishing practices regulated by the EU Common fisheries policy and the Marine Strategy Framework
738 Directive. Long-term natural resource planning and policy requires genetic diversity and gene flow
739 information in increasing numbers of species to reach the best management decisions without
740 compromising the resilience and adaptive potential of ecosystems (G-BIKE, 2020). Novel
741 developments and adaptations of the policy framework will be necessary to allow for ambitious MGs
742 to adapt natural resources to future needs. For example, legal recognition of hybrids in conservation
743 and natural resource policies would make a significant step forward to enhance such MGs, recognizing
744 that species are not fixed but evolving entities (Draper et al., 2021; Fitzpatrick et al., 2015). Other
745 ambitious policy developments that genomic data can support through proposing consensus methods
746 concern the taxonomic delimitation of closely related species in species complexes (Coates et al.,
747 2018) and the conservation of adaptive potential (Funk et al., 2019).

748

749 **E4. Genomics applications in natural resource management in practice**

750 The scientific community is increasingly well organised, in conjunction with natural resource managers,
751 to use the most powerful scientific knowledge to promote and achieve ambitious goals for biodiversity
752 in policy and practice, e.g., through collaborative instruments such as the EU COST Action G-BIKE
753 (Genomic Biodiversity Knowledge for Resilient Ecosystems, G-BiKE, 2019) or the Coalition for
754 Conservation Genetics that federates four eminent organisations (Kershaw et al., 2022). Scientists
755 increasingly recognize the power of genome-wide data for monitoring and managing genetic diversity
756 (e.g., Meuwissen et al., 2020), with the great promise of mitigating the ever intensifying environmental
757 change. At the same time, natural resource managers are increasingly aware of the benefits provided
758 by genomic monitoring tools, and teaming up with geneticists for timely interventions and optimising
759 ES. There remains a need to enhance standardisation and simplification of genomic data acquisition
760 and analysis workflows to reduce the cost, increase the speed and facilitate the practical deployment
761 of genomics in MAs (Rossetto et al., 2021; von Thaden et al., 2020). Synergies between scientists
762 and ES managers need to be increasingly fostered not only at international (Kershaw et al., 2022) but
763 also national and local levels to bridge the science-ES management application gap. Ambitious goals
764 for biodiversity conservation, its sustainable use and provision of ES can be achieved by merging the
765 high level of expertise required to analyse the genomic data and the expertise of real-world ES
766 management using appropriate workflows, deploying genomics training to ES managers, and
767 incorporating indigenous and local knowledge into science-informed MAs (e.g., Díaz et al., 2020). In
768 COST Action G-BIKE we follow this rationale, and in this work in particular, we prepared a “Brief for
769 nature managers” (Supplementary material S2) that summarizes our main findings and provides
770 application examples targeted to biodiversity and ES managers. The brief will be made available on
771 the G-BIKE website (<https://g-bikegenetics.eu/>) in a user-friendly layout with illustrations and
772 translated to several languages for dissemination. Another example framework for science-informed
773 biodiversity and conservation actions on the ground is the Biodiversity and Ecosystem Services
774 Network (BES-Net) that builds capacity and commitment for biodiversity action across the world by
775 translating the latest IPBES products into action, but BES-Net still lacks the implementation of
776 genomics. Governments and natural resource managers need to embrace the huge potential of
777 genomics for ES, particularly in this time of rapid changes in our ecosystems as a result of
778 anthropogenic effects.

779

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794

795

796 **Declaration of interests**

797 The authors declare that they have no known competing financial interests or personal relationships
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799

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1619 **Author contributions**

- 1620 Conceptualization: MH, PGG, JAMR, SBC, JG, BR, PR, TG, BJM, ST, AVa, AVe
1621 Data curation: MH, TG, PGG
1622 Formal analysis: MH, TG, PGG
1623 Funding acquisition: SH, CV
1624 Investigation: MH, PGG, SBC, JG, BR, PR, TG, JAMR, ST
1625 Methodology: PGG, MH, SBC, JG, BR, PR, TG, JAMR, ST
1626 Project administration: CV
1627 Resources: CV
1628 Visualisation: JMIB, PGG, MH, JG, ST, BR
1629 Roles/Writing - original draft: MH, PGG, SBC, JG, BR, PR, TG, JAMR, ST, AVa, SCGM, IP, AVe
1630 Writing - review & editing: MH, PGG, SBC, JG, BR, PR, TA, IA, JMIB, HC, RG, SCGM, TG, SH, AK,
1631 BJM, IP, JAMR, ST, AVa, AVe, CV

1634 **Supplementary materials**

1636 **S1 Keyword analysis - How does genomics link to ecosystem services in** 1637 **the scientific literature?**

- 1638 To systematically and quantitatively examine the links between the concepts of genomics, biodiversity
1639 and different types of ecosystem services in the scientific literature, we assessed and analysed the
1640 co-occurrence of keywords attributed to these concepts in the abstracts of published articles.

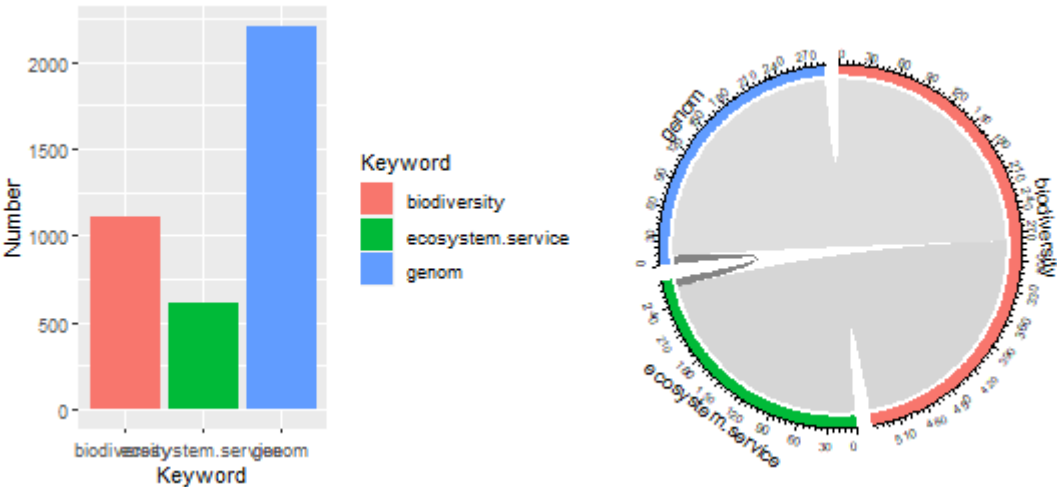
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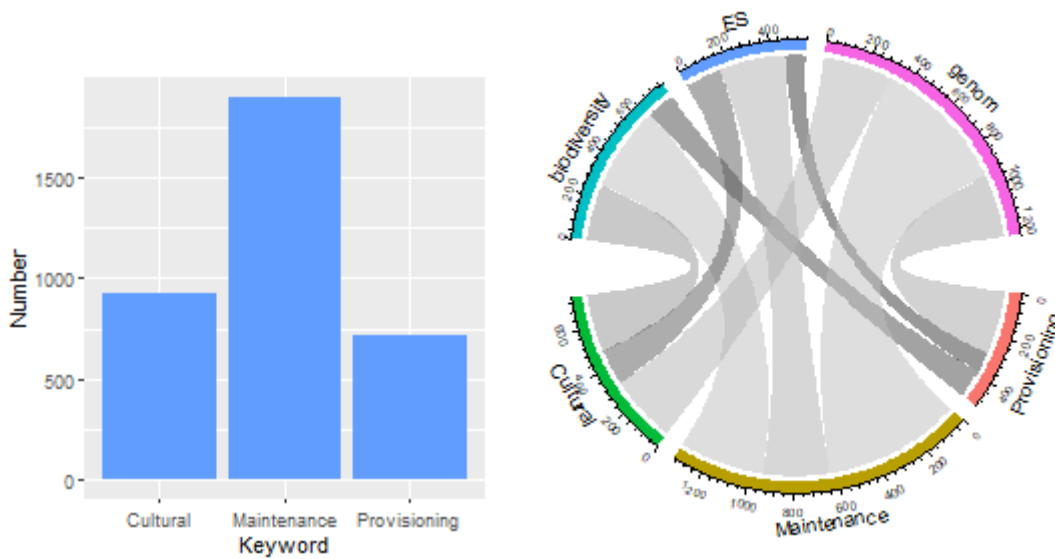
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Methods - We conducted a terminology research on Pubmed Central (<https://www.ncbi.nlm.nih.gov/pmc/>) for pairwise combinations of the terms “biodiversity”, “ecosystem service” and “genomics” in the body text of articles on **October 8th, 2020**, using the “Advanced search” tools. The search command was formulated as “(ecosystem service[Body - All Words] AND biodiversity[Body - All Words]) OR (ecosystem service[Body - All Words] AND genomics[Body - All Words]) OR (biodiversity[Body - All Words] AND genomics[Body - All Words])”. Abstracts of all retrieved papers were searched with 1. Target keywords (“ecosystem service”, “genom” and “biodiversity”); 2. Keywords or combinations of keywords describing ES *Classes* belonging to the three ES *Sections* Provisioning ES, Regulation and maintenance ES, and Cultural ES, as defined by the Common International Classification of Ecosystem Services, v5.1 available at <https://cices.eu/>. CICES classifies ES in a system of four hierarchical levels, 1) *Sections*, 2) *Divisions*, 3) *Groups*, and 4) *Classes*. We attributed each retrieved paper to one or more *Classes* (four-number code of CICES) based on keywords found in the abstract that matched the corresponding CICES *Class* descriptions.

Results - Our keyword research yielded 6417 references, the earliest published in 1993; 6064 papers had an abstract and were analysed. The target keywords “biodiversity”, “ecosystem service” and “genom” appeared in the abstracts of 2211, 616 and 1114 retrieved papers, respectively, representing a total of 2871 papers (Figure S1). We discovered that only 9 papers mentioned “genom” (contained in genome, genomic, genomics) and “ecosystem service” simultaneously in the abstract although both concepts are well connected through biodiversity (Figure S1). The links between the keywords “genomics” and “ecosystem services” appear poorly exploited in the literature, but the strong connection of both concepts with biodiversity illustrates that there is potential of genomic studies for ES valuation.

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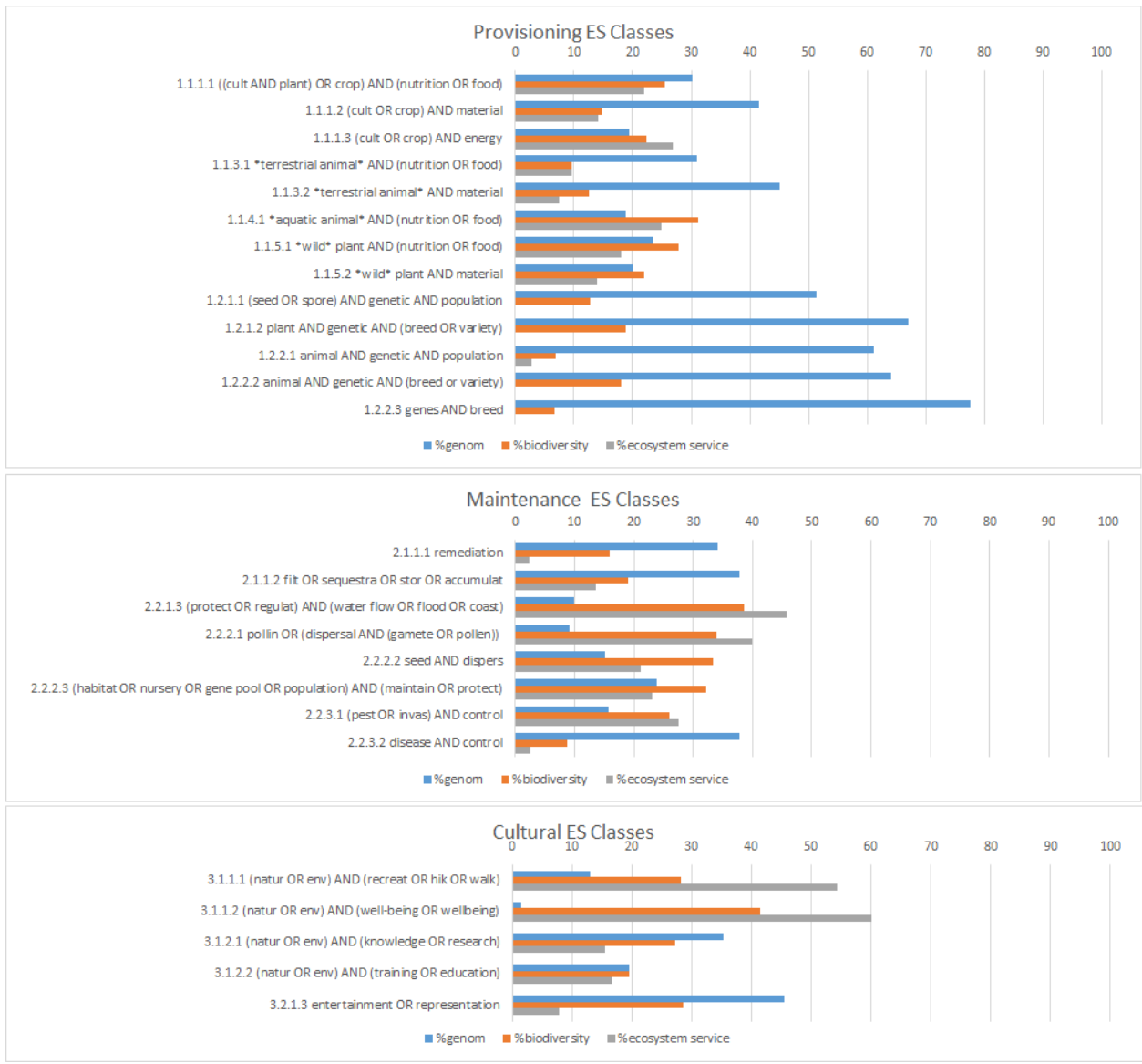
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1669 Figure S1. Articles retrieved in a search on Pubmed Central (<https://www.ncbi.nlm.nih.gov/pmc/>) for
1670 pairwise combinations of the terms “biodiversity”, “ecosystem service” and “genomics” in the body text
1671 of articles, on October 20, 2020.

1672

1673 A total of 2871 papers were attributed to specific ES Sections, 720 to the Provisioning Section, 1903
1674 to the Regulation and Maintenance section and 929 to the Cultural Section (Figure S2); multiple
1675 attributions were possible. The “genom” term was associated with articles from the three Sections in
1676 proportions similar to the number of articles retrieved.

1677 Within the Provisioning ES Section, the retrieved papers were unevenly distributed across Classes:
1678 Studies on plants as food crops (1.1.1.1) or for materials (1.1.1.2) were represented about four times
1679 more frequently than such studies on animals (1.1.3.1 and 1.1.3.2). Genetic resources as materials
1680 for breeding (1.2.1.2, 1.2.2.2, 1.2.2.3) or population conservation (1.2.1.1, 1.2.2.1) were also well
1681 represented (see Supplementary material).



1682

1683 Figure S2. Attribution of articles with the target keywords “biodiversity”, “ecosystem service” or
 1684 “genom” appearing in their abstracts to Sections and Classes of Ecosystem Services as defined by
 1685 CICES. Only classes with more than 30 attributed studies are represented.

1686 In the Classes of the Provisioning Section with more than 30 studies represented (Figure S2), we
 1687 illustrate the percentage of studies in which our target keywords occurred in the abstract. The “genom”
 1688 term occurred in over 50% of the studies on breeding or population establishment or conservation
 1689 (1.2.1.1., 1.2.1.2, 1.2.2.1, 1.2.2.2, 1.2.2.3), and was more frequent in classes on food (1.1.1.1, 1.1.3.1)
 1690 and materials (1.1.1.2, 1.1.3.2) than energy (1.1.1.3). The ecosystem service term was, strikingly, very
 1691 poorly represented in these Classes on breeding or conservation, suggesting that studies on the
 1692 provision of genetic materials or resources are not commonly presented as targeting an ES. The

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1693 biodiversity term was mentioned as the most frequently associated keywords in Classes on fisheries
1694 (1.1.4.1) or wild-sourced food or materials (1.1.5.1, 1.1.5.2). When characterizing genetic materials
1695 using genomic tools, scientists are fulfilling a Provisioning ES, a link that could be made more visible
1696 in future genomic studies.

1697 In the Regulation and Maintenance ES Section, the retrieved studies were attributed to Classes in a
1698 strongly uneven way, with a strong overrepresentation of studies attributed to the Class on filtration,
1699 sequestration, storage or accumulation (2.1.1.2) and a near-absence of studies in the Classes that
1700 focus on the contribution of living organisms in the regulation of soils (2.2.4.x, 2.2.5.x). The “genom”
1701 term (Figure 2B) was mostly associated with bioremediation (2.1.1.1), filtration / sequestration /
1702 storage / accumulation (2.1.1.2) and disease control (2.2.3.2). These Classes are much less
1703 associated with the ES term, and thus not explicitly valued as ecosystem services. Genomics was little
1704 associated with water flow regulation (2.2.1.3), and perhaps, unexpectedly, with pollen or seed
1705 dispersal (2.2.2.1, 2.2.2.2) and control of invasives (2.2.3.1). The latter categories are strongly
1706 associated with the biodiversity and ES terms though, and thus correctly valued as such in the
1707 literature.

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1709 In the ES Section on Culture, most retrieved studies were attributed to the Class on nature-related
1710 knowledge or research (3.1.2.1), and accessorially to the one on nature-related training or education
1711 (3.1.2.2); Classes on nature-related experiences and wellbeing (3.1.1.1, 3.1.1.2) or entertainment and
1712 representation (3.2.1.3) were also significantly represented (> 30 studies/ Class; Figure 2C). Classes
1713 related to natural heritage, aesthetic, spiritual or religious experiences were little represented.
1714 Genomics was predominantly associated with the class on nature-related knowledge or research
1715 (3.1.2.1) and that on representation (3.2.1.3), although the latter could be an artifact due to multiple
1716 meanings of the term “representation”; genomics was little associated with nature-related experiences
1717 and human well-being (3.1.1.1, 3.1.1.2), although the latter classes are clearly associated with
1718 biodiversity and ecosystem services.

1719 Our keyword analysis on the terms genomics, biodiversity and ecosystem services in the scientific
1720 literature has limitations, especially due to the fact that the words used to define ES classes can have
1721 multiple meanings and that CICES categories are unevenly covered in the scientific literature. The
1722 analysis allows us to conclude that the link between genomics and ecosystem services is exploited in
1723 breeding and biodiversity conservation studies, but that there is potential for genomics studies in other
1724 fields to highlight more clearly their contribution to ES.

- 1725 - For Provisioning ES, the genomic characterization of materials can be better promoted as an
1726 ES.
- 1727 - For Regulation and Maintenance ES, genomic studies relating to bioremediation, filtration,
1728 sequestration, storage or accumulation and with disease control have potential to be better
1729 values as delivering ES.
- 1730 - For Cultural ES, genomic applications are not much represented beyond knowledge
1731 generation, thus there is no clear potential identified to value them as ES.

1732 To better exploit this link, researchers could use a multidirectional approach based on 1. identifying
1733 the ES that match the object of their genomic work, instead of using biodiversity-centered approach
1734 only; 2. targeting genomic studies toward ES that have received little contributions from genomics but
1735 where a potential may exist, through including genome-ES studies into existing and future projects
1736 and programmes.

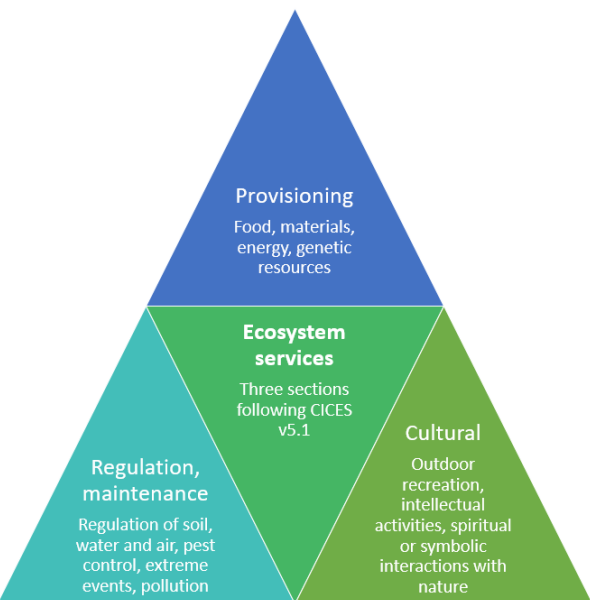
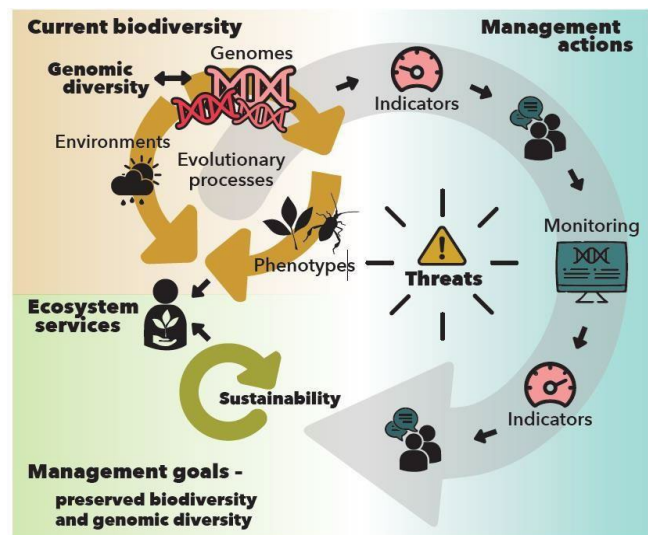
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S2 Brief for nature managers - Genomic applications for the conservation and management of biodiversity and ecosystem services

- The ongoing loss of biodiversity impacts ecosystem services (ES), the benefits that ecosystems provide to people (e.g., pollination, timber production, water filtration)
- High biodiversity within species, i.e., genetic diversity, allows populations and species to adapt and be resilient in the long-term
- Long-term resilient communities yield sustainable ES
- Nature managers can use genetic diversity information to more effectively
 - achieve biodiversity conservation and sustainable nature management goals
 - comply with biodiversity policies

WHY AND HOW – Collaboration with scientists can provide genetic or genomic diversity knowledge (BOX) that benefits nature managers to:

- Design management actions based on genetic indicators to meet their ES goals
- Monitor the success of implemented management actions
- Adjust management actions as necessary to achieve sustainability



Nature management goals that support sustainable ecosystem services and benefit from genomic diversity knowledge

- Conservation of threatened species and delineation of conservation/management areas
- Management
 - for sustainable productivity
 - for adaptation to climate change
 - of invasive species
 - of host-microbe interaction, e.g., pest control, symbionts
 - of microbial communities
 - for ES derived from water, soils and sediments
- Species, habitat and ecosystem restoration

gap: Genomics for biodiversity and ecosystem service management. *Biological Conservation* 2023 ;Volum 278. [10.1016/j.biocon.2022.109883](https://doi.org/10.1016/j.biocon.2022.109883)

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- Implementation of new biodiversity policies

BOX: Genetic diversity is the intraspecific diversity between individuals within a species, encoded in DNA and expressed in diverse phenotypes and adaptations to environments.

Genetic diversity

- Determines species' adaptive potential to environmental change,
- Increases ecosystem resilience in the face of climate change and anthropogenic risks,
- Supports all the other levels of biodiversity that deliver ecosystem services, benefiting people

Genomic diversity refers to genetic diversity measured at hundreds to millions of DNA sites spread across the genome. It provides highly detailed information on

- Genetic diversity and inbreeding within populations
- Genetic structure among populations
- Species' past demographic and selection history
- Genes involved in adaptive variation and adaptive potential
- Genomic signatures of hybridization

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WHICH DATA - Genomic diversity information to support management can be collected

- in a species threatened by extinction
- in the species most relevant for the ecosystem function or service of interest
- in interacting species, e.g., invasive species, hybrids, host-pest systems
- in a community of microbes

Management goals	Genomics-informed management actions
Population or species conservation	reduce inbreeding to prevent inbreeding depression, preserve gene pools, assist colonisation, design conservation areas that maximise adaptive potential
Sustainable productivity	identify populations (stocks) for management, breed for/promote productivity while conserving genetic diversity
Climate adaptation	favour adaptive alleles while conserving genetic diversity, assisted gene flow, assisted colonization
Restoration	perform climate-adjusted provenancing while conserving genetic diversity
Pest control	monitor disease dynamics, identify and promote co-evolved resistance, prevent pest spillover

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Microbial community management	characterise community function and manage it, e.g., through associated vegetation or inoculation to promote desired properties
Control of invasives	identify alien species to prevent invasion, identify invasive genotypes

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IN PRACTICE, NATURE MANAGERS CAN

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- Collaborate with scientists on data, methods and implementation of new policies
- Discuss the need for genomic data, its collection and use for a given management goal
- Use genomic information to identify risks of management options, including inaction
 - e.g., inbreeding, maladaptation and local extinction risks in the absence of active management
 - e.g., risks of co-translocated pathogens in the case of translocation or population supplementation
- Implement the best genomics-informed management actions and monitor their risks and successes

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Examples of genomic applications for nature management

Illustration of Atlantic cod	Genomic applications help to secure the future of seafood. Genomic applications revealed the geographic distribution of distinct Atlantic cod ecotypes and the genome regions responsible for their differential adaptation.	Illustration of a bat of genus <i>Myotis</i>	Including information on adaptive genomic variation in species distribution modelling improves projections for future range losses and the potential for population rescue using population genetic connectivity or assisted colonization.
Illustration of Australian Acacia woodland	Genomics-informed provenancing strategies for woodland restoration that account for the drivers of genomic divergence achieve better proofing to future climates than strategies based on distribution similarity of tree species.	Illustration of a pine seedling	Monitoring of gene flow from exotic plantations into native relict stands of Mediterranean conifers demonstrated that the proportion of exotic-sired offspring decreased from seeds to established seedlings. Exotic pollen did not lead to fitness reduction in offspring in native stands.

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<p>Illustration of one of the pest species or leaf lesions from the paper</p>	<p>Genomic biosurveillance of tree pathogens and pests can be reliably conducted on plant lesions, even <i>in situ</i> in remote forests, allowing for fast and accurate identification that can speed up management interventions.</p>	<p>Illustration of an abandoned mining site</p>	<p>Metabarcoding of soil microbial communities informs on the effectiveness of soil reclamation activities, as shown on the site of an abandoned iron and sulfur mine in southern Poland where soil restoration measures were conducted in the 1970s.</p>
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BENEFITS FOR POLICY IMPLEMENTATION

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Genomics-informed management is adapted to an ambitious policy framework for nature conservation and management. It helps to meet the requirements of

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- the EU Habitat directives,

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- the EU Natura 2000 network management,

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- the CBD Post-2020 global biodiversity framework,

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- the UN 2030 sustainable development goals,

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- the EU 2030 Biodiversity strategies,

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- the EU Forest strategy for 2030,

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- the EU Green deal and infrastructure strategy,

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- the EU Water Framework Directive,

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- the EU Common fisheries policy and Marine Strategy Framework Directive

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The content of this brief for nature managers is based on research published in *Biological Conservation* and developed by COST Action G-Bike (Genomic biodiversity knowledge for resilient ecosystems) under working group 3 Genomics and ecosystem services <https://g-bikegenetics.eu/en>

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