

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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20 **Keywords**

21 Biodiversity; citizen science; conservation; commercial exploitation; ERGA; European
22 Reference Genome Atlas; genetic diversity; genomes; Genome Atlas of Faroese Ecology;
23 sustainability.

24 **Abstract**

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

46 **Background**

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

51

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

67

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

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

84

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

91

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

104

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

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

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

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

129

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

139

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

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

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

151

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

175

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

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

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

185

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

193

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

200

201 **Biodiversity and conservation**

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

211

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

231

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

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

256

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

272

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

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

287

288 **Sustainability and commercial exploitation**

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

306

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

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

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

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

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

360

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

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

387

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

403

404 **Interaction between species**

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

409

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

416

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

429

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

446

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

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

465

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

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

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

486

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

494

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

511

512 **Incidental insights**

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

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

528

529 **Acknowledgments**

530 The authors are grateful to ERGA for inspiration and support. We deeply acknowledge
531 Professor Mark Blaxter and the Tree of Life project (Wellcome Sanger Institute, UK) for the
532 willingness to carry the financial costs for sequencing and assembling the initial genomes
533 from Faroese species. We gratefully acknowledge Mark Blaxter, Dorte Bekkevold (Technical
534 University of Denmark, DTU Aqua, Denmark), Pamela Woods and Magnús Thorlacius
535 (Marine and Freshwater Research Institute, Iceland), and Torild Johansen and Elvar
536 Hallfredsson (Marine Research Institute, Norway) for being partners in our many applications
537 to finance the initial phase of the Gen@FarE project. We are also very grateful to Professor
538 Tom Gilbert (Yggdrasil sequencing core facility and Globe Institute, University of
539 Copenhagen) for the sequencing and assembly of the genome from the lesser silver smelt. We
540 are thankful to the partners and their institutions for carrying substantial in-kind contributions
541 to the project. In addition to the mentioned authors, the present national participants in the
542 Gen@FarE project are: Hans Blaasvær and Eyðfinn Magnussen (Faculty of Science and
543 Technology, University of the Faroe Islands), Sjúrdur Hammer and Lise H. Ofstad (Faroese
544 Environment Agency), Petur Steingrund (Faroese Marine Research Institute), and Amanda
545 Vang (Aquaculture Research Station of Faroe Islands). We thank Sjúrdur Hammer, Lise H.
546 Ofstad, Eyðfinn Magnussen for commenting on the manuscript.

547

548 **Funding**

549 The present activities of Gen@FarE are financially supported by the University of Faroe
550 Islands, the Faroese Research Council (grant no. 0469), the Faroese Fishery Research Fund

551 (grant no. 22/22427), Nordic Arctic Co-operation Programme (NAPA; grant no. 23-11-0006),
552 and Føroyagrunnurin.

553

554 **Authors' contributions**

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

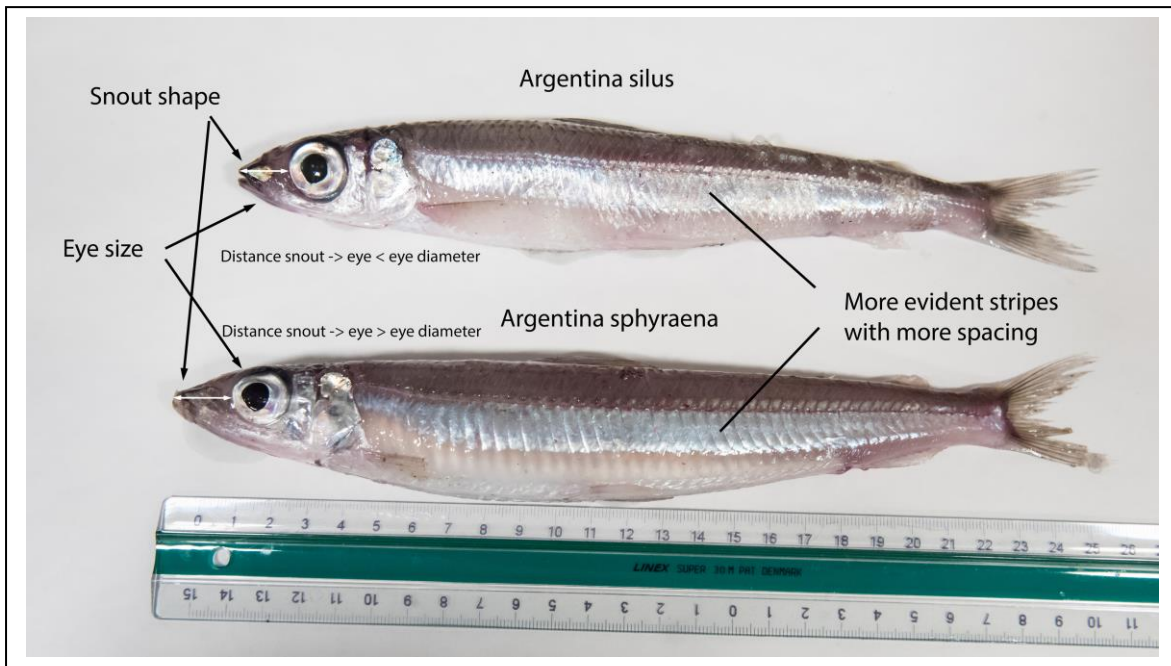
558

559 **Conflict of interest disclosure**

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

562 **Figures**

563



564

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

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