

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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19 **Keywords**

20 Biodiversity; citizen science; conservation; commercial exploitation; ERGA; European
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22 sustainability.

23 **Abstract**

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

45 **Background**

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

50

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

66

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

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

83

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

90

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

103

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

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

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

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

128

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

138

139 **Genome Atlas of Faroese Ecology (Gen@FarE)**

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

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

150

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

174

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

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

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

184

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

192

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

199

200 **Biodiversity and conservation**

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

210

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

230

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

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

255

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

271

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

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

286

287 **Sustainability and commercial exploitation**

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

305

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

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

323

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

336

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

347 [65]. These were the major reasons why the greater silver smelt was suggested as a Faroese
348 ERGA pilot species. Through the ERGA efforts, its genome assembly became available in
349 the spring 2023 (GenBank GCA_951799395). This genome assembly is the first available
350 genome from the order Argentiniformes. The genome will give us insight into the biology of
351 the species, and help to develop population genetic markers (which we presently are doing),
352 making it possible to assess the population substructure in the North Atlantic, and thereby
353 improve the management of this species. Additionally, we are also working on the genome
354 assembly of a sister species, the lesser silver smelt (a.k.a. lesser argentine; *Argentina*
355 *sphyraena*). The two species are morphologically rather similar (Fig. 1) and have overlapping
356 geographical distributions, and there is a risk of mixed catches. With their genomes available,
357 genetic tools can be developed to easily assess the presence of one or the other or both
358 species even in industrial fish products in the supermarket (e.g., [66]).

359

360 The lesser sandeel (*Ammodytes marinus*) is another Faroese ERGA pilot species. The ERGA
361 efforts made its genome assembly available in the spring 2023 (GenBank GCA_949987685).
362 The lesser sandeel is one of several species collectively known as sandeels or sand lances.
363 These species are important prey for birds, larger fishes and marine mammals, and they are
364 an important link between the primary production and higher trophic levels [67-69]. The
365 sandeels have typical seasonal behaviours, and burrow into sandy sea bottom during much of
366 the winter. They are little used for human food, but are industrially fished, especially by
367 countries around the North Sea. The total annual catches have varied between 100 000 and 1
368 million tonnes [70]. The intense fishery may influence seabirds at different stages of life [71-
369 73], and thereby contribute to the observed decreases in seabird populations [74, 75]. It is
370 poorly understood whether the sandeel populations in the different regions of the North Sea
371 and the Northeast Atlantic are genetically distinct populations and to which degree there is
372 gene-flow from one region to another [76]. Knowing the genome sequence of the lesser
373 sandeel (and for the related species) would be highly valuable for developing genetic panels
374 for such investigations, and we are presently working to establish its population genetics in
375 the Northeast Atlantic Ocean. Better knowledge on sandeel subpopulations and their genetic
376 interconnections would improve the basis for quota determination in different management
377 areas. At the time the ERGA pilot project was initiated, there were no publicly available
378 genome assemblies from the taxonomic order Uranoscopiformes, to which the sandeels
379 belong. During 2022 and 2023, genome assemblies from four species in this order became
380 available, including the mentioned genome assembly from *Ammodytes marinus*. These

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

386

387 An important aspect in sustainable exploitation of wild species, is to ensure that the
388 population and the potential subpopulations are large enough to endure the harvesting
389 pressure - in essence, that the species is maintained at a sufficiently sized population, within
390 its natural fluctuations. Moreover, there are a number of species where commercial interests
391 have more or less concrete wishes for developing new fisheries, or are in the early phases of
392 exploitation. The targeted species may range from deep-water fish to zooplankton (like krill
393 or *Calanus* spp.), and we know little about how this will affect the both the species itself and
394 interacting species. Acquiring adequate knowledge and overview of species that are
395 commercially exploited or suggested for commercial exploitation, should be common sense.
396 High-quality genome assemblies are likely *the* best basis to acquire such knowledge, as it can
397 later be diversified into separate and specialised sub-tools for specific questions and
398 investigations. One such question is how intensive fisheries are influencing the genetic future
399 of the species. Intensive fisheries may give selection pressures influencing traits such as size-
400 at-age and age-at-maturation [77, 78], but we know less if, and how, this influences the
401 ecosystem in small [79] or large scale, or the long-term trajectories of genetic diversity.

402

403 **Interaction between species**

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

408

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

415

416 Planktonic algae (together with bacteria and viruses) form the bio-basis of the entire marine
417 ecosystem on which the Faroese economy relies. Many algae are difficult to distinguish
418 morphologically, and DNA has become an important tool for routine algal biodiversity
419 monitoring. However, there are taxonomic uncertainties, and probably many cryptic species
420 and much unknown intraspecies genetic variations among algae [80]. Thus, there are still
421 many gaps for algae in the sequence databases. This also includes toxin-producing algae [81-
422 83], which are of interest for people collecting mussels, the shellfish industry and fish
423 aquaculture. Furthermore, the combined influence of climate change and the unintended
424 transport and release of algae and other marine species, especially by ballast water or by
425 attaching to the hull of ships, is likely to be an increasing problem in northern regions [e.g.,
426 ref. 84]. The ability to detect invasive species, including unexpected invasive species, will
427 increase as the genomic databases become more complete.

428

429 Invasive species are generally unwanted because they may affect the local native species and
430 the ecosystem in adverse ways. Island biodiversity is particularly vulnerable to the impact
431 from invasive alien species as is recognised in Kunming-Montreal target 6 for stemming
432 biodiversity loss. As elsewhere in the world, rats [85] and mice [86, 87] are invasive species
433 also in the Faroe Islands. There is a particular worry that rats will spread to the few rat-free
434 islands, especially as the rat-free Sandoy was connected to the rat-infected Streymoy by an
435 undersea tunnel in December 2023. However, there are also more subtle invasive species in
436 the Faroes. The New Zealand flatworm (*Arthurdendyus triangulatus*) was first reported in the
437 Faroe Islands in 1982, possibly introduced from Scotland or New Zealand by soil following
438 imported plants or trees [88]. The New Zealand flatworm preys on local earthworms, thereby
439 over time possibly degrading the quality and the properties of the soil. Although there is some
440 knowledge about genetic variations in the flatworm [89], a recent evaluation concluded that
441 there are large gaps in the sequence data from this and related species, making it impossible
442 to assess the reliability of the DNA markers [90]. Thus, having a genome assembly would be
443 the basis for much better tools to follow the routes of spreading (for example, by eDNA), and
444 possibly also to find potential targets for countermeasures.

445

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

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

464

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

466 The third main aim of Gen@FarE is to establish an information databank in Faroese,
467 covering all Faroese species and nature types. It is a scholarly obligation to inform the public
468 in various ways, like educational and outreach programmes, museum exhibitions and events,
469 popular science presentations, etc. Museums and public collections have a long tradition in
470 natural history, and have been highly important in disseminating knowledge and information
471 to the society, whether we consider school classes, single individuals or the authorities. At the
472 same time, many are interested in different aspects of biodiversity, and this is reflected in
473 citizen science projects like iNaturalist [91] and eBird [92]. More than 1.5 million
474 observation lists (usually with several species and many individuals of each species in each
475 list) were submitted to eBird during February 2023, and more than 1.3 million single
476 observations were added to iNaturalist in the same period. When the scale of the collected
477 data is big enough, the geographical and seasonal distribution and abundance of species
478 become apparent, and over time disclose population trends, as noticeably illustrated by eBird
479 [93-95]. Additionally, and possibly undervalued, highly skilled non-professionals and
480 laypersons contribute considerably to the identification and description of new species [5],
481 and even more so for geographical distribution of species [96]. Of course, citizen science data
482 may not rise to the same standards as professionally collected data [97], but the shortcomings

483 can be more or less counteracted by diverse measures [98-101], and time and again, citizen
484 science data have shown their value as indicated by the references above [5, 93-96].

485

486 Our Nordic neighbours have organised national searchable public biological information
487 banks interlinked with the possibility of registration of citizen science observations (Sweden
488 with Artdatabanken and Artportalen [102, 103]; Norway with Artsdatabanken and
489 Artsobservasjoner [104, 105]); and Denmark with Arter.dk [106]). Both the national and
490 international citizen science initiatives mentioned above have identification tools, either
491 integrated into the website or as free-standing mobile telephone apps [107-110], which
492 significantly lowers the threshold for contributing to citizen science.

493

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

510

511 **Incidental insights**

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

517 more about the genetic processes, physiological processes, the immune system, protection
518 against pathogens, and lots of other areas that give us deeper insight into life and basic
519 processes of life [14, 111], and some of which may find applications in the future for
520 improving our food production, and give new medical treatments, new materials, more eco-
521 friendly industrial processes, etc. We can safely assume that there will be a continued
522 advancement in methods, instruments, and bioinformatics, which will give us new and
523 efficient tools that also can be applied to various questions and purposes. In short, we will
524 have more insight into being humans, our own biology and genetics, and similarly for our
525 fellow beings, and understand more about taking care of nature and the Earth, which
526 ultimately is to take care of ourselves.

527

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552

553 **Authors' contributions**

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

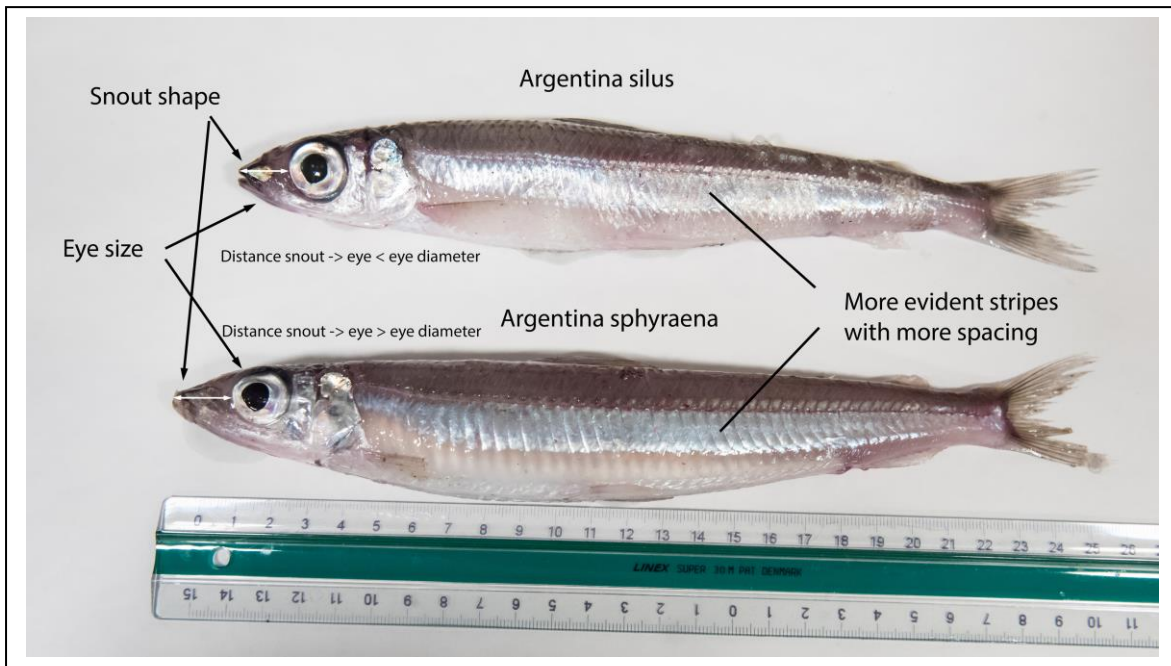
557

558 **Conflict of interest disclosure**

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

561 **Figures**

562



563

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

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617 [un-programme-de-recherche-ambitieux-pour-plonger-au-coeur-du-genome-marin](https://www.gouvernement.fr/france-2030-atlasea-un-programme-de-recherche-ambitieux-pour-plonger-au-coeur-du-genome-marin).
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