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

Svein-Ole Mikalsen[1,4]**, Jari í Hjøllum**[1]**, Ian Salter**[2]**, Sjúrður Hammer**[1,3]**, Anni Djurhuus**[1]**, and Sunnvør í Kongsstovu**[1]

[1] Faculty of Science and Technology, University of the Faroe Islands, Vestara Bryggja 15, FO-100 Tórshavn, The Faroe Islands
[2] Faroe Marine Research Institute, Nóatún 1, FO-100 Tórshavn, The Faroe Islands
[3] Faroese Environment Agency, Traðagøta 38, FO-100 Tórshavn, The Faroe Islands
[4] Corresponding author. E-mail: sveinom@setur.fo

SOM: ORCID 0000-0002-7128-4464; sveinom@setur.fo
JíH: ORCID 0000-0003-2388-9378; jarih@setur.fo
IS: ORCID 0000-0002-4513-0314; ians@hav.fo
SH: ORCID 0000-0002-3986-5074; sjurdurh@us.fo
AD: ORCID 0000-0002-3517-7522; annid@setur.fo
SíK: ORCID 0000-0001-6631-2347; sunnvork@setur.fo

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Abstract

Biodiversity is under pressure, mainly due to anthropocentric activities and climate change. At the international policy level, it is now recognised that genetic diversity is an important part of biodiversity. The availability of high-quality reference genomes gives the best basis for using genetics and genetic diversity towards the global aims of (i) protection of species, biodiversity, and nature, and (ii) in management of biodiversity for achieving sustainable harvesting of nature. Protecting biodiversity is a global responsibility, also resting on small nations, like the Faroe Islands. Being in the middle of the North Atlantic Ocean and having large fisheries activity, the nation has a particular responsibility towards maritime matters. We here provide the reasoning behind Genome Atlas of Faroese Ecology (Gen@FarE), a project based on our participation in the European Reference Genome Atlas consortium (ERGA). Gen@FarE has three major aims: (i) To acquire high-quality genomes of all eukaryotic species in the Faroe Islands and Faroese waters. (ii) To establish population genetics for species of commercial or ecological interest. (iii) 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 environments. Altogether, we believe that this will enhance the society's interest in and awareness of biodiversity, thereby protecting the foundations of our lives. Furthermore, the combination of a wide and highly competent ERGA umbrella and more targeted national projects will help fulfilling the formal and moral responsibilities that all nations, also those of limited resources, have in protecting biodiversity and achieving sustainability in harvesting from nature.

Background

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

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

It is of utmost importance that we, as the main caretaker of the Earth, are aware of the biodiversity and the existing genetic diversity. Within each single species, and within each single individual, the material of inheritance, the genome, is the basis and the main frame for the present diversity and carrying the diversity forward to the future generations. It is also recognized that genetic diversity within a species is pivotal for adaptation in a changing world, which is even more important in times of climate change. Thus, knowing the genome sequences from as many species as possible is central in the understanding and knowledge of the full span of biodiversity. With the strong influence that humans have on the ecosystems and the Earth, we will only be able to maintain the diversity and exploit it in a sustainable way by being aware of it. It is difficult or impossible to take care of the things we do not know. The sustainable utilisation and management of biological resources require a serious effort to establish current status (which is not necessarily the same as the historical status) and monitor future changes of biodiversity in diverse environments.

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

In international policy, **sustainability** and **biodiversity** seriously entered the stage through the UN report "Our Common Future" from 1987 [7] and the Convention on Biological Diversity (CBD) from 1992 [8]. Article 1 of CBD states that "*The objectives ... are... the conservation of biological diversity, (and) the sustainable use of its components...*" [8]. The balance of conservation and sustainable use of nature are repeated in several of the subsequent articles of CBD. All parties of the CBD, including the Faroe Islands (through the Kingdom of Denmark), commit to these objectives. CBD is the basis for additional international agreements and protocols, some of which the Faroe Islands have not joined (like the Nagoya protocol and the Aarhus convention). The Kunming-Montreal global diversity framework from December 2022, better known as UN CBD Conference of Parties 15 (COP15) [9], underlined the importance of genetics and genetic diversity in biodiversity and sustainability, as reflected in their direct mentioning in two of the four overarching goals:

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

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

- *Target 4: Ensure urgent management actions, to halt human induced extinction of known threatened species and for the recovery and conservation of species, in particular threatened species, to significantly reduce extinction risk, as well as to maintain and restore the **genetic diversity** within and between populations of native, wild and domesticated species....*

- *Target 13: Take effective legal, policy, administrative and capacity-building measures at all levels, as appropriate, to ensure the fair and equitable sharing of benefits that arise from the utilization of* ***genetic*** *resources...*
- *Target 21: Ensure that the best available data, information and knowledge* (this undoubtedly include genetic data, information and knowledge; authors' comments), *are accessible to decision makers, practitioners and the public to guide effective and equitable governance, integrated and participatory management of biodiversity, and to strengthen communication, awareness-raising, education, monitoring, research and knowledge management...*

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

Genome Atlas of Faroese Ecology (Gen@FarE)

Knowledge of the full genome of each species and the genetic diversity within each species, provide powerful tools to monitor, and through that preserve and manage biodiversity [2, 10]. This knowledge can be used in different ways and for different purposes. On the very practical and applied side, management of commercially exploited resources and protection of species and/or habitats, can be much improved by such tools. It will also give us better tools to survey the environment, whether it is for invasive species or population estimates. Equally important, such knowledge is valuable for understanding the diversity of life in all its aspects and functions, and it will undoubtedly initiate further questions and give new avenues to explore (see section *Incidental insights*). But above all, we will understand and know life on Earth in a much more detailed way, helping us to protect and maintain a healthy Earth for mankind and all its fellow beings.

National and regional initiatives are taking place both in Europe and globally by people and institutions recognising the need for - and the potential of - such knowledge [11-15]. This is a highly international task, where all nations need to contribute and collaborate. We all, as individuals, as industry, as society, as nations, have responsibility for the future of the Earth and its nature, and the politicians and governments must set the frames so this can become possible to achieve. Realising the urgency and needs in protecting biodiversity, and that genomics and genetics are essential tools in achieving this purpose, more than 700 European scientists, some of the present authors among them [16], have gone together to form the European Reference Genome Atlas project (ERGA) [11, 17] as a collaborative and interdisciplinary network. Also small nations, like the Faroe Islands (1 400 km^2 and 54 000 inhabitants), should contribute to this effort, partly as a global and moral obligation, and partly to ensure sustainability in its exploitation of biological resources in accordance with CBD [8]. Utilising the ERGA network and its dedication to a decentralised and equitable biodiversity genomics [18], the present authors have initiated the Genome Atlas of Faroese Ecology (Gen@FarE), and we participate in the ERGA Pilot project [18]. Although being a small nation, the Faroe Islands have a sizable economic zone (274 000 km^2) in the middle of the North Atlantic Ocean, and it has large fisheries activity. Thereby the nation has a particular responsibility towards maritime matters. The authors represent Faroese institutions with responsibilities for education, research, monitoring, and dissemination of knowledge within Faroese and North Atlantic biology and biodiversity, and advising the authorities about stock management and nature in general. We jointly see the advantage of increased genomic and genetic knowledge for protecting biodiversity and achieving sustainability in the region.

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

- To establish high-quality genomes of all eukaryotic species in the Faroe Islands and 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 may have more optimistic views on how fast such an aim will be achieved, but a large upscaling of capacities is needed [12, 19]. 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 storm petrel (*Hydrobates pelagicus*), one of the last remains of (claimed) wild type rock pigeon (*Columba livia*), and recognized subspecies of several other birds (European starling, *Sturnus vulgaris faroensis*; Eurasian wren, *Troglodytes troglodytes borealis*; common eider, *Somateria mollissima faeroeensis*; etc.) (see [20] for more information). However, we will in this paper not focus on this particular part of biodiversity.

The Red List status is often an important part in decisions for "what to do" and "how to do" in conservation and protection of species. The assessment of the Red List status is based on population trends and some other parameters [21], some of which are not always easy to assess for different reasons. One could imagine the inclusion of genetic diversity status into this assessment, both as an independent parameter and as an indirect parameter for assessing effective population size [22, 23]. It is well known that low effective population size increases the rate of homozygosity. Runs of homozygosity have been used for estimating historical bottlenecks for certain species [24-26]. It might be possible to take similar models into use for practical conservation and protection purposes, like the national and regional Red Lists. However, there is – perhaps surprisingly - no direct correlation of the Red List status and runs of homozygosity for a limited set of mammals [26] (please note that there is somewhat conflicting evidence regarding the correlation of the red list status and runs (or degree) of homozygosity; see refs. in [26]). As hinted at [26], there could be several explanations, like (i) the populations have not reached sufficiently low level to erode genetic variation in the individuals, or (ii) that when the decline is rapid (as it is in many cases) and without any particular genetic selection pressure, the relative degree of heterozygosity is maintained for quite a while, and runs of homozygosity only become evidently apparent after some generations of low population size.

Next generation sequencing and in particular third generation sequencing have shown that structural genetic variants are more common than previously thought. In some cases, structural variants are probably decisive for ecological adaptation and migration [27, 28] (see also section *Sustainability and commercial exploitation*), and in other cases they influence morphotypes and behaviour. In the Palearctic wader, ruff (*Philomachus pugnax*), an inverted chromosomal region controls three male phenotypes affecting behaviour, body size and plumage colour [29, 30], although not creating a reproductive barrier. The redpoll finch complex is presently regarded as three species (hoary redpoll, *Acanthis hornemanni*; common redpoll, *Acanthis flammea*; lesser redpoll, *Acanthis cabaret*), but they have considerable overlap in geographical distribution and may hybridise to some degree. Again, these three redpoll phenotypes are controlled by a large inversion [31]. In principle, an inversion does not necessarily change the frequency and identity of single nucleotide polymorphisms (SNPs) that are located in the inverted area, unless the genes and other genetic elements in the inverted area are under some kind of selection pressure. And certainly, the most comprehensive way to detect new or previously unknown SNPs and structural variants is by genome sequencing. Even so, short-read sequencing, a powerful approach to detect both known and previously unknown SNPs, may have problems in detecting the inversion itself, especially when low-coverage sequencing is used. Long-read sequencing, like nanopore (Oxford Nanopores) or Single Molecule Real Time (SMRT; PacBio) sequencing are presently the ultimate tools for this purpose, and these methods are central in the ERGA approach to achieve high-quality genome assemblies. Thus, for both population genetics and for basic biological research in all kinds of species, it is a great advantage to establish a high-quality species-specific reference genome, and from this develop genomic tools in investigating a particular species and its subpopulations.

Since the development of large-scale and sensitive DNA sequencing technologies, the use of environmental DNA (eDNA) and metabarcoding have gained popularity for different purposes, including the assessment of biodiversity [32-37], estimates of spatial distribution [38, 39], invasive species detection [40, 41], and predator-prey interactions [37]. These methods are likely to be valuable tools in future assessments of biodiversity trends and changes in relation to anthropogenic pressures. In the Faroe Islands, eDNA programs for monitoring of marine biodiversity have been ongoing since 2018 onwards. These approaches have already increased the number of species registered in the Faroese marine environment (Salter et al., submitted). However, these methods rely on the exactness and completeness of the relevant genetic databases, but also taxonomic expertise for correct registration of species. We know that the databases are far from complete, although there has been great effort in different barcoding projects, like the Barcode of Life [42] and Bioscan Europe [43].

Another factor that may influence both the completeness and the exactness of the databases are cryptic species, *i.e.*, that two or more distinct species are classified as a single species due to their morphological similarities [44]. Cryptic species are found within all organismal groups [45], and is a different concept than subspecies, where morphological criteria can distinguish between (usually geographic) subpopulations. Still, both concepts can lead to the definition of new species. It was only a few years ago that a well-known animal like the giraffe was divided into four species [46], and approximately every year subspecies of birds are split out as unique species, or the other way around. Genome sequencing is probably the most definitive way to sort out cryptic species (or if a subspecies should be split out as a distinct species), although there is no specific limit of genetic differences that defines the transition from one species to another. In any case, having high quality genome assemblies available from as many species as possible will improve the genetic databases, and thereby making the results from environmental metabarcoding more complete and more reliable. Thus, whole genomes on the one hand and eDNA metabarcoding on the other hand are complementary methods, and in particular, the genome sequencing of more species will improve the outcomes of the metabarcoding.

The sustainability of harvesting (presently) abundant species is often not thought of as a part of a conservation process or mechanism. We here briefly remind about the collapses in the stocks of Northwest Atlantic cod (*Gadus morhua*) [47] and Northeast Atlantic herring (*Clupea harengus*) [48], and the extinction of passenger pigeon (*Ectopistes migratorius*) [49], showing that such considerations should be taken. We must generally assume that common species have more ecological importance than rare, but potentially more iconic, species. A major exception to this notion is top predators (the highest trophic level), as they almost by definition are sparce, but still, they may shape their habitat and ecosystem [e.g., ref. 50]. We underline the advantage - and need - of maintaining subpopulations and genetic diversity in a changing world, and genome sequencing is a crucial tool to achieve the conclusive assessment of subpopulations and population structure (see section *Sustainability and commercial exploitation*). However, there are also other reasons, angles and aspects of genomics in conservation, some of which will briefly be described below.

Sustainability and commercial exploitation

The Faroe Islands is a maritime nation, where fisheries are of crucial importance. In the Faroe Islands, and elsewhere, certain fish species are commercially harvested, despite that the knowledge of their biology is limited. This is perhaps most evident for species where industrial fisheries have developed during the last few decades. There are also a number of species where commercial interests have more or less concrete wishes for developing new fisheries, or are in the early phases of exploitation. The targeted species may range from deep-water fish to zooplankton (like krill or *Calanus* spp.).

For some fish species, it has been known for a long time that the population consists of several stocks, *i.e.*, subpopulations that breed independently. *E.g.*, Atlantic herring consists of stocks that spawn in different areas of the North Sea and the North Atlantic, and with some stocks spawning in the spring and other in the autumn. Still, herring gather in large schools migrating across the Northeast Atlantic, and the different stocks often mix in such schools. It is of importance that it is possible to estimate the fraction of each stock in catches from such mixed schools to avoid overexploitation of certain stocks. History has shown that it is possible to overexploit fish stocks [51], like herring and cod, resulting in a collapse from which it may take decades to recover. Traditionally, the assessment of stock mixing in catches has been based on phenotypic properties (morphology, otoliths), although genetic tools have entered some fisheries. Phenotypic analysis is time-consuming and not necessarily exact. Based on recent high-quality genomes [52, 53], it has been possible to refine genetic markers in the herring genome, improving the potential in distinguishing between different stocks of herring in the Northeast Atlantic [54], which are exposed to one of the world's largest fisheries. Many of the genetic markers are positioned in an area of herring chromosome 12 that is associated with ecological adaptation [28, 54], and which in some stocks contains an inverted part of the chromosome [28]. This type of inversion is often called a "supergene", and contains a set of tightly linked genes giving rise to a certain and stable phenotype.

Similarly, Atlantic cod are divided into numerous stocks, some of which are migratory and other are stationary, and with limited gene flow between these stocks, despite some of them spawning in the same area and season. This is again associated with certain inverted supergenes [27, 55, 56]. Faroese waters have two distinct populations of cod, one at the Faroe Plateau and one at the Faroe Bank. The latter is fast-growing, large-sized fish [57], and locally known for its superior quality. We are confident that the Faroe Bank phenotype is strongly associated with certain, as yet unknown, genetic properties, possibly a genetic inversion. By being able to genetically separate Faroe Bank cod from other local cod stocks we would get a valuable tool in the search for the feeding grounds of the young Faroe Bank cod (age 0.5 to 3 years), which are not known today. Additionally, knowing the genetic properties associated with rapid growth and high quality may help in the efforts to make farmed cod a commercial reality.

The lesser sandeel (*Ammodytes marinus;* an ERGA pilot species) is one of several species collectively known as sandeels or sand lances. These species are important prey for birds, larger fishes and marine mammals, and they are an important link between the primary production and higher trophic levels [58-60]. The sandeels have typical seasonal behaviours, and burrow into sandy sea bottom during much of the winter. They are little used for human food, but are industrially fished, especially by countries around the North Sea. The total annual catches have varied between 100 000 and 1 million tonnes [61]. The intense fishery may influence seabirds at different stages of life [62-64], and thereby contribute to the observed decreases in seabird populations [65, 66]. It is poorly understood whether the sandeel populations in the different regions of the North Sea and the Northeast Atlantic are genetically distinct populations and to which degree there is gene-flow from one region to another [67]. Having the genome sequence of the lesser sandeel (and later for the related species) would be highly valuable for developing genetic panels for such investigations. Better knowledge on sandeel subpopulations and their genetic interconnections would improve the basis for quota determination in different management areas. Even more importantly, the genome sequence could be a tool in ecological studies, both to improve the knowledge of the sandeel biology in general, and for investigations of species interactions (see other examples below). At the time the ERGA pilot project was initiated, there were no publicly available genome assemblies from the taxonomic order Uranoscopiformes, to which the sandeels belong. During 2022 and 2023, genome assemblies from four species in this order became available, including our genome assembly from *Ammodytes marinus* (GenBank GCA_949987685).

Greater silver smelt (*Argentina silus;* an ERGA pilot species) is a relatively new, but, as yet, limited target for commercial fisheries, with an average annual catch of around 50 000 tonnes in the Northeast Atlantic, much of this in Faroese waters [57, 68]. It is commonly found at depths of 150-1400 m and it is long-lived and slow-growing [69]. Species with these characteristics are vulnerable to overexploitation, because the longer the time to reach maturity, the longer it takes to increase the population after a potential collapse. The stock structure is unknown [ref. 68 with stock annex]. Spawning may occur in several seasons or in prolonged periods of the year, and spread around in vast areas [69]. The International Council for the Exploration of the Sea (better known by its abbreviation, ICES) has divided the greater silver smelt into four assessment units, despite the lacking knowledge on separate biological populations [68]. Again, the genome would give us insight into the biology of the species, and help to develop population genetic markers, making it possible to assess the population substructure in the North Atlantic. Our genome assembly (GenBank GCA_951799395) is the first available genome from the order Argentiniformes.

An important aspect in sustainable exploitation of wild species, is to ensure that the population and the potential subpopulations are large enough to endure the harvesting pressure - in essence, that the species is maintained at a sufficiently sized population, within its natural fluctuations. Acquiring a good knowledge and overview of species that are commercially exploited or suggested for commercial exploitation, should be common sense. High-quality genome assemblies are one of the best tools, likely *the* best tool, to acquire such knowledge, and it can later be diversified into separate and specialised sub-tools for specific questions and investigations. One such question is how intensive fisheries are influencing the genetic future of the species. Intensive fisheries may give selection pressures influencing traits such as size-at-age and age-at-maturation [70, 71], but we know less if, and how, this influences the ecosystem in small [72] or large scale, or the long-term trajectories of genetic diversity.

Interaction between species

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

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

Planktonic algae form the basis of the entire marine ecosystem on which the Faroese economy relies. Many algae are difficult to distinguish morphologically, and DNA has become an important tool for routine algal biodiversity monitoring. However, there is probably much genetic variation and many cryptic species among algae that are unknown. Thus, there are still many gaps in our sequence databases for algae. This also includes toxin-producing algae [73-75], which are of interest for people collecting of mussels, the shellfish industry and fish aquaculture. Furthermore, the combined influence of climate change and the unintended transport and release of algae and other marine species, especially by ballast water or by attaching to the hull of ships, is likely to be an increasing problem in northern regions [e.g., ref. 76]. The ability to detect invasive species, including unexpected invasive species, will increase as the genomic databases become more complete.

Invasive species are generally unwanted because they may affect the local native species and the ecosystem in adverse ways. The New Zealand flatworm (*Arthurdendyus triangulatus*) was first reported in the Faroe Islands in 1982, possibly co-introduced from Scotland or New Zealand by soil following imported plants or trees [77]. The New Zealand flatworm preys on local earthworms, thereby over time possibly degrading the quality and the properties of the soil. Although there is some knowledge about genetic variation in the flatworm [78], a recent evaluation concluded that there are large gaps in the sequence data from this and related species, making it impossible to assess the reliability of the DNA markers [79]. Thus, having a genome assembly would be the basis for much better tools to follow the routes of spreading (for example, by eDNA), and possibly also to find potential targets for countermeasures.

In the Faroe Islands, there are no native terrestrial mammals. Among typical free-roaming herbivores, only mountain hare (*Lepus timidus*) and domestic sheep have been introduced, the former with four animals (from Norway) in 1855, and the latter probably with the first settlers well before year 1000 (and with many subsequent import events). Hunting of hare is a popular tradition, and the registered yield is between 3000 and 9000 hares/year (Eyðfinn Magnussen, pers. comm.), which is extremely high considering an area of 1400 km^2. One may imagine that hare and sheep could compete for food resources, given the high density of both species. This could be possible to investigate using different genetic tools, provided that the necessary genetic data are available for the local plants. Another interesting question is microevolution in hare, as all the local populations are founded from the first few animals introduced nearly 170 years ago.

Incidental insights

As genomes from more and more species are sequenced, it is evident that we will learn much about each single species. However, a single species does not exist without being connected to other species, not only in their habitats, in their ecosystems, and in their food webs, but they are also genetically connected to other species through evolution and the process of speciation. As more genome assemblies become available, we will undoubtedly understand more about the genetic processes, physiological processes, the immune system, protection against pathogens, and lots of other areas that give us deeper insight into life and basic processes of life [12, 80], and some of which may find applications in the future for improving our food production, and give new medical treatments, new materials, more eco-friendly industrial processes, etc. We can safely assume that there will be a continued advancement in methods, instruments, and bioinformatics, which will give us new and efficient tools that also can be applied to various questions and purposes. In short, we will have more insight into being humans, our own biology and genetics, and similarly for our fellow beings, and understand more about taking care of nature and the Earth, which ultimately is to take care of ourselves.

Interactions with and dissemination to the society

The third main aim of Gen@FarE is to establish an information databank in Faroese, covering all Faroese species and nature types. It is a scholarly obligation to inform the public in various ways, such as educational and outreach programmes, museum exhibitions and events, popular science presentations, etc. Museums and public collections have a long tradition in natural history, and have been highly important in disseminating knowledge and information to the society, whether we consider school classes, single individuals or the authorities. At the same time, many are interested in different aspects of biodiversity, and this is reflected in citizen science projects like iNaturalist [81] and eBird [82]. More than 1.5 million observation lists (usually with several species and many individuals of each species in each list) were submitted to eBird during February 2023, and more than 1.3 million single observations were added to iNaturalist in the same period. When the scale of the collected data is big enough, the geographical and seasonal distribution and abundance of species become apparent, and over time disclose population trends, as noticeably illustrated by eBird [83-85]. Additionally, and possibly undervalued, highly skilled non-professionals and laypersons contribute considerably to the identification and description of new species [5], and even more so for geographical distribution of species [86].

Our Nordic neighbours have organised national searchable public biological information banks interlinked with the possibility of registration of citizen science observations (Sweden with Artdatabanken and Artportalen [87, 88]; Norway with Artsdatabanken and Artsobservasjoner [89, 90]); and Denmark with Arter.dk [91]). Both the national and international citizen science initiatives mentioned above have identification tools, either integrated into the website or as free-standing mobile telephone apps [92-95], which significantly lowers the threshold for contributing to citizen science.

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

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Authors' contributions

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

Conflict of interest disclosure

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

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