

1 **The need of decoding life for taking care of biodiversity and the sustainable**
2 **use of nature in the Anthropocene – a Faroese perspective**

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4 **Svein-Ole Mikalsen^{1,4,3}, Jari í Hjøllum¹, Ian Salter², ~~Sjúrdur Hammer^{1,3}~~, Anni**
5 **Djurhuus¹, and Sunnvør í Kongsstovu¹**

6

7 ¹ Faculty of Science and Technology, University of the Faroe Islands, Vestara Bryggja 15,
8 FO-100 Tórshavn, The Faroe Islands

9 ² Faroe Marine Research Institute, Nóatún 1, FO-100 Tórshavn, The Faroe Islands

10 ~~³ Faroese Environment Agency, Traðagøta 38, FO-100 Tórshavn, The Faroe Islands~~

11 ^{4,3} Corresponding author. E-mail: sveinom@setur.fo

12

13 SOM: ORCID 0000-0002-7128-4464; sveinom@setur.fo

14 JíH: ORCID 0000-0003-2388-9378; jarih@setur.fo

15 IS: ORCID 0000-0002-4513-0314; ians@hav.fo

16 ~~SH: ORCID 0000-0002-3986-5074; sjurdurh@us.fo~~

17 AD: ORCID 0000-0002-3517-7522; annid@setur.fo

18 SíK: ORCID 0000-0001-6631-2347; sunnvork@setur.fo

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21 **Keywords**

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24 sustainability.

25 **Abstract**

26 Biodiversity is under pressure, mainly due to human anthropocentric activities and climate
27 change. At the international policy level, it is now recognised that genetic diversity is an
28 important part of biodiversity. The availability of high-quality reference genomes gives the
29 best basis for using genetics and genetic diversity towards the global aims of (i) protection of
30 species, biodiversity, and nature, and (ii) in management of biodiversity for achieving
31 sustainable harvesting of nature. Protecting biodiversity is a global responsibility, also resting
32 on small nations, like the Faroe Islands. Being in the middle of the North Atlantic Ocean and
33 having large fisheries activity, the nation has a particular responsibility towards maritime
34 matters. We here provide the reasoning behind Genome Atlas of Faroese Ecology
35 (Gen@FarE), a project based on our participation in the European Reference Genome Atlas
36 consortium (ERGA). Gen@FarE has three major aims: (i) To acquire high-quality genomes
37 of all eukaryotic species in the Faroe Islands and Faroese waters. (ii) To establish population
38 genetics for species of commercial or ecological interest. (iii) To establish an information
39 databank for all Faroese species, combined with a citizen science registration database,
40 making it possible for the public to participate in acquiring and maintaining the overview of
41 Faroese species in both terrestrial and marine environments. Altogether, we believe that this
42 will enhance the society's interest in and awareness of biodiversity, thereby protecting the
43 foundations of our lives. Furthermore, the combination of a wide and highly competent
44 ERGA umbrella and more targeted national projects will help fulfilling the formal and moral
45 responsibilities that all nations, also those of limited resources, have in protecting biodiversity
46 and achieving sustainability in harvesting from nature.

47 **Background**

48 The Faroe Islands, and all nations in the world, live from nature. Mankind gets its food and
49 raw materials from nature, directly or indirectly. We are now affecting the Earth so heavily
50 and fundamentally that it is proposed to call the present time the Anthropocene - the
51 geological epoch of human influence [1].

52

53 A well-functioning nature is dependent on healthy ecosystems, which again are intimately
54 linked with biodiversity. The term "biodiversity" includes the full set of all life forms, their
55 variations and functions, and their community structures in the different habitats and
56 ecosystems [2]. The total biodiversity is a composite of several "sub"-diversities, and among
57 them, genetic diversity (additionally, and subject to the definition of choice, diversity in
58 species, ecosystems, functions, and evolution are often included) [2, 3]. It may well be argued
59 that genetic diversity is the foundation for each of the other "sub"-diversities, and thereby
60 also the total biodiversity. Biodiversity is central in maintaining ecosystems both locally and
61 globally. However, many species, ecosystems, and even global biodiversity are today
62 threatened by overexploitation, fragmentation of nature, loss of habitats, invasive species, and
63 climate change [4]. Thus, all aspects of conservation, like protection of species and their
64 genetic diversity, and the protection of the areas and resources that the species depend on,
65 need to be considered to preserve biodiversity, ecosystems and nature as a whole, and at the
66 same time achieve sustainable exploitation to ensure that humans can live in a healthy world
67 in the future [2].

68

69 It is of utmost importance that we, as the main caretaker of the Earth, are aware of the
70 biodiversity and the existing genetic diversity. Within each single species, and within each
71 single individual, the material of inheritance, the genome, is the basis and the main frame for
72 the present diversity and carrying the diversity forward to the future generations. It is also
73 recognized that genetic diversity within a species is pivotal for adaptation in a changing
74 world, which is even more important in times of climate change. Thus, knowing the genome
75 sequences from as many species as possible is central in the understanding and knowledge of
76 the full span of biodiversity. With the strong influence that humans have on the ecosystems
77 and the Earth, we will only be able to maintain the diversity and exploit it in a sustainable
78 way by having relevant knowledge about the diversity. It is difficult or impossible to take
79 unknown or undetected species into considerations in a management plan, or to make proper
80 management plans for species, an ecosystem, or a geographical area when relevant and

81 significant biological knowledge is not available. The sustainable utilisation and management
82 of biological resources require a determined effort to establish current status (which is not
83 necessarily the same as the historical status) and monitor future changes of biodiversity in
84 diverse environments.

85

86 We should be fully aware that we presently do not know all species, as new species are
87 discovered every year, even in well-explored areas like Europe [5]. The marine environments
88 are likely to hide many unknown species [6]. Furthermore, we have limited biological
89 knowledge of many of the species we do know, even among species that are commercially
90 exploited, *e.g.*, their full geographical distribution, subpopulations, population dynamics,
91 interactions with other species, the influences of climate change or human harvesting, etc.

92

93 In international policy, the terms "sustainability" and "biodiversity" became much more
94 frequently used after the UN report "Our Common Future" from 1987 [7] and the Convention
95 on Biological Diversity (CBD) from 1992 [8]. Article 1 of CBD states that "*The objectives ...*
96 *are... the conservation of biological diversity, (and) the sustainable use of its components...*"
97 [8]. The balance of conservation and sustainable use of nature is repeated in several of the
98 subsequent articles of CBD. All parties of the CBD, including the Faroe Islands (through the
99 Kingdom of Denmark), commit to these objectives. CBD is the basis for additional
100 international agreements and protocols. The Faroe Islands have committed to some of these,
101 like the UN Agenda 2030 for Sustainable Development and its Sustainability Development
102 Goals (SDG) [9, 10], but not to others, like the Nagoya protocol and the Aarhus convention.
103 Not being a member of EU (despite that Denmark is a member), Faroe Islands are also less
104 restrained by EU regulations and agreements.

105

106 The Kunming-Montreal global diversity framework from December 2022, better known as
107 UN CBD Conference of Parties 15 (COP15) [11], underlined the importance of genetics and
108 genetic diversity in biodiversity and sustainability, as reflected in their direct mentioning in
109 two of the four overarching goals:

- 110 • *The **genetic diversity** within populations of wild and domesticated species is*
111 *maintained, safeguarding their adaptive potential.*
- 112 • *The monetary and non-monetary benefits for the utilization of **genetic** resources ...*
113 *are shared fairly and equitably...*

114 This is also repeated in some of the corresponding 23 targets for the Kunming-Montreal
115 framework:

- 116 • *Target 4: Ensure urgent management actions, to halt human induced extinction of*
117 *known threatened species and for the recovery and conservation of species, in*
118 *particular threatened species, to significantly reduce extinction risk, as well as to*
119 *maintain and restore the **genetic diversity** within and between populations of native,*
120 *wild and domesticated species...*
- 121 • *Target 13: Take effective legal, policy, administrative and capacity-building measures*
122 *at all levels, as appropriate, to ensure the fair and equitable sharing of benefits that*
123 *arise from the utilization of **genetic** resources...*
- 124 • *Target 21: Ensure that the best available data, information and knowledge (this*
125 *undoubtedly include genetic data, information and knowledge; authors' comment), are*
126 *accessible to decision makers, practitioners and the public to guide effective and*
127 *equitable governance, integrated and participatory management of biodiversity, and*
128 *to strengthen communication, awareness-raising, education, monitoring, research*
129 *and knowledge management...*

130
131 Indirectly, having the species' genome assemblies and knowing the genetic diversities will
132 wholeheartedly support the other COP15 overarching goals and targets for the Kunming-
133 Montreal framework that involve sustainability and sustainable management, and **further** the
134 integration of biodiversity into policies, planning and regulations, including the protection of
135 species, habitats, ecosystems and areas, etc. The four overarching goals and the 23 more
136 specified targets can be seen as an elaboration and specification from previous international
137 agreements and protocols. We will here have a main focus on how genomes and the
138 knowledge of genetic diversity can help us in protecting biodiversity and maintaining
139 sustainability to reach different aims and potentials.

140 141 **Genome Atlas of Faroese Ecology (Gen@FarE)**

142 Knowledge of the full genome of each species and the genetic diversity within each species,
143 provide powerful tools to monitor **biodiversity**, and through that, **manage** and **preserve it** [2,
144 12]. This knowledge can be used in different ways and for different purposes. On the very
145 practical and applied side, management of commercially exploited resources and protection
146 of species and/or habitats, can be much improved by such tools. It will also give us better

147 tools to survey the environment, whether it is for invasive species or population estimates.
148 Equally important, such knowledge is valuable for understanding the diversity of life in all its
149 aspects and functions, and it will undoubtedly initiate further questions and give new avenues
150 to explore (see section *Incidental insights*). But above all, [this will](#) help us [in protecting](#) and
151 [maintain](#)ing a healthy Earth for mankind and all its fellow beings.

152
153 National and regional initiatives are taking place both in Europe and globally by people and
154 institutions recognising the need for, and the potential of, [genomic](#) knowledge [13-17]. This
155 is a highly international task, where all nations need to contribute and collaborate. We all, as
156 individuals, as industry, as society, as nations, have responsibility for the future of the Earth
157 and its nature, and the politicians and governments must set the frames so this can become
158 possible to achieve. Realising the urgency and needs in protecting biodiversity, and that
159 genomics and genetics are essential tools in achieving this purpose, more than 700 European
160 scientists, some of the present authors among them [18], have gone together to form the
161 European Reference Genome Atlas project (ERGA) [13, 19, 20] as a collaborative and
162 interdisciplinary network. Also small nations, like the Faroe Islands (1 400 km² and 54 000
163 inhabitants), should contribute to this effort, partly as a global and moral obligation, and
164 partly to ensure sustainability in its exploitation of biological resources in accordance with
165 CBD [8]. Utilising the ERGA network and its dedication to a decentralised and equitable
166 biodiversity genomics [21], the present authors have initiated the Genome Atlas of Faroese
167 Ecology (Gen@FarE), and we participate in the ERGA Pilot project [21]. Although being a
168 small nation, the Faroe Islands have a sizable economic zone (274 000 km²) in the middle of
169 the North Atlantic Ocean, and it has large fisheries activity. Thereby the nation has a
170 particular responsibility towards maritime matters. The authors represent Faroese institutions
171 with responsibilities for education, research, monitoring, and dissemination of knowledge
172 within Faroese and North Atlantic biology and biodiversity, and advising the authorities
173 about stock management and nature in general. We jointly see the advantage of increased
174 genomic and genetic knowledge for protecting biodiversity and achieving sustainability in the
175 region.

176
177 The Genome Atlas of Faroese Ecology has three major long-term aims:

- 178 • To establish high-quality genomes of all eukaryotic species in the Faroe Islands and
179 Faroese waters.

- To establish population genetics for all species that are commercially exploited or are of ecological interest.
- To establish an information databank for all Faroese species, combined with a citizen science registration database, making it possible for the public to participate in acquiring and maintaining the overview of Faroese species in both terrestrial and marine areas.

We expect that it will take many years, maybe decades, before having high-quality genome assemblies from all species, despite the expected technological advances and the consorted accumulation of relevant genomes and data from other countries. We are aware that other projects, [like the Earth BioGenome Project](#), may have more optimistic views on how fast such an aim will be achieved, but a large upscaling of capacities is needed [14, 22]. The urgency of protection and maintaining the biodiversity and ensuring sustainability in the harvesting of nature, requires that it is worked on all three aims in parallel.

In the long-term process, there are many other direct and indirect aims, some of which we may not yet be aware of, some that are general, and others that are associated with a particular species. In particular, we would like to point out the close link to biomonitoring using metabarcoding (see section *Biodiversity and conservation*), as the product from this project will help closing the lacks and gaps in reference sequence databases due to absence of species or genes, or intraspecies variability in marker genes.

Biodiversity and conservation

Of course, partly as a consequence of the CBD, each nation has an added moral responsibility for diversity existing only (or mainly) within their national borders and maritime economical zone. Although there are few known endemic species in the Faroe Islands, it has its share of bird diversity with the world's largest colony of [European](#) storm petrel (*Hydrobates pelagicus*), one of the [few](#) last remains of (claimed) wild type rock pigeon (*Columba livia*), and recognized subspecies of several other birds (European starling, *Sturnus vulgaris feroensis*; Eurasian wren, *Troglodytes troglodytes borealis*; common eider, *Somateria mollissima faeroensis*; etc.) (see [23] for more information). However, we will in this paper not focus on this particular part of biodiversity.

213 The Red List status is often an important part in decisions for "what to do" and "how to do" in
214 conservation and protection of species. The assessment of the Red List status is based on
215 population trends and some other parameters [24], some of which are not always easy to
216 assess for different reasons. One could imagine the inclusion of genetic diversity status into
217 this assessment, both as an independent parameter and as an indirect parameter for assessing
218 effective population size [25, 26]. It is well known that low effective population size
219 increases the rate of homozygosity. Runs of homozygosity have been used for estimating
220 historical bottlenecks for certain species [27-29] as they are recognizable long after a
221 potential expansion of the population following a bottleneck. It might be possible to take
222 similar models into use for practical conservation and protection purposes, like the national
223 and regional Red Lists. However, there is – perhaps surprisingly - no direct correlation of the
224 Red List status and runs of homozygosity for a limited set of mammals [29] (please note that
225 there is somewhat conflicting evidence regarding the correlation of the Red List status and
226 runs (or degree) of homozygosity or loss of heterozygosity; see refs. in [29, 30]). As hinted at
227 [29], there could be several explanations, like (i) the populations have not reached
228 sufficiently low level to erode genetic variation in the individuals, or (ii) when the decline is
229 rapid (as it is in many cases) and without any particular genetic selection pressure, the
230 relative degree of heterozygosity is maintained for quite a while, and runs of homozygosity
231 only become evidently apparent after some generations at low population size.

232

233 Next generation sequencing and in particular third generation sequencing have shown that
234 structural genetic variants are more common than previously thought. In some cases,
235 structural variants are probably decisive for ecological adaptation and migration [31, 32] (see
236 also section *Sustainability and commercial exploitation*), and in other cases they influence
237 morphotypes and behaviour. In the Palearctic wader, ruff (*Philomachus pugnax*), an inverted
238 chromosomal region controls three male phenotypes affecting behaviour, body size and
239 plumage colour [33, 34], although not creating a reproductive barrier. The redpoll finch
240 complex is presently regarded as three species (hoary redpoll, *Acanthis hornemanni*; common
241 redpoll, *Acanthis flammea*; lesser redpoll, *Acanthis cabaret*), but they have considerable
242 overlap in geographical distribution and may hybridise to some degree. Again, these three
243 redpoll phenotypes are controlled by a large inversion [35]. In principle, a recent inversion
244 does not necessarily change the frequency and identity of single nucleotide polymorphisms
245 (SNPs) that are located in the inverted area, unless the genes and other genetic elements in
246 the inverted area are under some kind of selection pressure. And certainly, the most

247 comprehensive way to detect new or previously unknown SNPs and structural variants is by
248 genome sequencing. Even so, short-read sequencing, a powerful approach to detect both
249 known and previously unknown SNPs, may have problems in detecting the inversion itself,
250 especially when low-coverage sequencing is used. Long-read sequencing, like nanopore
251 (Oxford [Nanopore Technologies](#)) or [in particular](#) Single Molecule Real Time (SMRT;
252 PacBio) sequencing are presently the ultimate tools for this purpose. [Additionally, SMRT](#)
253 [sequencing is](#) central in the ERGA approach to achieve high-quality genome assemblies.
254 Thus, both [for](#) population genetics and for basic biological research in all kinds of species, it
255 is a great advantage to establish a high-quality species-specific reference genome, and from
256 this develop genomic tools in investigating a particular species and its subpopulations.

257
258 Since the development of large-scale and sensitive DNA sequencing technologies, the use of
259 environmental DNA (eDNA) and metabarcoding have gained popularity for different
260 purposes, including the assessment of biodiversity [36-41], estimates of spatial distribution
261 [42, 43], invasive species detection [44, 45], and predator-prey interactions [41]. These
262 methods are likely to be valuable tools in future assessments of biodiversity trends and
263 changes in relation to anthropogenic pressures. In the Faroe Islands, eDNA programs for
264 monitoring of marine biodiversity have been ongoing since 2018 onwards. These approaches
265 have already increased the number of species registered in the Faroese marine environment
266 (Salter et al., submitted). However, these methods rely on the exactness and completeness of
267 the relevant genetic databases, but also taxonomic expertise for correct registration of species.
268 We know that the databases are far from complete, although there has been great effort in
269 different barcoding projects, like the Barcode of Life [46] and Bioscan Europe [47]. [Thus,](#)
270 [assembling high-quality genomes and eDNA metabarcoding are complementary methods,](#)
271 [and in particular, the genome sequencing of more species will improve the outcomes of](#)
272 [eDNA and metabarcoding approaches.](#)

273
274 Another factor that may influence both the completeness and the exactness of the databases
275 are cryptic species, *i.e.*, that two or more distinct species are classified as a single species due
276 to their morphological similarities [48]. Cryptic species are found within all organismal
277 groups [49], and is a different concept than subspecies, where morphological criteria can
278 distinguish between (usually geographic) subpopulations. Still, both concepts can lead to the
279 definition of new species. It was only a few years ago that a well-known animal like the
280 giraffe was divided into four species [50], and approximately every year subspecies of birds

281 are split out as unique species, or the other way around. Genome sequencing is probably the
282 most definitive way to sort out cryptic species (or if a subspecies should be split out as a
283 distinct species), although there is no specific limit of genetic differences that defines the
284 transition from one species to another. In any case, having high quality genome assemblies
285 available from as many species as possible will improve the genetic databases and their
286 practical use for many purposes, including the ability to describe new species whether based
287 on previously known subspecies or cryptic species.

289 **Sustainability and commercial exploitation**

290 The sustainability of harvesting (presently) abundant species is often not thought of as a part
291 of a conservation process or mechanism. We here briefly remind about the extinction of the
292 once abundant passenger pigeon (*Ectopistes migratorius*) [51] and the collapses in the stocks
293 of Northwest Atlantic cod (*Gadus morhua*) [52] and Northeast Atlantic herring (*Clupea*
294 *harengus*) [53] indicating that such considerations should be taken. The Faroe Islands is a
295 maritime nation, where fisheries are of crucial importance. Thus, UN SDG 14 Life Below
296 Water ("*Conserve and sustainably use the oceans, seas and marine resources for sustainable*
297 *development*") is particularly relevant. Fishing is considered the main threat to the Faroese
298 marine ecosystem [54]. In the Faroe Islands, and elsewhere, certain fish species are
299 commercially harvested despite that the knowledge of their biology is limited. This is perhaps
300 most evident for species where industrial fisheries have developed during the last few
301 decades. History has repeatedly shown that it is possible to overexploit fish stocks, resulting
302 in a collapse from which it may take decades to recover [55]. It has been estimated that one
303 third of fish stocks are presently overfished [56]. Also for commercially exploited species it
304 is an advantage - and need - of maintaining subpopulations and genetic diversity in a
305 changing world. Genome sequencing is a crucial tool to achieve the conclusive assessment of
306 subpopulations and population structure.

307
308 For some fish species, it has been known for a long time that the population consists of
309 several stocks, *i.e.*, subpopulations that breed independently. *E.g.*, Atlantic herring consists of
310 stocks that spawn in different areas of the North Sea and the North Atlantic, and with some
311 stocks spawning in the spring and other in the autumn. Still, herring gather in large schools
312 migrating across the Northeast Atlantic, and the different stocks often mix in such schools. It
313 is important to estimate the fraction of each stock in catches from such mixed schools to
314 avoid overexploitation of certain stocks. Traditionally, the assessment of stock mixing in

315 catches has been based on phenotypic properties (morphology, otoliths), although genetic
316 tools have entered some fisheries. Phenotypic analysis is time-consuming and not necessarily
317 exact. Based on recent and better genomes assemblies [57, 58], it has been possible to refine
318 genetic markers in the herring genome, improving the potential in distinguishing between
319 different stocks of herring in the Northeast Atlantic [59], which are exposed to one of the
320 world's largest fisheries. Many of the genetic markers are positioned in an area of herring
321 chromosome 12 that is associated with ecological adaptation [32, 59], and which in some
322 stocks contains an inverted part of the chromosome [32]. This type of inversion is often
323 called a "supergene", and contains a set of tightly linked genes giving rise to a certain and
324 stable phenotype.

325
326 Similarly, Atlantic cod are divided into numerous stocks, some of which are migratory and
327 other are stationary, and with limited gene flow between these stocks, despite some of them
328 spawning in the same area and season. This is (at least partly) associated with certain inverted
329 supergenes [31, 60, 61]. Faroese waters have two distinct populations of cod, one at the Faroe
330 Plateau and one at the Faroe Bank. The latter is fast-growing, large-sized fish [62], and
331 locally known for its superior quality. We are confident that the Faroe Bank phenotype is
332 strongly associated with certain, as yet unknown, genetic properties. By being able to
333 genetically separate Faroe Bank cod from other local cod stocks we would get a valuable tool
334 in the search for the feeding grounds of the young Faroe Bank cod (age 0.5 to 3 years), which
335 are not known today, although it is presumed they are local on the Faroe Bank [63].
336 Additionally, identifying the genetic properties associated with rapid growth and high quality
337 may help in the efforts to make farmed cod a commercial reality.

338
339 The greater silver smelt (*Argentina silus*) is a relatively new, but, as yet, limited target for
340 commercial fisheries, with an average annual catch of around 50 000 tonnes in the Northeast
341 Atlantic, much of this in Faroese waters [62, 64]. It is commonly found at depths of 150-1400
342 m and it is long-lived and slow-growing [65]. Species with these characteristics are
343 vulnerable to overexploitation, because the longer the time to reach maturity, the longer it
344 takes to increase the population after a potential collapse. The stock structure is unknown
345 [ref. 64 with stock annex]. The International Council for the Exploration of the Sea (better
346 known by its abbreviation, ICES) has divided the greater silver smelt into four assessment
347 units, despite the lacking knowledge on separate biological populations [64]. Spawning may
348 occur in several seasons or in prolonged periods of the year, and spread around in vast areas

349 [65]. These were the major reasons why the greater silver smelt was suggested as a Faroese
350 ERGA pilot species. Through the ERGA efforts, its genome assembly became available in
351 the spring 2023 (GenBank GCA_951799395). This genome assembly is the first available
352 genome from the order Argentiniformes. The genome will give us insight into the biology of
353 the species, and help to develop population genetic markers (which we presently are doing),
354 making it possible to assess the population substructure in the North Atlantic, and thereby
355 improve the management of this species. [66, 67] Additionally, we are also working on the
356 genome assembly of a sister species, the lesser silver smelt (a.k.a. lesser argentine; *Argentina*
357 *sphyraena*). The two species are morphologically rather similar (Fig. 1) and have overlapping
358 geographical distributions, and there is a risk of mixed catches. With their genomes available,
359 genetic tools can be developed to easily assess the presence of one or the other or both
360 species even in industrial fish products in the supermarket (e.g., [68]).

361

362 The lesser sandeel (*Ammodytes marinus*) is another Faroese ERGA pilot species. The ERGA
363 efforts made its genome assembly available in the spring 2023 (GenBank GCA_949987685).

364 The lesser sandeel is one of several species collectively known as sandeels or sand lances.

365 These species are important prey for birds, larger fishes and marine mammals, and they are
366 an important link between the primary production and higher trophic levels [69-71]. The
367 sandeels have typical seasonal behaviours, and burrow into sandy sea bottom during much of
368 the winter. They are little used for human food, but are industrially fished, especially by
369 countries around the North Sea. The total annual catches have varied between 100 000 and 1
370 million tonnes [72]. The intense fishery may influence seabirds at different stages of life [73-
371 75], and thereby contribute to the observed decreases in seabird populations [76, 77]. It is
372 poorly understood whether the sandeel populations in the different regions of the North Sea
373 and the Northeast Atlantic are genetically distinct populations and to which degree there is
374 gene-flow from one region to another [78]. Knowing the genome sequence of the lesser
375 sandeel (and for the related species) would be highly valuable for developing genetic panels
376 for such investigations, and we are presently working to establish its population genetics in
377 the Northeast Atlantic Ocean. Better knowledge on sandeel subpopulations and their genetic
378 interconnections would improve the basis for quota determination in different management
379 areas. At the time the ERGA pilot project was initiated, there were no publicly available
380 genome assemblies from the taxonomic order Uranoscopiformes, to which the sandeels
381 belong. During 2022 and 2023, genome assemblies from four species in this order became
382 available, including the mentioned genome assembly from *Ammodytes marinus*. These

383 genomes will make it easier to assess whether these species, which are morphologically
384 rather similar and have overlapping geographical distributions, are prone to mixed catches.
385 Even more importantly, the genome assemblies could be a tool in ecological studies, both to
386 improve the knowledge of the sandeel biology in general, and for investigations of species
387 interactions.

388

389 An important aspect in sustainable exploitation of wild species, is to ensure that the
390 population and the potential subpopulations are large enough to endure the harvesting
391 pressure - in essence, that the species is maintained at a sufficiently sized population, within
392 its natural fluctuations. Moreover, there are a number of species where commercial interests
393 have more or less concrete wishes for developing new fisheries, or are in the early phases of
394 exploitation. The targeted species may range from deep-water fish to zooplankton (like krill
395 or *Calanus* spp.), and we know little about how this will affect the both the species itself and
396 interacting species. Acquiring adequate knowledge and overview of species that are
397 commercially exploited or suggested for commercial exploitation, should be common sense.
398 High-quality genome assemblies are likely *the* best basis to acquire such knowledge, as it can
399 later be diversified into separate and specialised sub-tools for specific questions and
400 investigations. One such question is how intensive fisheries are influencing the genetic future
401 of the species. Intensive fisheries may give selection pressures influencing traits such as size-
402 at-age and age-at-maturation [79, 80], but we know less if, and how, this influences the
403 ecosystem in small [81] or large scale, or the long-term trajectories of genetic diversity.

404

405 **Interaction between species**

406 Species interact in all kinds of ways: in food webs being prey and predator, by symbiosis and
407 parasitism, by living permanently or temporarily in the mixed groups, by competing or
408 collaborating, etc. DNA investigations may reveal much about such species interactions and
409 ecosystem services.

410

411 The public attention is much directed towards "visible" species, but for many purposes,
412 "invisible" species may sometimes have large consequences, whether they have a lifestyle
413 that hide them from the human eye (night activity, under water, in soil), or they in fact are so
414 small that they really are invisible to the naked human eye. We will mention a few more or
415 less local examples, two of which concern "invisible" species, where genomic knowledge
416 could be translated into practical tools or managerial choices and decisions.

417

418 Planktonic algae (together with bacteria and viruses) form the bio-basis of the entire marine
419 ecosystem on which the Faroese economy relies. Many algae are difficult to distinguish
420 morphologically, and DNA has become an important tool for routine algal biodiversity
421 monitoring. However, there are taxonomic uncertainties, and probably many cryptic species
422 and much unknown intraspecies genetic variations among algae [82]. Thus, there are still
423 many gaps for algae in the sequence databases. This also includes toxin-producing algae [83-
424 85], which are of interest for people collecting mussels, the shellfish industry and fish
425 aquaculture. Furthermore, the combined influence of climate change and the unintended
426 transport and release of algae and other marine species, especially by ballast water or by
427 attaching to the hull of ships, is likely to be an increasing problem in northern regions [e.g.,
428 ref. 86]. The ability to detect invasive species, including unexpected invasive species, will
429 increase as the genomic databases become more complete.

430

431 Invasive species are generally unwanted because they may affect the local native species and
432 the ecosystem in adverse ways. Island biodiversity is particularly vulnerable to the impact
433 from invasive alien species as is recognised in Kunming-Montreal Target 6 for stemming
434 biodiversity loss. As elsewhere in the world, rats [87] and mice [88, 89] are invasive species
435 also in the Faroe Islands. There is a particular worry that rats will spread to the few rat-free
436 islands, especially as the rat-free Sandoy that was connected to the rat-infected Streymoy by
437 an undersea tunnel in December 2023. However, there are also more subtle invasive species
438 in the Faroes. The New Zealand flatworm (*Arthurdendyus triangulatus*) was first reported in
439 the Faroe Islands in 1982, possibly introduced from Scotland or New Zealand by soil
440 following imported plants or trees [90]. The New Zealand flatworm preys on local
441 earthworms, thereby over time possibly degrading the quality and the properties of the soil.
442 Although there is some knowledge about genetic variations in the flatworm [91], a recent
443 evaluation concluded that there are large gaps in the sequence data from this and related
444 species, making it impossible to assess the reliability of the DNA markers [92]. Thus, having
445 a genome assembly would be the basis for much better tools to follow the routes of spreading
446 (for example, by eDNA), and possibly also to find potential targets for countermeasures.

447

448 There are no native terrestrial mammals in the Faroe Islands. Among typical free-roaming
449 herbivores, only mountain hare (*Lepus timidus*) and domestic sheep have been introduced, the
450 former with four animals (from coastal Norway) in 1855, and the latter probably with the first

451 settlers well before year 1000 (and with many subsequent import events). Hunting of hare is a
452 popular tradition, and the registered yield is between 3000 and 9000 hares/year (Eyðfinn
453 Magnussen, pers. comm.), which is extremely high considering an area of 1400 km². One
454 may imagine that hare and sheep could compete for food resources, given the high density of
455 both species. This could be possible to investigate using different genetic tools, provided that
456 the necessary genetic data are available for the local plants. Another interesting question is
457 microevolution in hare, as all the local populations are founded from the first few animals
458 introduced nearly 170 years ago. This includes the genetics behind the grey winter fur of
459 Faroese hare. Grey winter fur is also known from parts of coastal southern Norway, and we
460 would suppose that the grey winter furs of Faroese and local Norwegian hares have the same
461 genetic background. Hypothetically, the grey winter fur could be caused a recessive allele in
462 the introduced animals, and it probably became fixed in the population as the white hares
463 were more easily shot during the late fall hunting in (usually) snow-less conditions (hunting
464 of hares started only a few years after introduction, and the first legislation on hare-hunting is
465 from 1881).

466

467 **Interactions with and dissemination to the society**

468 The third main aim of Gen@FarE is to establish an information databank in Faroese,
469 covering all Faroese species and nature types. It is a scholarly obligation to inform the public
470 in various ways, like educational and outreach programmes, museum exhibitions and events,
471 popular science presentations, etc. Museums and public collections have a long tradition in
472 natural history, and have been highly important in disseminating knowledge and information
473 to the society, whether we consider school classes, single individuals or the authorities. At the
474 same time, many are interested in different aspects of biodiversity, and this is reflected in
475 citizen science projects like iNaturalist [93] and eBird [94]. More than 1.5 million
476 observation lists (usually with several species and many individuals of each species in each
477 list) were submitted to eBird during February 2023, and more than 1.3 million single
478 observations were added to iNaturalist in the same period. When the scale of the collected
479 data is big enough, the geographical and seasonal distribution and abundance of species
480 become apparent, and over time disclose population trends, as noticeably illustrated by eBird
481 [95-97]. Additionally, and possibly undervalued, highly skilled non-professionals and
482 laypersons contribute considerably to the identification and description of new species [5],
483 and even more so for geographical distribution of species [98]. Of course, citizen science data
484 may not rise to the same standards as professionally collected data [99], but the shortcomings

485 can be more or less counteracted by diverse measures [100-103], and time and again, citizen
486 science data have shown their value as indicated by the references above [5, 95-98].

487

488 Our Nordic neighbours have organised national searchable public biological information
489 banks interlinked with the possibility of registration of citizen science observations (Sweden
490 with Artdatabanken and Artportalen [104, 105]; Norway with Artsdatabanken and
491 Artsobservasjoner [106, 107]); and Denmark with Arter.dk [108]). Both the national and
492 international citizen science initiatives mentioned above have identification tools, either
493 integrated into the website or as free-standing mobile telephone apps [109-112], which
494 significantly lowers the threshold for contributing to citizen science.

495

496 Consistent with article 13a *Public Education and Awareness* in CBD ("*The Contracting*
497 *Parties shall promote and encourage understanding of the importance of, and the measures*
498 *required for, the conservation of biological diversity, as well as its propagation through*
499 *media, and the inclusion of these topics in educational programmes*") and target 21 in the
500 Kunming-Montreal agreement (see *Background* section), we believe that the ability to easily
501 access the established knowledge on species and the possibility of the public in contributing
502 to the knowledge building, will increase the interest in the species and in nature values in
503 general. The combined data from organised research and citizen science will over time
504 indicate abundance and trends, and point out geographical areas with particular values of
505 nature (*e.g.*, rare type of biological or geological landscape at national or international level;
506 high biodiversity; habitat of rare or threatened species, etc.). This information will help in
507 management decisions of various kinds, like protection of species, development of area plans,
508 conservation of smaller or larger areas, etc. It will increase the transparency and the
509 interactions between the scientists, the authorities, the politicians, and the public for many
510 aspects of preservation of species, management and conservation of areas, and management
511 and sustainable exploitation of species.

512

513 **Incidental insights**

514 As genomes from more and more species are sequenced, it is evident that we will learn much
515 about each single species. However, a single species does not exist without being connected
516 to other species, not only in their habitats, in their ecosystems, and in their food webs, but
517 they are also genetically connected to other species through evolution and the process of
518 speciation. As more genome assemblies become available, we will undoubtedly understand

519 more about the genetic processes, physiological processes, the immune system, protection
520 against pathogens, and lots of other areas that give us deeper insight into life and basic
521 processes of life [14, 113], and some of which may find applications in the future for
522 improving our food production, and give new medical treatments, new materials, more eco-
523 friendly industrial processes, etc. We can safely assume that there will be a continued
524 advancement in methods, instruments, and bioinformatics, which will give us new and
525 efficient tools that also can be applied to various questions and purposes. In short, we will
526 have more insight into being humans, our own biology and genetics, and similarly for our
527 fellow beings, and understand more about taking care of nature and the Earth, which
528 ultimately is to take care of ourselves.

529

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554

555 **Authors' contributions**

556 SOM wrote the manuscript. SíK commented throughout the writing process. JíH, IS, SH and
557 AD commented on the manuscript. All authors read and accepted the final version of the
558 manuscript.

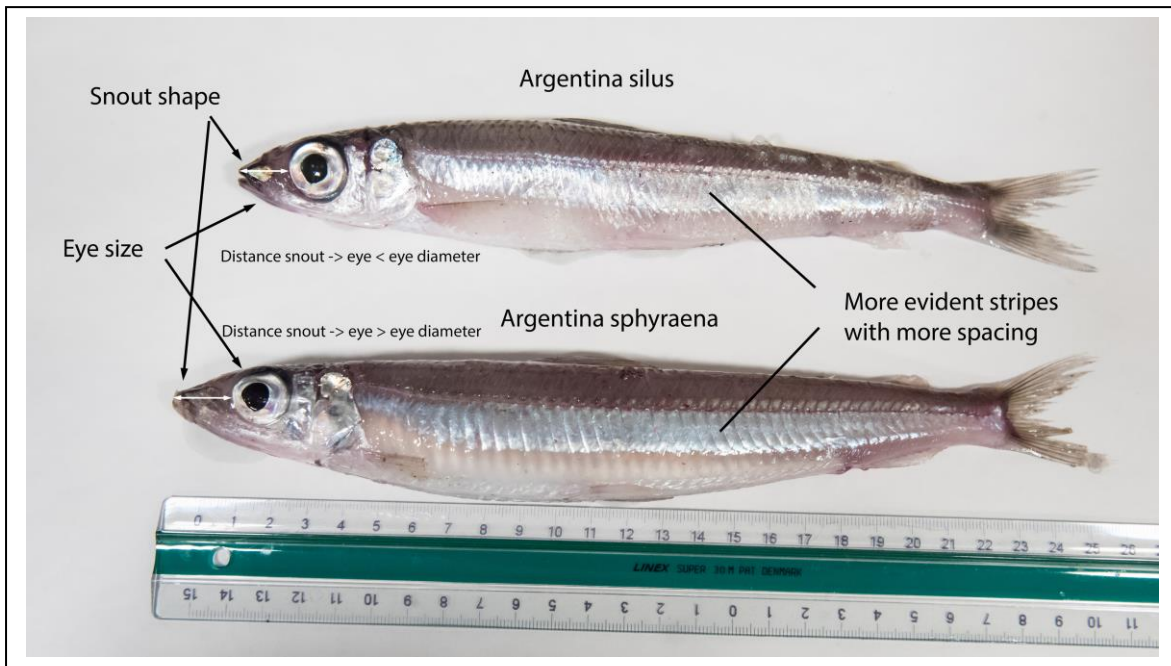
559

560 **Conflict of interest disclosure**

561 The authors declare that they comply with the PCI rule of having no financial conflict of
562 interest in relation to the content of the article.

563 **Figures**

564



565

566 **Fig. 1.** Greater silver smelt (*Argentina silus*) and lesser silver smelt (*Argentina sphyraena*)
567 have quite similar appearances, and have overlapping geographical distributions. The shown
568 individuals are (lower) adult lesser silver smelt (max. length 35 cm) and (upper) subadult
569 greater silver smelt (max. length 70 cm). The two individuals were caught in the same 1 h
570 trawl haul (survey cruise with RV Jákup Sverri) at 200-220 m depth (decimal position 61.60
571 N, 7.45 W) on the 9th of August 2023. Greater silver smelt is also known as greater argentine,
572 Atlantic argentine or herring smelt. Lesser silver smelt is also known as lesser argentine.
573 Photo and labelling by SOM.

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