SCIENTIFIC COMMITTEE WORKING GROUP ON GENETICS

28 October 2025

Online

REPORT

Presented to the 32nd meeting of the Scientific Committee as NAMMCO/SC/32/07

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Chair

Morten Tange Olsen

Rapporteur

Maria Garagouni

Authors

Rachel Ball, Ricardo de Almeida Mendes, Maria Garagouni, Sunnvør Klettskarð í Kongsstovu, Marie Louis, Morgan McCarthy, Tommi Nyman, Christophe Pampoulie, María Quintela Sánchez, Mioko Taguchi, Morten Tange Olsen, Sven Winter.

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EXECUTIVE SUMMARY

The Working Group on Genetics (Genetics WG) met online on 28 October 2025. The meeting was chaired by Morten Tange Olsen. The agenda and full list of participants are available in Appendices 1 and 2, respectively. The aim of the meeting was to review new information on pilot whale genetic structure in the North Atlantic and compare it with existing literature on the subject; these documents are listed in Appendix 3. The conclusions drawn here will inform the stock assessment that will be conducted by the Pilot Whale Working Group (PWWG) later this year.

Preliminary results of the DolphinUnit project, a comprehensive genomic study spanning the entire North Atlantic, suggest no population structure of long-finned pilot whales. This pattern is consistent across several molecular markers, including autosomal DNA, mitochondrial DNA, and the X chromosome. This lack of structure contrasts with the outcomes of former studies, namely, of a north-south genetic differentiation in the Northeast Atlantic, and of a West Greenland differentiation that was inferred from microsatellite and mitochondrial DNA analyses. While these new data show clear evidence of gene flow across the North Atlantic, they do not entirely preclude the possibility of genetic structure, e.g., genomic islands of divergence.

The analyses presented here concur with the previous conclusion that pilot whales in the Mediterranean are genetically distinct from the Atlantic, although there is evidence of some admixture (gene flow between populations) with animals sampled in France. This admixture could potentially explain the previous indications of a north-south differentiation, as the relevant studies did not include animals from the Mediterranean (that is, the differentiation of more southerly animals would not have seemed strong if the truly distinct Mediterranean animals had also been included).

The Genetics WG made a series of **recommendations for further analyses**, namely to:

- Test for selection and genomic islands of divergence within the North Atlantic dataset;
- Examine relatedness between different regions, compared to intra-locality relatedness levels;
- Investigate the higher levels of heterozygosity in Irish and Canadian samples, which might be due to degradation of the DNA;
- Test for isolation by distance using approximate locations;
- Investigate the divergence history (demographic history, inbreeding, divergence time, migration rates, putative selection) of the Mediterranean and North Atlantic populations;
- Compare the current dataset with samples from the Southern Hemisphere and with short-finned pilot whales.

REPORT

The Working Group on Genetics (Genetics WG) met online on 28 October 2025. The meeting was chaired by Morten Tange Olsen (Globe Institute). The full list of participants is available in Appendix 2. The aim of the meeting was to review new information on pilot whale genetic structure in the North Atlantic and compare it with existing literature on the subject.

1. WELCOME FROM THE CHAIR

The Chair welcomed participants and mentioned that the outcomes of this meeting will help inform the upcoming pilot whale stock assessment by the Pilot Whale Working Group (PWWG). He also reminded that a thorough review of existing literature on pilot whale genetics in the North Atlantic had been conducted by the Genetics WG in 2024, and that new information would be compared against that background. Finally, he called for a round of introductions.

2. ADOPTION OF AGENDA

The meeting agenda was adopted with no modifications, as seen in Appendix 1.

3. APPOINTMENT OF RAPPORTEURS

Deputy Secretary Maria Garagouni was appointed as rapporteur, with support from NAMMCO Intern Ricardo de Almeida Mendes and other participants, as needed.

4. REVIEW OF AVAILABLE DOCUMENTS

A list of documents made available prior to the meeting is shown in Appendix 3.

5. LONG-FINNED PILOT WHALE GENETIC STRUCTURE IN THE NORTH ATLANTIC

5.1 DOLPHINUNIT PRELIMINARY RESULTS

Sven Winter presented some preliminary results from the DolphinUnit project.

Summary

Knowledge of long-finned pilot whale population structure within the Northern Hemisphere has been lacking. Studies using mitochondrial DNA (mtDNA) or microsatellites previously indicated a distinct Mediterranean population and suggested a north-south distinction in the eastern North Atlantic. Differentiation between the eastern and western North Atlantic was less conclusive, as the sample size from West Greenland was small and comprised hunted animals that may have been related. Initial results from newly generated whole-genome SNP data from 172 pilot whales currently support a clear distinction between the North Atlantic and the Mediterranean, but suggest that the structure observed might be caused by genetic drift in the Mediterranean population, due to small population numbers; this is also supported by a reduced genome-wide heterozygosity and a lack of accumulated substitutions in the mitochondrial genomes. Within the North Atlantic, standard population genomics analyses, such as PCA and admixture, are unable to detect significant population structure and instead suggest a rather uniform population. MtDNA analysis confirms the previously observed low diversity of the mtDNA, with most haplotypes showing only a one- or two-substitution difference to the most common haplotype, while being shared by pilot whales from across the North Atlantic. The only

haplogroup that substantially differs from the most common haplotype (15 substitutions) seems to be closely related to the short-finned pilot whale (*G. macrorhynchus*).

Discussion

The group **agreed** that the analyses presented show no indication of genetic structure in North Atlantic pilot whales. With the exception of samples from the Mediterranean, there is clear evidence of gene flow across all other areas. However, further analyses could potentially reveal adaptive variation and, therefore, the next step would be to examine specific regions of the autosomal genome for differentiation (e.g. genomic islands of divergence), as well as to conduct population structure analyses based on the Y chromosome, as male animals might reveal genetic structure, which was not detected in females based upon the X chromosome.

Certain samples from Canada and Ireland, in particular, showed higher heterozygosity levels than average. The group **concurred** that closer examination of the samples with high heterozygosity is warranted, as it is for those with more distinct mitogenomes (e.g., certain animals from East Greenland, the Faroe Islands, and Canada).

The overall low number of mitochondrial substitutions suggests that genetic drift is more likely than geographic separation between groups, but simulations of demographic changes under different scenarios would be useful to determine the most probable explanation. The integration of environmental data could also help identify putative patterns of isolation by environment.

5.2 COMPARISON WITH EXISTING LITERATURE

A review of existing literature had led the Genetics WG to conclude, at its previous meeting (NAMMCO 2024), that: “There is genetic evidence of a north-south differentiation of pilot whales in the eastern North Atlantic, with potentially distinct genetic clusters in the Faroe Islands, the UK and Ireland, and the Bay of Biscay/Iberian Peninsula, and a possible contact zone across UK and Irish waters. Pilot whales in the Mediterranean Sea form a separate genetic cluster. In the western North Atlantic, there appears to be a genetic link between Greenland and Canada, although more samples are required to confirm this. It is unclear whether these patterns are a result of geographic separation, isolation-by-distance, or skewed sampling of related individuals during stranding and hunting events.”

In contrast with the above, the data presented here do not support the existence of a north-south differentiation in pilot whale autosomal DNA, X chromosome, or mitochondrial DNA. Moreover, excluding the highly related West Greenland individuals (or duplicate samples, as the case may be) from the analysis completely erases any indication of structure between Canada and West Greenland. However, the samples from the Mediterranean Sea do form a distinct genetic cluster, as concluded previously, although with evidence of admixture with animals sampled in France (Bay of Biscay). It is possible that the north-south divergence indicated in older studies that did not include animals from the Mediterranean Sea was driven more by a fringe group of animals with this admixture signal.

As further analyses could explore differentiation in more detail, the group agreed that it would be premature to completely discount any kind of genetic structure. For example, a targeted comparison between samples taken from different areas where there are direct catches, such as West and East Greenland and the Faroe Islands, would help identify potential genomic islands of divergence, even with a small dataset. Re-running the PCA using geographically explicit locations (DAPC) or in windows across the genome (localPCA) would also be useful, as would comparing inter-population relatedness distributions with intra-population relatedness levels—although the latter case would require caution regarding samples collected from completely different sources, e.g., strandings versus drive hunts, where the chances of sampling relatives are very different.

5.3 CONCLUSIONS AND RECOMMENDATIONS

The Genetics WG **agreed** that the geographic extent and number of samples in the DolphinUnit dataset will lead to robust conclusions once the analyses are complete. This would be further served in the long term by a comparison with genomes and mitogenomes from long-finned pilot whales in the Southern Hemisphere, as well as short-finned pilot whales.

At present, the **conclusions** that can be safely drawn are as follows:

- Preliminary data based on 3.5 mil SNPs suggest high levels of gene flow in the North Atlantic, thus not necessarily supporting previous findings of a north-south differentiation in the Northeast Atlantic, nor the differentiation of a West Greenland population that was inferred from microsatellites and mtDNA. This pattern is consistent across autosomes and the X chromosome, as well as the mitogenome (Y chromosome analysis is in progress). The patterns suggested for West Greenland by previous studies may be a result of including related individuals or of family structure. Although the same individuals from a single group were included here, first to third order relatives were excluded from the analyses.
- The Mediterranean animals from Spain are distinct, and there is a slight signature of admixture with animals from the French Atlantic coast. It is currently unclear whether the overall distinction is a result of drift in small populations.

The Genetics WG made a series of **recommendations for further analyses**, namely to:

- Test for selection and genomic islands of divergence within the North Atlantic dataset;
- Examine relatedness between different regions, compared to intra-locality relatedness levels;
- Investigate the higher levels of heterozygosity in Irish and Canadian samples, which might be due to degradation of the DNA;
- Test for isolation by distance using approximate locations;
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6. REPORT ADOPTION AND MEETING CLOSE

A draft of the meeting conclusions and recommendations was agreed upon during the meeting. The final report was adopted by correspondence on 07 November 2025.

Participants thanked Winter for his very interesting presentation and congratulated the Chair for keeping the meeting on track despite technical setbacks. The Chair and Garagouni in turn thanked everyone for joining the meeting and for their vital contribution to the work of NAMMCO.

REFERENCES

NAMMCO-North Atlantic Marine Mammal Commission (2024). Report of the Scientific Committee Working Group on Genetics, October 2024, Copenhagen, Denmark. https://nammco.no/wp-content/uploads/2024/12/report_genetics-wg-2024.pdf

APPENDIX 1: AGENDA

1. **Welcome from the Chair**
2. **Adoption of agenda**
3. **Appointment of rapporteurs**
4. **Review of available documents**
5. **Long-finned pilot whale genetic structure in the North Atlantic**
    - 5.1. DolphinUnit preliminary results
    - 5.2. Comparison with existing literature
    - 5.3. Robustness of conclusions
6. **Report adoption**
7. **Meeting close**

APPENDIX 2: PARTICIPANT LIST

WG MEMBERS

Christophe Pampoulie
Marine and Freshwater Research Institute
christophe.s.pampoulie@hafogvatn.is

María Quintela Sánchez
Institute of Marine Research
maria.quintela.sanchez@hi.no

Marie Louis
Greenland Institute for Natural Resources
marie.louis@natur.gl

Mioko Taguchi
Institute for Cetacean Research
taguchi@cetacean.jp

Morgan McCarthy
Copenhagen University
morgan.lee.mccarthy@gmail.com

Morten Tange-Olsen (Chair)
Globe Institute
morten.olsen@sund.ku.dk

Sunnvør Klettskarð í Kongsstovu
University of the Faroe Islands
SunnvorK@setur.fo

Tommi Nyman
Norwegian Institute of Bioeconomy Research
tommi.nyman@nibio.no

INVITED EXPERTS

Rachel Ball
University of Glasgow
racheljb2708@gmail.com

Sven Winter
University of the Faroe Islands
svenw@setur.fo

NAMMCO SECRETARIAT

Maria Garagouni
Deputy Secretary
maria@nammco.org

Ricardo de Almeida Mendes
Intern
intern@nammco.org

APPENDIX 3: LIST OF DOCUMENTS

Document Reference	Title	Agenda Item
Working Documents		
Genetics WG/2025-01//01	Draft Agenda	2
Genetics WG/2025-01/02	Draft List of Participants	1
Genetics WG/2025-01/03	Draft List of Documents	4
For information documents		
Genetics WG/2025-01/FI/01	ICES Meeting Etiquette (2022)	All
Genetics WG/2025-01/FI/02	NAMMCO (2024) Report of the Genetics WG	5.2
Genetics WG/2025-01/FI/03	NAMMCO (2008) Report of the Pilot Whale WG	5
Genetics WG/2025-01/FI/04	Monteiro et al. (2015). Long-finned pilot whale population diversity and structure in Atlantic waters	5.2
Genetics WG/2025-01/FI/05	Ball et al. (2021). New haplotypes found in stranded long-finned pilot whales	5.2
Genetics WG/2025-01/FI/06	Kraft et al. (2020). Global phylogeography and genetic diversity of the long-finned pilot whale	5.2
Genetics WG/2025-01/FI/07	Marina et al. (2018). Long-finned pilot: Are there differences in their skulls?	5.2
Genetics WG/2025-01/FI/08	Monteiro et al. (2016). Major Histocompatibility Complex (MHC) class II sequence polymorphism in long-finned pilot whale	5.2
Genetics WG/2025-01/FI/09	Fullard et al. (2000). Population structure of long-finned pilot whales	5.2
Genetics WG/2025-01/FI/10	Oremus et al. (2009). Worldwide mitochondrial DNA diversity and phylogeography of pilot whales	5.2
Genetics WG/2025-01/FI/11	Verborgh & Desportes (2023). Long-Finned Pilot Whale, *Mammals of Europe*	5.2
Genetics WG/2025-01/FI/12	Gauffier et al. (2023) Long-finned pilot whales IUCN Red List Assessment	5
Genetics WG/2025-01/FI/13	Thorne & Nye (2021) Long-finned pilot whales trait-mediated poleward shifts	5