


The logo for Peer Community In Genomics features a stylized network of blue and black dots and lines, with a circular pattern of black and white segments on the left side. The text "Peer Community In Genomics" is written in a large, black, sans-serif font to the right of the graphic.

# Peer Community In Genomics

## Why sequence everything? *A raison d'être* for the Genome Atlas of Faroese Ecology

**Stephen Richards**  based on peer reviews by **Tereza Manousaki** and 1 anonymous reviewer

Svein-Ole Mikalsen, Jari í Hjøllum, Ian Salter, Anni Djurhuus, Sunnvør í Kongsstovu (2024) The need of decoding life for taking care of biodiversity and the sustainable use of nature in the Anthropocene - a Faroese perspective. EcoEvoRxive, ver. 3, peer-reviewed and recommended by Peer Community in Genomics. <https://doi.org/10.32942/X21S4C>

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When discussing the Earth BioGenome Project with scientists and potential funding agencies, one common question is: why sequence everything? Whether sequencing a subset would be more optimal is not an unreasonable question given what we know about the mathematics of importance and Pareto's 80:20 principle, that 80% of the benefits can come from 20% of the effort. However, one must remember that this principle is an observation made in hindsight and selecting the most effective 20% of experiments is difficult. As an example, few saw great applied value in comparative genomic analysis of the archaea *Haloferax mediterranei*, but this enabled the discovery of CRISPR/Cas9 technology (1). When discussing whether or not to sequence all life on our planet, smaller countries such as the Faroe Islands are seldom mentioned. Mikalsen and co-authors (2) provide strong arguments to appreciate, investigate and steward genetic diversity, from a Faroese viewpoint, a fishery viewpoint, and a global viewpoint. As readers, we learn to cherish the Faroe Islands, the Faroese, and perhaps by extension all of nature and the people of the world. The manuscript describes the proposed Faroese participation in the European Reference Genome Atlas (ERGA) consortium through Gen@FarE – the Genome Atlas of Faroese Ecology. Gen@FarE aims to: i) generate high-quality reference genomes for all eukaryotes on the islands and in its waters; ii) establish population genetics of all species of commercial or ecological interest; and iii) establish a "databank" for all Faroese species with citizen science tools for participation.

In the background section of the manuscript, the authors argue that as caretakers of the earth (and responsible for the current rapid decrease in biodiversity), humanity must be aware of the biodiversity and existing genetic diversity, to protect these for future generations. Thus, it is necessary to have reference genomes for as many species as possible, enabling estimation of population sizes and gene flow between ecosystem locations.

Without this the authors note that "...it is impossible to make relevant management plans for a species, an ecosystem or a geographical area...". Gen@FarE is important. The Faroe nation has a sizable economic zone in the North Atlantic and large fisheries. In terms of biodiversity and conservation, the authors list some species endemic to other Faroe islands, especially sea birds. The article discusses ongoing marine environmental-DNA-based monitoring programs that started in 2018, and how new reference genome databases will help these efforts to track and preserve marine biodiversity. They point to the lack of use of population genomics information for Red List decisions on which species are endangered, and the need for these techniques to inform sustainable harvesting of fisheries, given collapses in critical food species such as Northwest Atlantic cod and herring. In one example, they highlight how the herring chromosome 12 inversion contains a "supergene" collection of tightly linked genes associated with ecological adaptation. Genetic tools may also help enable the identification and nurturing of feeding grounds for young individuals. Critically, the Faroe Islands have a significant role to play in protecting the millions of tons of seafood caught annually upon which humanity relies. As the authors note, population genomics based on high-quality reference sequences is "likely the best tool" to monitor and protect commercial fisheries. There is an important section discussing the role of interactions between visible and "invisible" species in the marine ecosystem on which we all depend. Examples of "invisible" species include a wide range of morphologically similar planktonic algae, and invasive species transported by ballast water or ship hulls. As biologists, I believe we forget that our population studies of life on the earth have so far been mostly in the dark. Gen@FarE is but one light that can be switched on.

The authors conclude by discussing Gen@FarE plans for citizen science and education, perhaps the most important part of this project if humanity is to learn to cherish and care for the earth. Where initiatives such as the Human Genome Project did not need the collaborative efforts of the world for sample access, the Earth BioGenome Project most certainly does. In the same way, at a smaller scale, Gen@FarE requires the support and determination of the Faroese.

### **References:**

- 1 Mojica, F. J., Díez-Villaseñor, C. S., García-Martínez, J. & Soria, E. Intervening sequences of regularly spaced prokaryotic repeats derive from foreign genetic elements. *J Mol Evol* 60, 174-182 (2005).
- 2 Mikalsen, S-O., Hjøllum, J. í., Salter, I., Djurhuus, A. & Kongsstovu, S. í. The need of decoding life for taking care of biodiversity and the sustainable use of nature in the Anthropocene – a Faroese perspective. *EcoEvoRxiv* (2024), ver. 3 peer-reviewed and recommended by Peer Community in Genomics. <https://doi.org/10.32942/X21S4C>

## **Reviews**

### **Evaluation round #1**

DOI or URL of the preprint: <https://doi.org/10.32942/X21S4C>

Version of the preprint: 1

### **Authors' reply, 16 January 2024**

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**Decision by [Stephen Richards](#) , posted 22 November 2023, validated 23 November 2023**

**Revisions needed**

Hi,

I'm the recommender at PCI genomics for your pre-print "The need of decoding life for taking care of biodiversity and the sustainable use of nature in the Anthropocene – a Faroese perspective" and two reviewers have looked at your manuscript and generally liked it.

Both reviewers generally liked and appreciated the manuscript and the work you have put in to get this far.

Unfortunately, both had minor problems with the text, in terms of the words and structure you use to describe the project rather than the intellectual content.

I thought about recommending as is, but feel it would be better for you as authors if you had another round of edits to fix the text errors and proposed improvements found by the reviewers before it goes into the record for posterity.

I look forward to seeing the improved revision so we can move forward with the recommendation.

With best wishes,

Stephen Richards  
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[Download recommender's annotations](#)

**Reviewed by [Tereza Manousaki](#), 11 October 2023**

In this manuscript, Mikalsen et al. describe the building of a national initiative for genome sequencing of the Faroese species linked to ERGA. Their initiative is very important not only for Faroe Islands, but for other countries with limited capacity and sets the ground for future such initiatives across other countries as well. They explain very well the link of species management and protection to the genetic diversity and the importance of monitoring it. I have comments mostly about the structure of the manuscript which I think could be substantially improved, to help the reader go through this wonderful paper.

First, I would expect to reduce a bit the more horizontal expressions one can find across the manuscript such as L58-60. Same for L53,54, I believe that intact nature is not the target, or the main problem, but heavily exploiting without clear management plans.

In L78 I understand what the authors wish to say, but my feeling is that the phrases "by being aware of it" and "impossible to take care of the things we do not know" need to be rephrased.

Similarly, L90 needs to be rephrased.

L196 maybe replace moral with ethical?

Regarding structure I have the following comments.

For example the Biodiversity and conservation section includes very important information but the paragraphs should be connected and presented in a more reasonable flow. The paragraphs are Red list and importance of genome, then long read sequencing and structural variation, then the value of barcoding, then the value of genomics for cryptic species and finally the sustainability of abundant species. In my opinion, although each paragraph has something important to say, the meaning is lost due to the lack of structure.

L371 In the same lines, the contribution of Faroe Islands ERGA pilot is not clearly explained. For example the phrase "Our genome assembly" helped me understand that this is linked to the Faroe ERGA effort, but I still had to guess it. It is important to show why each species was selected and what avenues this opens for the future management.

L379 Reference genomes are an amazing tool, when coupled with population genomics data. Not the genome alone.

Again, the section interaction between species is not clear why it is separate from the biodiversity and conservation section.

I really enjoyed the "Incidental insights" paragraph and think that it fits better as the last paragraph of this paper.

Good luck,

Tereza Manousaki

### **Reviewed by anonymous reviewer 1, 21 September 2023**

The manuscript by Svein-Ole Mikalsen and coworkers represents a perspective paper regarding the local needs and opportunities to apply genomics and reference genome generation in the Faroe islands.

The manuscript is generally well written, although the first half of the introduction is quite manifest-like and could be made more concise. Due to the nature of this contribution, my comments are mainly suggestions to broaden or focus some parts of their work.

L70-> L195-> L294 etc: Mapping of genetic diversity is important, however I would like to know more what the authors mean by "establishing population genetics for all commercial species". What are these species and what would be sufficient sampling to achieve appropriate coverage? How does this work for the oceanic fish stocks, whose population encompasses the whole Northern Atlantic? I think these parts of the manuscript could be elaborated a bit.

L195: Not a single whale species is mentioned in this chapter?

L216: The runs of homozygosity do not correlate with the Red list status. It is fairly easy to think of examples (including our own species), which show relatively little variation but have huge populations. For example, invasive species have typically experienced a bottleneck when colonizing new areas, resulting in loss of homozygosity. However, it might still be useful to have a catalogue of SNP variation and their allele frequencies in a species to see how these might change over time. Generally, I would like the authors to discuss more the practicalities for their proposals. For example, what resources (money, personnel or infrastructure) does the genetic/genomic sampling require to be effective? What organism groups the citizen science projects can successfully target in the Faroese context?

L243 "Oxford Nanopores" -> Oxford Nanopore Technologies (ONT)

L294-> How about grindadrap or pilot whale / dolphin hunting? Certainly, a rather unique local tradition, whose sustainability is dependent on accurate evaluation of the whale populations. Also the species identification and existence of endangered cryptic species among whales is an issue that genomics could help to tackle. Might be worth to mention?

L424: Curiously, the Faroese hares seem to be grey in winter, which might be nice to mention as an adaptation?

L452: Are there any shortcomings for the Citizen science initiatives (frequent misidentifications, observations capturing mainly common or charismatic species)? Are there ways to improve these by targeted campaigns and expert help? What resources would be needed?

Despite these few suggestions, the manuscript is a very important contribution to describe some of the expectations from the ERGA initiative.