



SCIENTIFIC COMMITTEE WORKING GROUP ON GENETICS

*October 8 – 9, 2024
Faroese Representation, Copenhagen, Denmark*

REPORT

Presented to the 31st Meeting of the Scientific Committee as NAMMCO/SC/31/06



© North Atlantic Marine Mammal Commission

Please cite this report as:

NAMMCO-North Atlantic Marine Mammal Commission (2024). Report of the Scientific Committee Working Group on Genetics, October 2024, Copenhagen, Denmark.

Available at https://nammco.no/genwg_reports/

DISCLAIMER:

The content of this report contains the view of the Working Group and does not necessarily represent the views of the NAMMCO Scientific Committee or Council.

NAMMCO

Postbox 6400, Sykehusveien 21-23, N-9294 Tromsø, Norway, +47 77687371, nammco-sec@nammco.no,
www.nammco.no

TABLE OF CONTENTS

Table of contents.....	iii
Executive Summary	iv
Main report	8
1. Welcome from the Chair and Opening Remarks	8
2. Adoption of Agenda	8
3. Appointment of Rapporteurs.....	8
4. Review of available Meeting Documents.....	8
5. Pilot whale	9
5.1 Population structure across the North Atlantic.....	9
5.2 Information and guidance for Pilot Whale Stock Assessment.....	10
6. Narwhal	11
6.1 Population structure between Canada and Greenland	11
6.2 Genetic discreteness of putative small stocks in East Greenland.....	13
7. Beluga.....	15
7.1 Genetic provenance of animals occurring in East Greenland.....	15
7.2 Genetic relationship between west Greenland winter harvest and Southeast Baffin Island population ..	17
7.3 Stock structure in the High Arctic	17
8. Dolphins.....	18
8.1 White-beaked and white-sided dolphin population structure	18
9. Genetics in stock assessments.....	19
10. Future focal points.....	20
10.1 Harbour porpoise.....	20
10.2 Harbour and grey seal.....	21
10.3 Walrus.....	23
11. Any other business	24
12. Recommendations for research	24
12.1 Recommendations for Pilot Whales	24
12.2 Recommendations for Narwhal.....	24
12.3 Recommendations for Beluga.....	24
12.4 Recommendations for Dolphins	25
12.5 Recommendations for Coastal Seals.....	25
13. Adoption of Report and meeting close	25
References.....	25
APPENDIX 1: Agenda	31
APPENDIX 2: List of Participants	33
APPENDIX 3: List of Documents.....	34

EXECUTIVE SUMMARY

The NAMMCO Scientific Committee Working Group on Genetics held its 1st meeting in Copenhagen, Denmark, on the 8th and 9th of October 2024. The Working Group (WG) was chaired by Morten Tange Olsen (Globe Institute, Denmark). The Genetics WG was established as a means of improving the reliability of the stock structure information and/or hypotheses used in NAMMCO species/stock assessments and, therefore, the robustness of assessments.

The *Terms of Reference* of the WG are:

- i. *To review the genetic data that will be used in NAMMCO's species assessments.*
- ii. *To serve as a consultation body on topics related to genetics for NAMMCO's working groups.*
- iii. *To detect data and knowledge gaps needed for the assessment of specific species/stocks and provide NAMMCO with advice on how to move forward to fill such gaps.*

At its 30th meeting, the NAMMCO Scientific Committee prioritised the following tasks for this WG:

- **Pilot whales:** examination of the genetic connectivity between different hunting areas (East Greenland, West Greenland, Faroe Islands, Iceland), as well as population structure (if any) across the North Atlantic.
- **Narwhals:** examination of the genetic discreteness of putative small stocks in East Greenland, as well as population structure between Canada and Greenland.
- **Belugas:** further examination of the genetic provenance of the animals occurring in East Greenland; examination of the genetic relationship between the West Greenland winter harvest and the Southeast Baffin Island population; examination of stock structure of belugas in the High Arctic, namely those wintering in North Water, those available to the hunt in Northwest Greenland (Qaanaaq), and those available to the fall and winter hunt in West Greenland.

The WG examined existing literature and ongoing studies pertaining to the questions above, as well as to species that will undergo stock assessments in the next two years. Recommendations were formulated, which will help fill in knowledge gaps on these topics and allow for robust stock assessments in the near future. Finally, a draft of recommendations for genetic data collection and analysis methods was initiated (to be completed intersessionally by the WG), which will help establish standardised protocols across NAMMCO countries.

Pilot whale

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.

Narwhal

Recent investigations into the genetic structuring of narwhals show evidence of at least three genetic clusters in Arctic Canada, namely, a northern and southern cluster in the High Arctic, and another cluster in Naujaat Bay. This structure is further supported by these animals' migration patterns, as described in the Global Review of Monodontids.

Fine-scale genetic structure of narwhals harvested in East Greenland shows clear differentiation between the spring and summer hunt in Scoresby Sound (Management Area 1), as well as weaker

differentiation of the animals hunted in Tasilaq (Management Area 3). There is no robust genetic evidence that the animals harvested around Kangerlussuaq (Management Area 2) form a distinct cluster.

Beluga

Genetic clustering of belugas harvested in East Greenland in recent years (2017–2023) indicates that they originated from at least two geographically distant stocks, the Beaufort Sea and the Kara Sea. A single individual potentially originated from Svalbard, but this link should be further investigated.

Ongoing range-wide genetic studies of belugas indicate some potential differentiation between Cumberland Sound and Qeqertarsuaq. Moreover, belugas harvested in Grise Fiord originated from two distinct stocks, Cunningham Inlet and Qeqertarsuaq, with a single individual likely originating from Repulse Bay. There are also slight indications of genetic differentiation between Qaanaaq belugas and Cunningham Inlet belugas.

White-beaked and white-sided dolphins

There is strong genetic evidence of at least three distinct populations of white-beaked dolphins in the North Atlantic: one in the western North Atlantic (Canada and USA), one in the eastern North Atlantic (Barents Sea, western Svalbard, and Iceland), and one in more southern regions (North Sea, Britain, and Ireland). There is possibly a fourth genetic cluster in the southern North Sea (Germany and Denmark).

In contrast, Atlantic white-sided dolphins show no population structure across the central and eastern North Atlantic. A higher sample size is needed from the western North Atlantic in order to draw robust conclusions about east-west connectivity of this species.

Harbour porpoise

Current knowledge indicates that harbour porpoises in the North Atlantic form a large, near-panmictic population spanning from the USA and Canada to northern Norway. It is likely that this population has “seeded” smaller, localised genetic clusters which exist in West Greenland, Mauritania, the Iberian Peninsula, and the Black Sea, with still more clusters potentially existing in other parts of Europe and the Arctic. Ongoing analyses will shed further light on this in the near future.

Harbour and grey seals

Harbour seals exhibit high site fidelity, with multiple small, extremely localised genetic clusters confirmed along coastlines on both sides of the Atlantic. This could have serious implications for management, with regards to local extirpations of harbour seals. Further analyses should include more samples from Canada, East Greenland, and the Barents Sea.

Grey seals, in contrast, show greater mobility and several large and small genetic clusters have been identified in the eastern North Atlantic, as well as a large one in the western North Atlantic. There is currently very little genetic information regarding grey seals in Greenland, the Faroe Islands, and northern Norway.

Walrus

Existing studies have identified at least six genetic clusters of walrus across the North Atlantic, as well as two extinct populations in Iceland and the Canadian Maritimes. Ongoing whole-genome sequencing research across their entire range will shed light on precise population boundaries and substructure.

Recommendations for research for Pilot Whale

Recommendations to All Parties

- Determining population structure at the scale of the North Atlantic, and whether this structure is driven geographically or socially by range-wide sampling of family units and single individuals, and keeping exact track of where the samples are sourced.
- Conducting genetic analyses of tagged pilot whales, to compare movement, foraging, and social behaviour with relatedness, genetic structure, diversity, and potential adaptations.

Recommendations to the Faroe Islands and Greenland

- Initiating a dedicated genetic monitoring program based on archival and newly collected samples from harvested groups in Greenland and the Faroe Islands, as well as in mass stranding events wherever they occur, to determine:
 - i. family groupings and social structure,
 - ii. putative population of origin,
 - iii. the influence of removing entire family units during pilot whale hunts, for instance in terms of genetic diversity, inbreeding levels, mutation load, and standing genetic variation.

Recommendations for research for Narwhal

Recommendations to Greenland and Canada

- Generating high-coverage genome data for High Arctic–West Greenland narwhals to compare with the existing data from the Arctic Canada, to further elucidate population structure across the two regions.
- Conducting more in-depth research into the social structure of narwhal populations, including genetic relatedness and sex-based analyses.

Recommendations for research for Beluga

Recommendations to Greenland

- Conducting continuous genetic analysis of any harvested individuals from East Greenland, to determine the proportions of harvested belugas from different genetic stocks.

Recommendations to Greenland and Canada

- Conducting additional genetic analysis with more samples and high-coverage genome data of belugas from West Greenland and Canada to confirm (or negate) genetic differentiation.
- Conducting additional genetic analysis with more samples and high-coverage genome data of belugas from the High Arctic to confirm (or negate) genetic differentiation.

Recommendations for research for Dolphins

Recommendations to Greenland, Canada, and the USA

- Conducting range-wide analysis to fill in knowledge and sampling gaps for white-beaked and white-sided dolphins in the western North Atlantic, West Greenland, and East Greenland.

Recommendations for research for Coastal Seals

Recommendations to Greenland

- Sampling more harbour seals in Greenland to further investigate putative signals of genetic substructure. This could include analysis of archival samples, in addition to opportunistic sampling of by-caught individuals.

Recommendations to the Faroe Islands

- Sampling grey seals from the Faroe Islands to determine if they are a unique population or a part of a larger population in Scotland and/or southeast Iceland.

MAIN REPORT

The NAMMCO Scientific Committee Working Group on Genetics held its 1st meeting in Copenhagen, Denmark, on the 8th and 9th of October 2024. The Working Group (WG) was chaired by Morten Tange Olsen (Globe Institute, Denmark). The meeting agenda and list of participants are available in Appendix 1 and 2, respectively.

The Genetics WG was established as a means of improving the reliability of the stock structure information and/or hypotheses used in NAMMCO species/stock assessments and, therefore, the robustness of assessments. The Terms of Reference of the WG are:

- i. To review the genetic data that will be used in NAMMCO's species assessments.*
- ii. To serve as a consultation body on topics related to genetics for NAMMCO's working groups.*
- iii. To detect data and knowledge gaps needed for the assessment of specific species/stocks and provide NAMMCO with advice on how to move forward to fill such gaps.*

In light of the stock assessments presented at SC/30, as well as those planned for the next two years, the Scientific Committee (NAMMCO 2024) tasked the WG with the following priorities:

- **Pilot whales:** examination of the genetic connectivity between different areas (East Greenland, West Greenland, Faroe Islands, Iceland), as well as population structure (if any) across the North Atlantic.
- **Narwhals:** examination of the genetic discreteness of putative small stocks in East Greenland, as well as population structure between Canada and Greenland.
- **Belugas:** further examination of the genetic provenance of the animals occurring in East Greenland; examination of the genetic relationship between the West Greenland winter harvest and the Southeast Baffin Island population; examination of stock structure of belugas in the High Arctic, namely those wintering in North Water, those available to the hunt in Northwest Greenland (Qaanaaq), and those available to the fall and winter hunt in West Greenland.

1. WELCOME FROM THE CHAIR AND OPENING REMARKS

Tange Olsen welcomed the participants to the 1st physical meeting of the WG and thanked the Faroese Representation for hosting it. He then called for a round of introductions and provided the background for the meeting, as outlined above.

2. ADOPTION OF AGENDA

The agenda was adopted with no modifications.

3. APPOINTMENT OF RAPPORTEURS

NAMMCO Deputy Secretary Maria Garagouni was appointed as the primary rapporteur, with assistance from NAMMCO Intern, Noor Elias. Participants were asked to submit written summaries of presentations and interventions on agenda items, as needed.

4. REVIEW OF AVAILABLE MEETING DOCUMENTS

Working (WD) and For Information (FI) documents were shared with participants two weeks prior to the meeting itself. These were presented or referred to throughout the discussion of the remaining agenda items.

5. PILOT WHALE

5.1 POPULATION STRUCTURE ACROSS THE NORTH ATLANTIC

Rachel Ball presented an overview of existing literature on long-finned pilot whales, as well as her own recent findings (WD/06).

Summary

Knowledge of long-finned pilot whale population structure within the Northern Hemisphere is lacking. Several mitochondrial DNA (mtDNA) studies exist, indicating that the Mediterranean population is distinct, and that differentiation exists between Irish and Scottish waters. However, only one study has used nuclear markers to investigate population structure in the North Atlantic, suggesting a correlation with sea-surface temperatures. Samples originating from mass stranded individuals on Scottish and Irish coastlines, along with a grind pod from the Faroe Islands, were analysed with microsatellite markers to investigate group relatedness. Additional single stranded samples from Scotland and Ireland were added to that sample set and analysed with genomic sequencing to test for population structure within the eastern North Atlantic. Furthermore, the first direct comparison of nuclear markers between Northern and Southern Hemisphere long-finned pilot whales was conducted using stranded individuals from the Falkland Islands. The microsatellite analysis confirmed maternal centred pod structure, with multiple pod units found in every event examined. F_{ST} analysis found that some stranding events were significantly genetically differentiated from others, i.e., unrelated family groups, but this was not correlated to geographic location. The single nucleotide polymorphism (SNP) dataset did not support previous mtDNA patterns of differentiation between Ireland and Scotland. No neutral or adaptive divergence was found within the eastern North Atlantic. However, clear genetic difference was observed between the Northern and Southern Hemispheres.

Discussion

The WG discussed the robustness of some of the conclusions drawn in older publications, such as the apparent correlation of temperature and genetic diversity in FI/11, which, based on sample size, could potentially be due to random chance. In Ball's findings (WD/06), there appeared to be subtle patterns of population structure within the eastern North Atlantic, with the exception of the Faroese individuals. However, it was pointed out that the source of the samples (family units of closely related animals in the Faroese grind, as opposed to scattered stranding events in other areas) could potentially be driving this signal. The same might be true of animals hunted in West Greenland, samples of which could be biasing the conclusions of Fullard et al. (2000) (FI/11). Telemetry data from animals tagged in the Faroe Islands has shown large dispersal ranges, as far south as the Bay of Biscay; such long-distance movements could explain the overall lack of clear population structure. Tange Olsen presented some unpublished data that included samples from the Iberian Peninsula and the Mediterranean Sea for comparison, showing more distinct patterns. However, in all the literature discussed, samples were conspicuously absent from Iceland, Norway, and East Greenland, making it difficult to draw conclusions about the entire North Atlantic. A recently funded project (see also item 8.1) aims to analyse samples collected during tagging, biopsy, and hunting trips, across East Greenland, Canada, Iceland, and the Faroe Islands, with potential contributions from northern Norway, Gibraltar, the Mediterranean, the Bay of Biscay, and Ireland, as well as opportunistic hunts in West Greenland. The group recommended sampling family units as well as single individuals where possible, both within this project and in future studies.

Based on the combined evidence in all the studies examined, the WG agreed that there are robust differences in the pilot whale mitochondrial haplotypes between the Faroe Islands, the UK-Ireland, and the Iberian coast, with a possible north-south contact zone across the UK and Ireland. The WG further agreed that animals in the Mediterranean Sea are quite distinct from the rest of the north Atlantic and likely form their own stock. The evidence of differentiation between the eastern and

western Atlantic is less conclusive, as the sample size from West Greenland is small and based on hunted animals.

The group agreed that Ball's own work was analytically comprehensive and could serve as a guide for future sampling efforts, e.g., what to sample and which kinship relationships to examine. Examining family groupings within the data from mass strandings would give insights into family-based, rather than ecologically driven, population structure. Investigating the social structure within Faroese pods would provide similar insights, as would collecting biopsy samples of tagged animals, to assess behavioural influences. From a methodological perspective, it would also be interesting to compare the resolution of relatedness found with SNP data compared to microsatellite data. This would confirm parent-offspring relationships; however, it is not possible to achieve with the existing dataset.

Besides inferences useful for stock delineations, the group discussed other useful applications of genetic analyses within the NAMMCO remit. The WG recommended genetically examining the influence of removing entire family units during pilot whale drive hunts, for instance in terms of genetic diversity, inbreeding levels, mutation load, and standing genetic variation. Genetic diversity in particular is currently understudied in the Atlantic, and it is therefore entirely unclear how pilot whale hunts impact their adaptive capacity, or if there are ecotype-like specialisations in terms of habitat preferences, diet, susceptibility to diseases, and contaminant loads.

5.2 INFORMATION AND GUIDANCE FOR PILOT WHALE STOCK ASSESSMENT

Based on the best available current knowledge (Figure 1), the WG **agreed** that there is evidence of a north-south differentiation of pilot whales in the eastern North Atlantic, roughly into the following geographic regions: the Faroe Islands, the UK and Ireland, and the Iberian Peninsula. There is a possible contact zone across UK–Irish waters. The Mediterranean Sea animals likely form a distinct genetic population from the rest of the Atlantic. It is unclear whether the patterns currently observed in the North Atlantic (not including the Mediterranean) reflect geographically distinct populations, isolation-by-distance or the effect of social stratification, i.e., incidental sampling of related individuals.

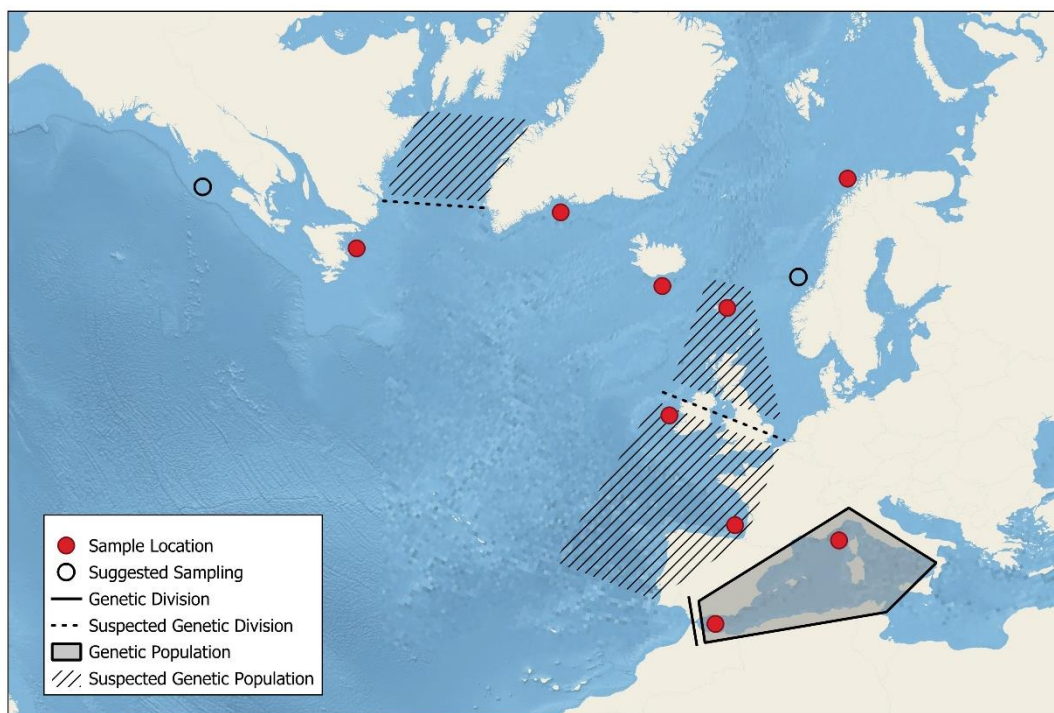


Figure 1. Putative long-finned pilot whale genetic populations in the North Atlantic. Sample locations and inferences about population structure are drawn from the following sources: Fullard et al. (2000) (FI/11), Kraft et al. (2020) (FI/08), and Monteiro et al. (2015) (FI/06)

For the purposes of a full stock assessment at the upcoming Pilot Whale Working Group in 2025, this **WG recommended:**

- i. Determining whether structure is driven geographically or socially by range-wide sampling of family units, as well as single individuals, and keeping exact track of where the samples are sourced.
- ii. Initiating a dedicated genetic monitoring program based on archival and newly collected samples from harvested groups in GL and FO, as well as in mass stranding events wherever they occur, to determine
 - a. family groupings and social structure,
 - b. putative population of origin,
 - c. the influence of removing entire family units during pilot whale hunts, for instance in terms of genetic diversity, inbreeding levels, mutation load, and standing genetic variation.
- iii. Conducting genetic analyses of tagged pilot whales, to compare movement, foraging, and social behaviour with relatedness, genetic structure, diversity, and potential adaptations.

6. NARWHAL

6.1 POPULATION STRUCTURE BETWEEN CANADA AND GREENLAND

Marie Louis presented recent findings on genetic structuring and demographic histories of narwhal populations in the NAMMCO region and beyond.

Summary

Based on 24 narwhal samples and 274,847 unlinked SNPs sequenced to 10-12x genome-wide coverage, and a larger set of 117 samples of lower genome-wide coverage and 486,710 unlinked SNPs, we identify three distinct clusters of narwhals in a Principal Component analysis: Canadian Arctic Archipelago and West Greenland (CAA/WG), Northeast Greenland and Svalbard (NEG/Sv), and Southeast Greenland (SEG, Figure 2a). No further structure was recovered within CAA/WG, possibly due to the low sequencing coverage of our data. Although not a separate cluster, Melville Bay narwhals tend to group together, and this may be due to sampling of related individuals.

To infer the timing and drivers of the observed population structuring, the demographic history of the three narwhal populations was reconstructed, using various methods. The results indicate each population had a low long-term effective population size (N_e), followed by an increase at the start of the Last Glacial period (around 100,000 years ago) and a post-glacial decrease (9,000-6,000 years ago) for the two populations east of Greenland (Figure 2b). Changes in (N_e) reflect rates of coalescence, which may reflect either change in population size or in population structure. This analysis indicates the three populations diverged less than 10,000 years ago, although this needs to be taken with caution, as gene flow is not considered in the model.

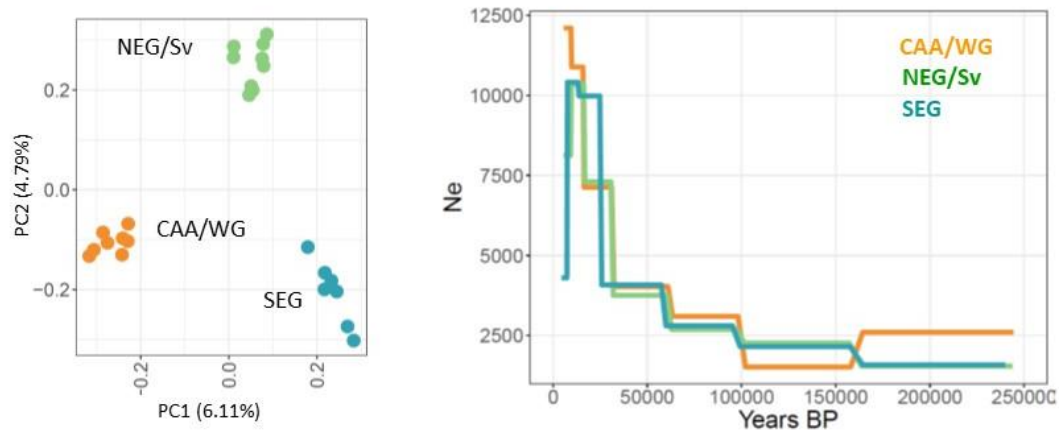


Figure 2. Genetic structuring and demographic history of narwhals. a) Principal component analysis of 24 narwhal individuals, with the proportion of genetic variance captured by the two first principal components (PC) indicated. b) Changes in effective population size through time inferred for each narwhal population using SMC++. Populations are: Canadian Arctic Archipelago and West Greenland (CAA/WG); Northeast Greenland and Svalbard (NEG/Sv); Southeast Greenland (SGE).

Very low levels of genome-wide diversity were found in all three populations, with mean heterozygosity levels (H_e) of ~ 0.00038 , which is amongst the lowest recorded in any mammal.

The variation in diversity levels among populations was further investigated by estimating runs of homozygosity (ROH). ROH are stretches in the genome with no variation. They arise when an offspring receives two copies of the same ancestral haplotype from its parents. The SEG population has a longer proportion of their genome in ROH, with the largest total length of long ROH fragments ($>4\text{Mb}$), while CAA/WG has the lowest. This is consistent with the SEG population currently having the lowest census size of the three populations, and the CAA/WG the largest. Genetic load estimations are consistent with expectations for a species that has maintained low diversity over a long time, with purging of highly deleterious mutations, but an accumulation of mildly to moderately deleterious mutations.

A study using intermediate coverage samples (3-24x) of 57 narwhals across the Canadian Arctic Archipelago reported substructure within the region (de Greef et al. 2024). The analyses support the differentiation of the Northern Hudson Bay narwhals with the rest of the region, and more subtle differentiation between northern and southern fjords/coastal areas in Baffin Bay.

Discussion

Áki Jarl Láruson inquired whether the effective population size of different populations shows the same patterns when analysed with other methods, noting that different approaches are best suited to different time-periods (i.e., more or less removed from the present). Louis confirmed that the stairway plot of the range-wide data shows the same overall population trends. The group agreed that these results highlight the importance of considering the genetic health of a population/stock when making management decisions.

The WG compared the subtle population structure of narwhals in the Canadian Arctic with the Global Review of Monodontids (GROM) (Hobbs et al. 2019), pointing out that the genetic clustering is somewhat reflected in the map of wintering/summering grounds in that region. Most notably, the distinct genetic cluster of samples from Nauyaat Bay matches the GROM's conclusion that animals from that area migrate further south than other narwhal groups for the winter. Tange Olsen noted that narwhals in Melville Bay and fjords around Qaanaaq are geographically closest to the northernmost Canadian cluster. Louis' PCA shows that samples from Melville Bay are slightly more distinct from those in northernmost Greenland and Canada, but she highlighted that this could be a result of relatedness-driven bias. She further mentioned anecdotal reports made by local hunters, that there are two phenotypically and behaviourally distinguishable types of narwhals in the area around Qaanaaq.

The WG **agreed** that there is sufficient evidence of at least three genetic clusters of narwhals in Arctic Canada, namely, one northern and one southern cluster in the High Arctic, and one cluster around Naujaat Bay. The WG **recommended** that high-coverage genome data are generated for High Arctic–West Greenland narwhals to compare with the existing data from Arctic Canada and to further elucidate population structure across the two regions.

6.2 GENETIC DISCRETENESS OF PUTATIVE SMALL STOCKS IN EAST GREENLAND

Louis then presented findings on the fine-scale genetic structure of narwhals in East Greenland (WD/04), which had also been shared with the *Ad hoc* WG on Narwhal in East Greenland (NEGWG) in 2023 (NAMMCO 2023).

Summary

Inferring the level of connectivity among narwhals in East Greenland and assessing the overall population structure of narwhals in the region is crucial for improving the scientific basis for informed species management. This study used whole genome re-sequencing to assess the genetic structure of narwhals in East Greenland based on 80 individual samples from all hunting areas between Tasiilaq and Ittoqqortoormiit (Figure 3a), and non-hunted areas in Northeast Greenland and Svalbard from various seasons.

Based on a Principal Component Analysis (PCA) of ~500,000 unlinked variable sites, and 62 samples (after removing close relatives present in the 80 samples) there were three clusters of narwhals with different levels of distinctness (Figure 3b):

- i. Northern cluster (lower right corner; $PC1 > 0.05$): All individuals from Svalbard (N=4); all individuals from Northeast Greenland (N=12), all individuals sampled in the spring, apart from one, at the mouth of Scoresby Sound (N=10); one narwhal sampled in July at the entrance of Scoresby Sound; two individuals from Kangerlussuaq; one individual from Nansen Fjord;
- ii. Scoresby Sound summer cluster (lower left corner; $PC1 < -0.05$): All individuals sampled in the summer in Scoresby Sound (N=17); individuals from other locations further south (three individuals from Kangerlussuaq, one from Nansen Fjord, one from Nuuaalik and one from Sermilik/Kuummiut);
- iii. Southern cluster (central strand; $-0.05 < PC1 < 0.05$): Three individuals from Sermilik/Kuummiut; four from south of Sermilik; one from Nuuaalik; one from the entrance of Scoresby Sound in the spring. This cluster was not as well defined as the others and needs further investigation (such as removing one individual from south of Sermilik for which there was little data).

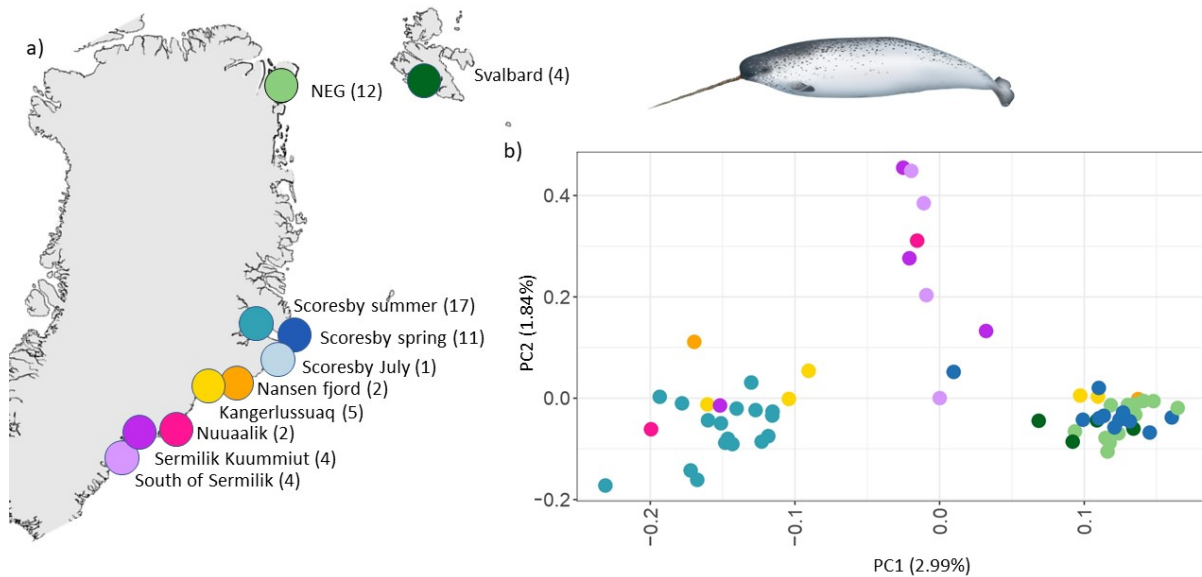


Figure 3. Narwhal sampling localities and population structure. **a)** Sample locations of the 62 narwhals analysed. **b)** Principal Component Analysis of the 62 narwhals with relatedness coefficient lower than 0.08, displaying first and second principal components (PCs), with the proportion of genetic variance captured by each component indicated in brackets. Narwhal illustration by Uko Gorter.

Importantly, narwhals harvested in summer within Scoresby Sound are genetically distinct compared to most animals harvested in the spring at the entrance of Scoresby Sound, confirming observations from local hunters that they are from different aggregations, which had been previously suggested based on differences in morphology. Mean relatedness was significantly higher in narwhals inhabiting Scoresby Sound in summer compared to animals in Northeast Greenland and Svalbard. This observation is consistent with a small size of the summer Scoresby Sound aggregation, where the chances of sampling relatives is high. Remaining analyses of this dataset will include estimating levels of diversity and inbreeding, and genetic sexing of the sampled individuals.

Discussion

During the discussion of the PCA results, Louis confirmed that Principal Components (PCs) beyond 1 and 2 did not show any notable patterns. The WG discussed whether structuring the data further according to temporal boundaries would be useful, but decided that the effects of this additional analysis would be minimal.

A key outcome of the study is the identification of three distinct genetic clusters of narwhals in East Greenland. These clusters are associated with different hunting seasons and geographical areas. Importantly, the group strongly supported the distinction between the narwhals hunted in summer and spring in Scoresby Sound. This genetic difference aligns with the observations made by local hunters regarding different morphological characteristics between the spring and summer aggregations.

The group then discussed the implications of the clustering scores for animals sampled in Management Area (MA) 2 (Nansen Fjord and Kangerlussuaq), namely, that they don't all fall into the same grouping—some animals cluster together with samples from Scoresby Sound in summer and others with samples originating in Northeast Greenland and Svalbard. Tange Olsen interpreted this to mean that animals from Northeast Greenland and Svalbard, which also supply the spring hunt in Scoresby Sound, may occasionally migrate even further south. The group agreed that this is the most likely inference, which then raised the question as to the value of defining this geographic region as a separate MA. Based on the given data, the WG agreed that there is no strong evidence to support separating the Nansen Fjord/Kangerlussuaq animals into a distinct genetic stock at this time (although

also acknowledging that genetics is not the only basis for management unit delineation, and agreeing with the precautionary approach applied by the NEGWG).

The group also discussed the possibility of investigating chromosomal structures or inversions, but Louis mentioned that such analyses have not been conducted yet on narwhals. Further exploration of this topic was suggested to provide additional insights into potential genetic adaptations. More in-depth research into the social structure of these populations, including genetic relatedness and sex-based analyses, was **recommended**, as little is currently known in this area.

The WG **agreed** that there is clear and robust genetic differentiation between the spring and summer hunt in Scoresby Sound, and a weaker signal of genetic differentiation in the south (MA 3, Tasiilaq). Based on the genetic data there is no basis for separating the Kangerlussuaq (MA 2) animals as a stock.

7. BELUGA

7.1 GENETIC PROVENANCE OF ANIMALS OCCURRING IN EAST GREENLAND

Mikkel Skovrind presented findings on the fine-scale population structure of East Greenland belugas (WD/05), which had also been shared with the NEGWG in 2023 (NAMMCO 2023).

Summary

While beluga harvests in East Greenland prior to 2017 are uncertain, between 2017 and 2023 there have been 37 confirmed takes. To investigate the geographic origin of the East Greenland belugas, a genomic dataset of 15 belugas collected on the east coast of Greenland between 2017 and 2023 was generated. These belugas were compared with an unpublished range-wide genomic reference dataset of 75 individuals. The PCA plot based on all 90 samples showed that Pacific and Atlantic belugas are separated by PC1, which captured 4.5% of the total variation. The Ittoqqortoormiit 2023 samples (N=4) clustered with the Beaufort Sea samples (Figure 4b, upper left) while the Ittoqqortoormiit 2017 (N=1) and 2020 (N=2) as well as the Tasiilaq 2022 (N=8) samples clustered together with the Svalbard and Kara Sea samples (upper centre). A subset of the dataset was selected including only samples from Kara Sea, Svalbard, and East Greenland (excluding the samples that clustered with the Beaufort Sea samples; four 2023 Ittoqqortoormiit samples and one 2021 Tasiilaq sample). A PCA run on this subset showed that the 2017 Ittoqqortoormiit sample clustered with the Svalbard samples, while the two 2020 Ittoqqortoormiit and seven Tasiilaq samples clustered with the Kara Sea samples (Figure 4d). The pattern shown in the two PCA plots was supported by the unrooted neighbour-joining tree based on the pairwise distance matrix (Figure 4c) leading to the most likely conclusion that the 15 beluga samples collected in East Greenland between 2017 and 2023 originated from three different populations, one from Svalbard, ten from the Kara Sea, and four from the Beaufort Sea.

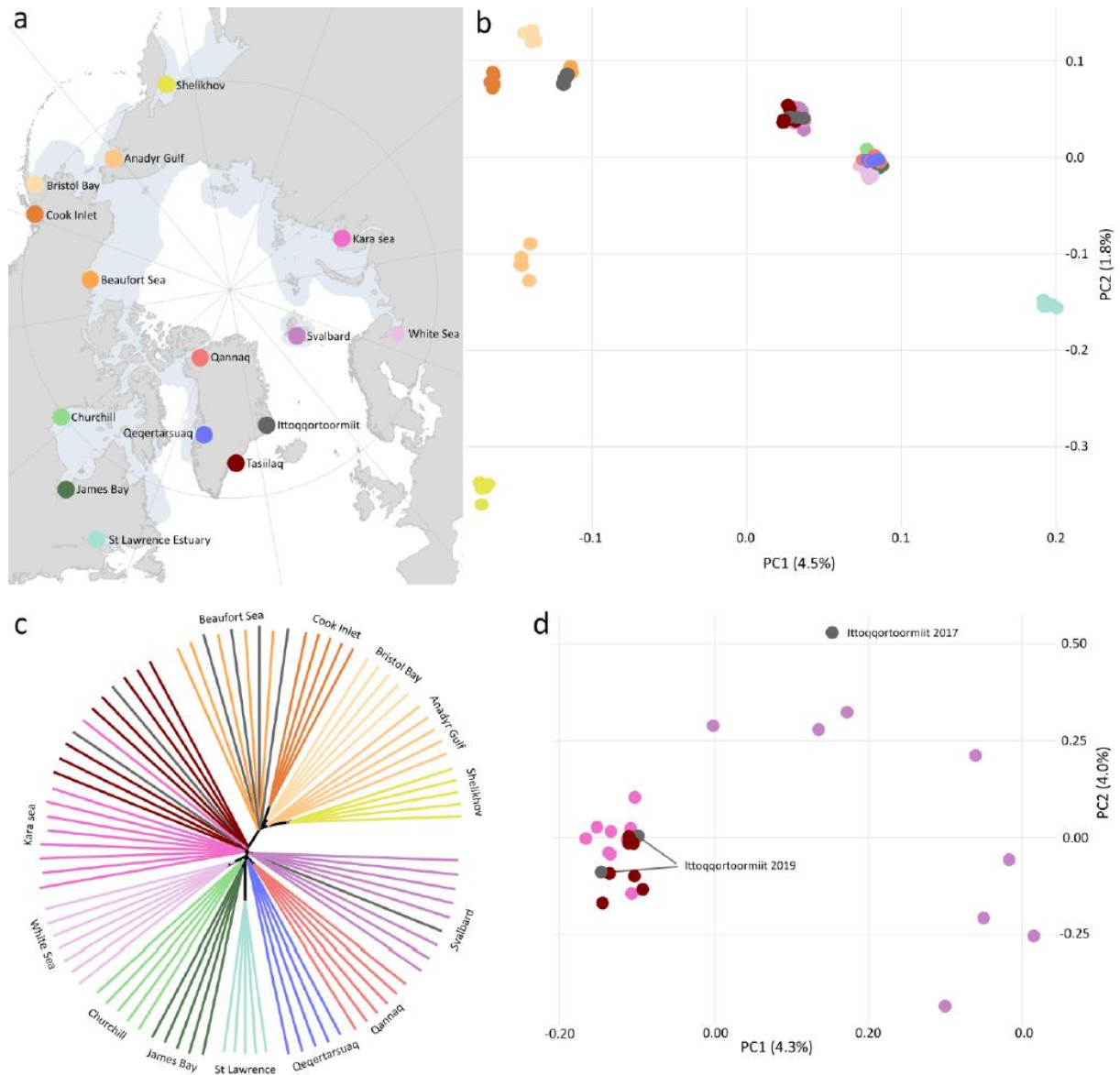


Figure 4. Sample localities and genetic clustering. **a)** Map of sampling localities of the 90 beluga genomes included in our analyses. Coloured circles indicate the sample localities. Light blue shading indicates the distribution of the species, which has not been observed in east Greenland waters until recently. **b)** Principal Component Analyses of 90 beluga genomes including 15 individuals from east Greenland sampled between 2017 and 2023. **c)** Neighbour-joining tree based on pairwise distance matrix. **d)** Principal Component Analysis of beluga genomes from east of Greenland, incl. Ittoqqortoormiit 2017 (N=1), Ittoqqortoormiit 2020 (N=2), Tasiilaq 2022 (N=7), Kara Sea (N=10), and Svalbard (N=8). Colours of b, c and d correspond to the localities on the map (a).

Discussion

The WG **agreed** that the belugas harvested in East Greenland since 2017 originated from at least two genetic stocks, namely the Beaufort Sea (N=4) and Kara Sea (N=10). In addition, a single animal from 2017 potentially originated from Svalbard, but that link should be further investigated. The WG **recommended** continuous genetic analysis of harvested individuals from East Greenland, to determine the proportions of harvested individuals from different genetic stocks.

7.2 GENETIC RELATIONSHIP BETWEEN WEST GREENLAND WINTER HARVEST AND SOUTHEAST BAFFIN ISLAND POPULATION

Skovrind presented results from ongoing genetic research on belugas with a range-wide perspective. The research includes nine samples from Cumberland Sound on the east coast of Baffin Island and six samples from Qeqertarsuaq on the west coast of Greenland, all sequenced to a mean read depth of 0.82x–2.39x.

Summary

Results from a PCA including 134 samples from 16 Atlantic localities showed that Cumberland Sound and Qeqertarsuaq belugas clustered together, suggesting that they either belong to a single population or two closely related populations. To explore this, the covariance matrix generated by the PCA analysis was passed through UMAP, a dimension reduction software enabling multidimensional data to be plotted in two dimensions. Results from UMAP showed that belugas from Cumberland Sound and Qeqertarsuaq formed distinct clusters, suggesting that they belong to separate populations. To further explore this potential genetic separation between Cumberland Sound and Qeqertarsuaq belugas, the data were subset to only include samples from Cumberland Sound and Qeqertarsuaq, as well as nine samples from Grise Fiord in northeastern Canada. The subset data was used as input for another PCA, which showed that Cumberland Sound and Qeqertarsuaq belugas form distinct clusters, thus supporting that they do belong to separate populations. However, it should be noted that these analyses were performed on a very limited sample size and that the differentiation between the clusters is very limited.

Discussion

The WG **agreed** that some genetic analyses, but not all, pointed to the genetic differentiation between Cumberland Sound and Qeqertarsuaq belugas. The WG **recommended** additional genetic analysis with more samples and high-coverage genome data to address this uncertainty.

7.3 STOCK STRUCTURE IN THE HIGH ARCTIC

Skovrind presented results from ongoing genetic research on belugas with a range-wide perspective, as described above. This research includes nine samples from Cunningham Inlet, nine samples from Grise Fiord and nine samples from Qaanaaq in northwestern Greenland, sequenced to a mean read depth of 0.82-2.39x.

Summary

To estimate the genetic differentiation of belugas in the high Arctic, 134 genomes from individuals harvested from 16 Atlantic localities were analysed. Results from a PCA showed that all individuals from Cunningham Inlet and Qaanaaq, as well as five samples from Grise Fiord, clustered together. The remaining four samples from Grise Fiord clustered with belugas from further south. Three samples clustered with Cumberland Sound and Qeqertarsuaq belugas and one individual clustered with Hudson Bay belugas. To further explore the relationship between high Arctic belugas, the data were parsed through UMAP, which suggested that belugas from Cunningham Inlet and Qaanaaq are in fact, two separate genetic lineages. The UMAP plot further suggested that the five individuals from Grise Fiord clustered with Cunningham Inlet, rather than Qaanaaq belugas. In addition, it indicated that three individuals clustered with Qeqertarsuaq rather than Cumberland Sound and that the individual clustering with Hudson Bay belugas likely came from Repulse Bay.

Discussion

The WG **agreed** that the animals harvested in Grise Fiord originated from two distinct genetic populations, namely Cunningham Inlet and Qeqertarsuaq, intercepted as they are passing by. In addition, a single individual originated from Western Hudson Bay, likely Repulse Bay. Some genetic

analyses, but not all, pointed to the genetic differentiation between Qaanaaq and Cunningham Inlet belugas. The WG **recommended** additional genetic analysis with more samples and high-coverage genome data to address this uncertainty.

8. DOLPHINS

8.1 WHITE-BEAKED AND WHITE-SIDED DOLPHIN POPULATION STRUCTURE

Louis presented an overview of the [DolphinUnit project](#) relating to the population structure of white-sided dolphins, white-beaked dolphins, and pilot whales in the NAMMCO region and beyond (in the context of the information published in FI/16 & FI/17).

Summary

The North Atlantic and Arctic are experiencing drastic and rapid environmental change, which are impacting the distribution of species. Temperate cetacean species, including white-beaked (WB) and white-sided (WS) dolphins and pilot whales (PW), are currently increasing in Arctic waters. Those species are hunted for subsistence in the Faroe Islands and Greenland. However, their genetic structure in the North Atlantic is not resolved, making it extremely difficult to estimate the impact of current levels of removals on populations and make recommendations for sustainable harvesting.

In this context, the team will use whole genome sequencing on 100–150 samples from across the North Atlantic and Arctic range of white-beaked (WB) and white-sided (WS) dolphins, *Lagenorhynchus albirostris* and *Lagenorhynchus acutus*, and pilot whales, *Globicephala melas* (Figure 5) to:

- i. define population structure, connectivity and local adaptation of each species;
- ii. infer their demographic histories, and how they responded to past climate change;
- iii. estimate their genetic vulnerability by estimating inbreeding levels and genetic load.

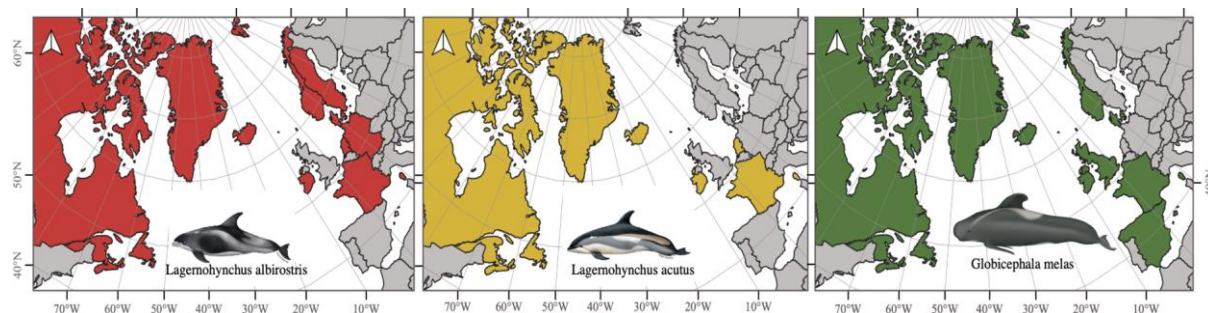


Figure 5. Countries of origin of the samples of white-beaked and white-sided dolphins and pilot whales included in our study.

The team plans to sequence 10–20 individuals per location depending on sample availability.

The results in particular on population structure will have practical implications for management. This study will also address fundamental questions on the impact of climate change on connectivity and the evolutionary ecology/history of the three species.

Discussion

The WG concurred that the findings of Gose et al. 2023 (FI/16) about the lack of population structure in white-sided dolphins across the eastern North Atlantic are robust, noting the high total number of samples and the combination of methods used. However, the small sample size from the western North Atlantic, particularly in relation to the overall population size, is insufficient to draw conclusive inferences about genetic distinctness across the eastern and western Atlantic basin.

In reviewing the genomic analyses of white-beaked dolphins from Gose et al. 2024 (FI/17), the WG agreed that the data revealed very clear clusters, indicating at least two genetically distinct populations

in the central and eastern North Atlantic. One cluster spans northern waters, including Iceland, the Barents Sea, and the western Svalbard margin. The genetic link between Iceland and the Barents Sea is noteworthy, given that decades of cetacean sightings surveys indicate a marked hiatus in white-beaked dolphin distribution between Iceland and northern Norway (Figure 6). Another cluster inhabits European waters, particularly the North Sea and the waters west of Britain and Ireland. Although no evidence of spatial segregation was found, the slight genetic differences between the North Sea and the region west of Britain and Ireland suggest the potential presence of two genetically distinct groups in close proximity.

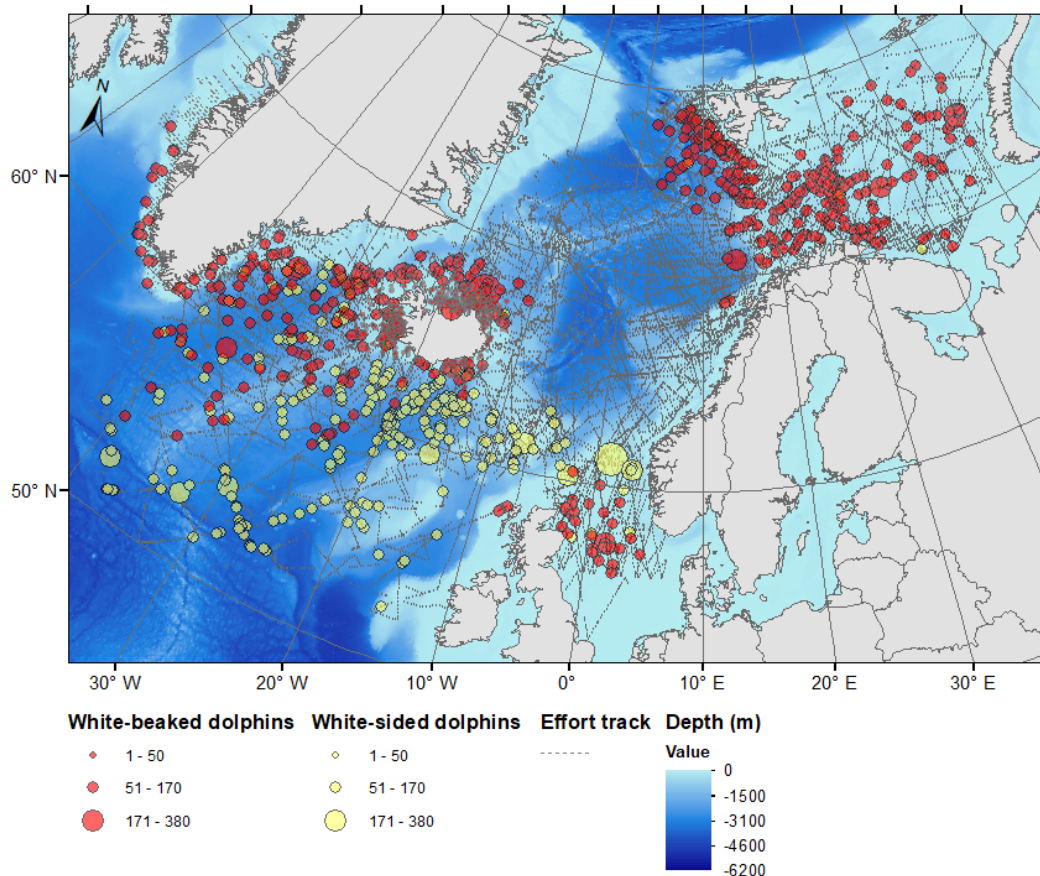


Figure 6. Map of all sightings of white-beaked and white-sided dolphins compiled from NASS, NILS, and Greenlandic surveys from 1986 to 2016 (Ramirez-Martinez 2021).

The WG **agreed** that the genetic data on white-sided dolphins show no population structure across the central and eastern North Atlantic, whereas the data on white-beaked dolphins indicate the existence of at least three distinct populations in the North Atlantic—one in the western North Atlantic (Canada and USA), one in the eastern North Atlantic (Barents Sea, western Svalbard, and Iceland), and one in more southern regions (North Sea, Britain, and Ireland). In addition, there might be a genetically distinct stock in the southern North Sea (Germany and Denmark). The WG further **recommended** range-wide analysis to fill in knowledge and sampling gaps for both species in the western North Atlantic, West Greenland, and East Greenland.

9. GENETICS IN STOCK ASSESSMENTS

The WG discussed potential recommendations for data collection and analysis methods that should be standardised across the board for all NAMMCO countries. A draft document was compiled, which will be refined and circulated following the meeting.

10. FUTURE FOCAL POINTS

10.1 HARBOUR PORPOISE

Tange Olsen presented a summary of genetic studies on harbour porpoise in the North Atlantic.

Summary

Harbour porpoises in the North Atlantic and neighboring regions have been subject to several genetic studies based on mitochondrial and nuclear genetic markers, including full nuclear genomes (Fontaine, Baird et al. 2007, Fontaine, Tolley et al. 2010, Fontaine, Snirc et al. 2012, Fontaine, Roland et al. 2014, Lah, Trense et al. 2016, Fontaine, Thatcher et al. 2017, Chehida, Loughnane et al. 2021, Olsen, Nielsen et al. 2022, Celemín, Autenrieth et al. 2023, Autenrieth, Havenstein et al. 2024). These studies agree on an overall pattern of population genetic structure consisting of a major near-panmictic population occupying much of the North Atlantic from the USA and Canada to northern Norway; multiple local populations in West Greenland, Mauritania, Iberia, Black Sea, and the Belt Sea, as well as possibly smaller and partly admixed populations in the Bay of Biscay, southeastern North Sea, and the Baltic Sea proper (Figure 7). Unresolved issues regarding population structure pertain to the putative genetic independence of porpoises in the Bay of Biscay, Wadden Sea and Baltic Sea proper, as well as porpoises in Arctic Canada, NW Greenland, Svalbard and Russia.

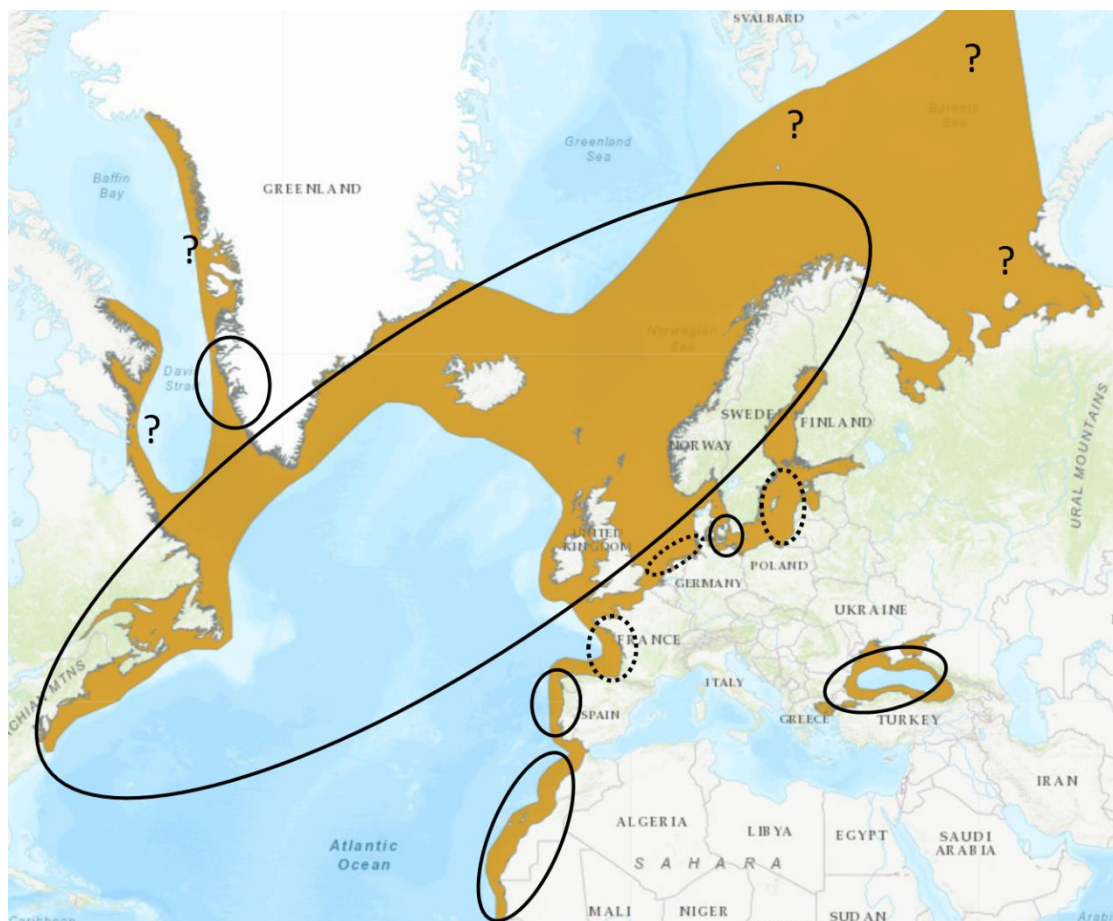


Figure 7: Harbour porpoise genetic populations in the North Atlantic. Full circles are populations confirmed by nuclear genetic markers (microsatellite, RADseq or full genome), stippled circles denote suggested but not fully confirmed populations, and question marks denote regions with no or little genetic data. Species distribution map is from IUCN Red List.

Discussion

The WG acknowledged the body of genetics literature that was presented for this species in the Atlantic. It was highlighted that tagging studies, which have generally supported the notion that harbour porpoises favour coastal habitats and do not travel long distances, have all been conducted in Danish waters, which form their own genetic cluster. Conversely, genetic indications of a large offshore population that has “seeded” smaller coastal ones suggest a much greater capacity for long-range movement in this small cetacean. Ongoing analyses of full nuclear genome data should shed further light on this in the near future.

10.2 HARBOUR AND GREY SEAL

Tange Olsen presented existing information on the genetics of harbour seals and grey seals.

Summary

The harbour seal is highly site-fidelic and characterised by fine-scale genetic structure (Goodman 1998, Andersen and Olsen 2010, Andersen, Lydersen et al. 2011, Olsen, Andersen et al. 2014, Olsen, Islas et al. 2017, Carroll, Hall et al. 2020, Liu, Rønhøj Schjøtt et al. 2022, Steinmetz et al. 2022). A recent study of North Atlantic harbour seals using genome-based sequencing (GBS) data identified at least 14 genetic populations (Liu, Rønhøj Schjøtt et al. 2022), which, combined with findings from previous studies, brings the total to at least 19 genetic populations in the North Atlantic (Figure 8). Uncertainties exist regarding the putative genetic uniqueness of harbour seals in Arctic Canada, possible substructure within Greenland, and whether there is additional substructure in northern Norway and Russia.

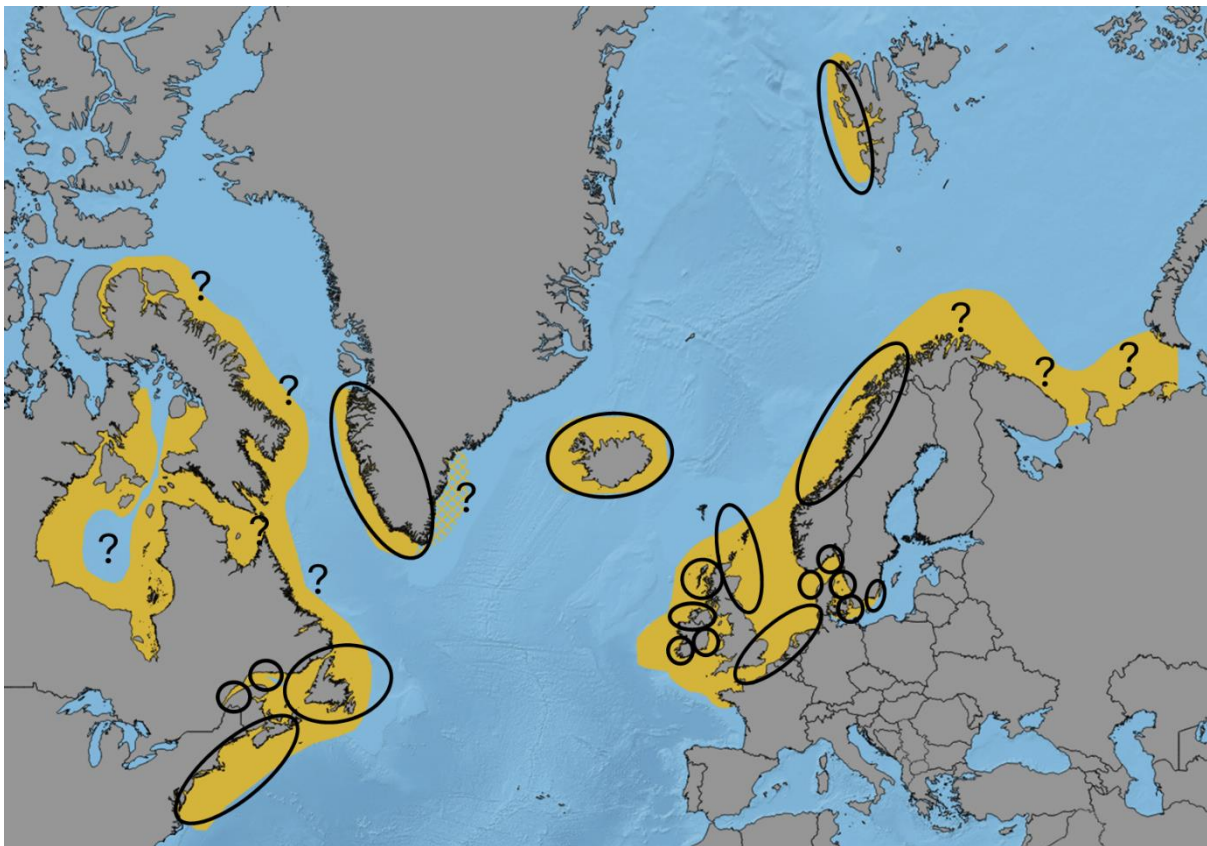


Figure 8: Harbour seal genetic populations in the North Atlantic. Full circles are populations confirmed by nuclear genetic markers (microsatellites or GBS) and question marks denote regions with no or little genetic data. Species distribution map is from IUCN Red List. Note that tagging data suggest the presence of harbour seals in SE Greenland (Rosing-Asvid, Teilmann et al. 2020).

The grey seal comprises at least three main genetic populations in the Northwest (NW) Atlantic, Northeast (NE) Atlantic, and Baltic Sea, respectively (Boskovic, Kovacs et al. 1996, Klimova, Phillips et al. 2014), yet uncertainties remain as to the status of these as subspecies, evolutionary significant units, and/or demographic independent segments (Berta and Churchill 2012, Olsen, Galatius et al. 2016, Galatius, Svendsen et al. 2022). Moreover, local studies have suggested the existence of additional genetic substructure within these three main genetic populations (Allen, Amos et al. 1995, Gaggiotti, Jones et al. 2002, Graves, Helyar et al. 2009, Fietz, Graves et al. 2013, Fietz, Galatius et al. 2016, Decker, Hassani et al. 2017, Steinmetz, Murphy et al. 2024), however these are still to be confirmed by more detailed range-wide nuclear genome analyses. An ongoing study provides the first range-wide insight on population structure based on nuclear genome data (ddRADseq), finding no additional substructure within the NW Atlantic, potential differentiation of Belt Sea grey seals from Baltic Sea, and substantial evidence of additional substructure within the NE Atlantic, including populations in Iceland, Norway, Russia, the North Sea/Faroe Islands, and Ireland/southwestern UK/France, respectively (Olsen, pers. comm.) (Figure 9). Additional data and analyses are required to confirm this pattern, as well as determine the putative genetic uniqueness of grey seals in southern Norway and the Danish Belt Sea.

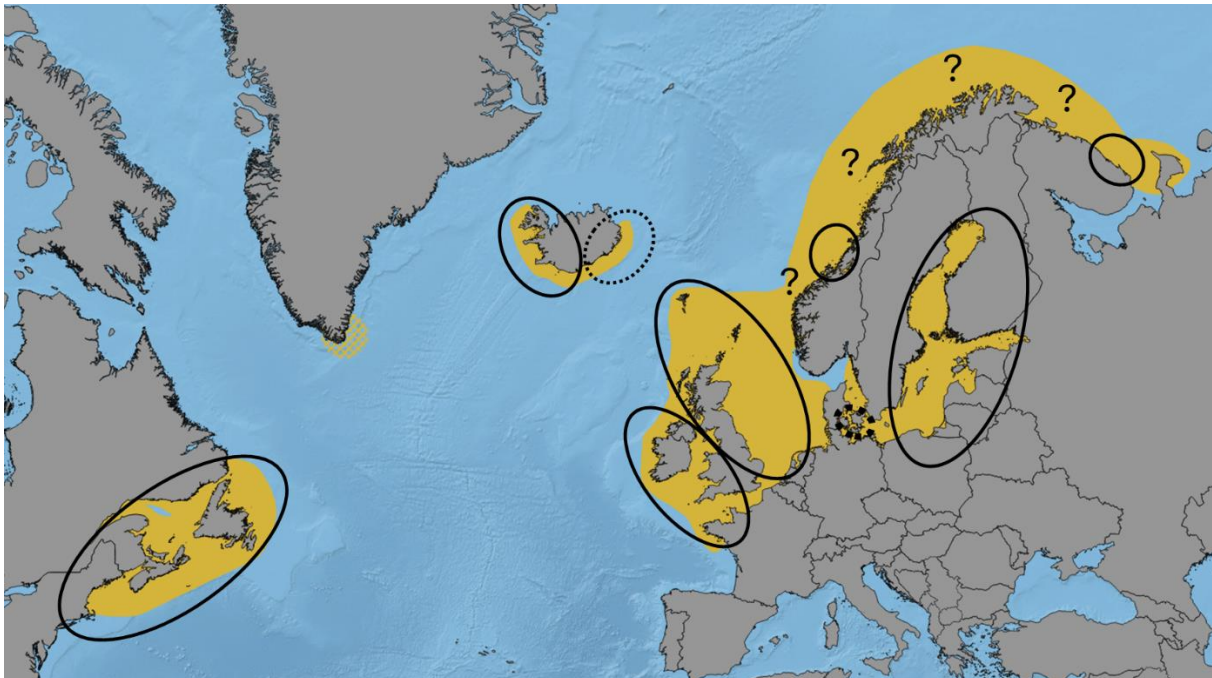


Figure 9: Grey seal genetic populations in the North Atlantic. Full circles are populations confirmed by nuclear genetic markers (microsatellite or ddRADseq), stippled circles denote suggested but not fully confirmed populations, and question marks denote regions with no or little genetic data. Species distribution map is from IUCN Red List. Grey seals have been observed in S Greenland, but these are assumed to be occasional visitors from NW Iceland (Rosing-Asvid, Teilmann et al. 2010).

Discussion

The WG concurred that multiple genetic approaches show the same pattern of extreme site fidelity in harbour seals, to ranges of approximately 100 km. From a management perspective, this means that locally extirpated populations could take several hundreds of years, if at all, to be re-established. In UK waters, there is perhaps a meta-population that could seed local sub-populations following local extirpations. Quintela informed of a study covering harbour seals along the entire Norwegian coastline (samples from 522 individuals) that will be published in the very near future.

Conversely, grey seals show much higher mobility, raising the question as to why there is a genetically distinct cluster in the Baltic Sea, given they clearly have the capacity to travel much further, into the Atlantic. Possible explanations put forward by the group included an artefact of hunting having

historically eliminated and “stepping stone” breeding areas between the two regions, or the effect of different breeding strategies (breeding on ice in the Baltic Sea, but on beaches in the Atlantic).

The WG **recommended** sampling more harbour seals in Greenland to further investigate putative signals of genetic substructure. This could include analysis of archival samples, in addition to opportunistic sampling of by-caught individuals. The group further **recommended** sampling grey seals from the Faroe Islands to determine if they are a unique population or a part of a larger population in Scotland and/or southeast Iceland.

10.3 WALRUS

Tange Olsen showed an overview of known information on walrus population structure.

Summary

The Atlantic walrus was among one of the first marine mammal species subject to genetic analysis of population structure with several follow-up studies using RFLP, short mtDNA fragments, microsatellites, and/or entire mitogenomes, and in the Canadian Arctic also GBS data (Cronin, Hills et al. 1994, Andersen, Born et al. 1998, Born, Andersen et al. 2001, Andersen, Born et al. 2009, Shafer, Davis et al. 2014, Shafer, Gattepaille et al. 2015, Andersen, Jacobsen et al. 2017, Star, Barrett et al. 2018, Ruiz-Puerta, Keighley et al. 2023). These studies have collectively identified at least 6 genetic populations across the species current North Atlantic range, including High Arctic Canada-NW Greenland (North Water), Foxe Basin-Hudson Bay, E Baffin Island-W Greenland (Davis Strait), E Greenland, Svalbard-Franz Josef Land, and the Barents/Kara/Pechora Seas, as well as two now extinct genetic populations in the Canadian Maritimes and Iceland (McLeod, Frasier et al. 2014, Keighley, Pálsson et al. 2019, Ruiz-Puerta, Keighley et al. 2023) (Figure 10). There are some uncertainties regarding precise population boundaries and putative substructure within populations, in particular in the Canadian Arctic and western Greenland. Resolving this will likely require a range-wide genetic analysis using full nuclear genome data.

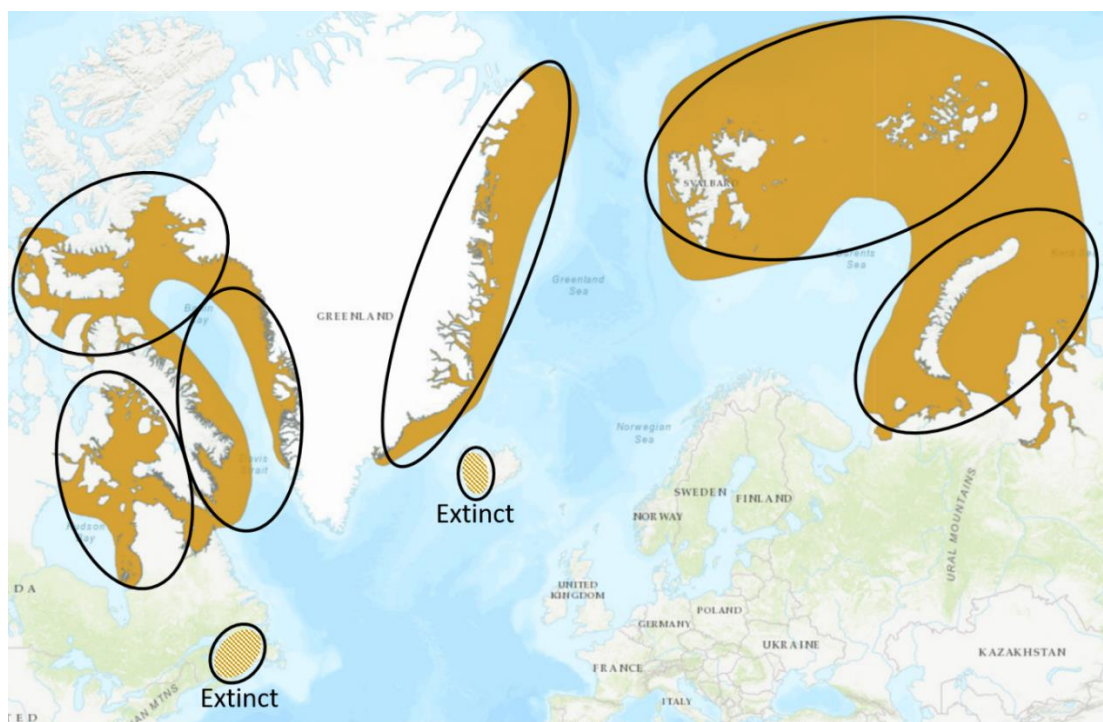


Figure 10: Walrus genetic populations in the North Atlantic. Full circles are populations confirmed by nuclear genetic markers (microsatellites or GBS) and/or mitogenomes, stippled circles denote suggested but not fully confirmed populations, and question marks denote regions with no or little genetic data. Extinct populations are included. Species distribution map is from IUCN Red List.

Discussion

The group expressed great interest in the ongoing whole-genome sequencing work, as well as in the possibility of elucidating what genetic adaptations the (now extinct) southern populations of walrus had that allowed them to live and breed in sub-arctic conditions.

11. ANY OTHER BUSINESS

No other business was discussed.

12. RECOMMENDATIONS FOR RESEARCH

12.1 RECOMMENDATIONS FOR PILOT WHALES

Recommendations to All Parties

- Determining population structure at the scale of the North Atlantic, and whether this structure is driven geographically or socially by range-wide sampling of family units and single individuals, and keeping exact track of where the samples are sourced.
- Conducting genetic analyses of tagged pilot whales, to compare movement, foraging, and social behaviour with relatedness, genetic structure, diversity, and potential adaptations.

Recommendations to the Faroe Islands and Greenland

- Initiating a dedicated genetic monitoring program based on archival and newly collected samples from harvested groups in Greenland and the Faroe Islands, as well as in mass stranding events wherever they occur, to determine:
 - i. family groupings and social structure,
 - ii. putative population of origin,
 - iii. the influence of removing entire family units during pilot whale hunts, for instance in terms of genetic diversity, inbreeding levels, mutation load, and standing genetic variation.

12.2 RECOMMENDATIONS FOR NARWHAL

Recommendations to Greenland and Canada

- Generating high-coverage genome data for High Arctic–West Greenland narwhals to compare with the existing data from the Arctic Canada, to further elucidate population structure across the two regions.
- Conducting more in-depth research into the social structure of narwhal populations, including genetic relatedness and sex-based analyses.

12.3 RECOMMENDATIONS FOR BELUGA

Recommendations to Greenland

- Conducting continuous genetic analysis of any harvested individuals from East Greenland, to determine the proportions of harvested belugas from different genetic stocks.

Recommendations to Greenland and Canada

- Conducting additional genetic analysis with more samples and high-coverage genome data of belugas from West Greenland and Canada to confirm (or negate) genetic differentiation.
- Conducting additional genetic analysis with more samples and high-coverage genome data of belugas from the High Arctic to confirm (or negate) genetic differentiation.

12.4 RECOMMENDATIONS FOR DOLPHINS

Recommendations to Greenland, Canada, and the USA

- Conducting range-wide analysis to fill in knowledge and sampling gaps for white-beaked and white-sided dolphins in the western North Atlantic, West Greenland, and East Greenland.

12.5 RECOMMENDATIONS FOR COASTAL SEALS

Recommendations to Greenland

- Sampling more harbour seals in Greenland to further investigate putative signals of genetic substructure. This could include analysis of archival samples, in addition to opportunistic sampling of by-caught individuals.

Recommendations to the Faroe Islands

- Sampling grey seals from the Faroe Islands to determine if they are a unique population or a part of a larger population in Scotland and/or southeast Iceland.

13. ADOPTION OF REPORT AND MEETING CLOSE

The Chair thanked all participants for their enthusiasm and engagement, which resulted in a highly productive meeting. The group, in turn, thanked Tange Olsen for his able chairing, as well as Garagouni and Elias for their rapporteuring and organisational skills. All expressed that this first meeting of the WG had accomplished its goals and hoped that such meetings will feature regularly in the NAMMCO workplans.

REFERENCES

- Allen, P. J., Amos, W., Pomeroy, P. P., & Twiss, S. D. (1995). Microsatellite variation in grey seals (*Halichoerus grypus*) shows evidence of genetic differentiation between two British breeding colonies. *Molecular Ecology*, 4(6), 653–662. <https://doi.org/10.1111/j.1365-294x.1995.tb00266.x>
- Andersen, L., Born, E., Doidge, D., Gjertz, I., Wiig, Ø., & Waples, R. (2009). Genetic signals of historic and recent migration between sub-populations of Atlantic walrus (*Odobenus rosmarus rosmarus*) west and east of Greenland. *Endangered Species Research*, 9, 197–211. <https://doi.org/10.3354/esr00242>
- Andersen, L., & Olsen, M. T. (2010). Distribution and population structure of North Atlantic harbour seals (*Phoca vitulina*). *NAMMCO Scientific Publications*, 8, 15. <https://doi.org/10.7557/3.2669>
- Andersen, L. W., Born, E. W., Gjertz, I., Wiig, Ø., Holm, L., & Bendixen, C. (1998). Population structure and gene flow of the Atlantic walrus (*Odobenus rosmarus rosmarus*) in the eastern Atlantic Arctic based on mitochondrial DNA and microsatellite variation. *Molecular Ecology*, 7(10), 1323–1336. <https://doi.org/10.1046/j.1365-294x.1998.00455.x>
- Andersen, L. W., Jacobsen, M. W., Lydersen, C., Semenova, V., Boltunov, A., Born, E. W., Wiig, Ø., & Kovacs, K. M. (2017). Walruses (*Odobenus rosmarus rosmarus*) in the Pechora Sea in the context of contemporary population structure of Northeast Atlantic walruses. *Biological Journal of the Linnean Society*, 122(4), 897–915. <https://doi.org/10.1093/biolinnean/blx093>

- Andersen, L. W., Lydersen, C., Frie, A. K., Rosing-Asvid, A., Hauksson, E., & Kovacs, K. M. (2011). A population on the edge: genetic diversity and population structure of the world's northernmost harbour seals (*Phoca vitulina*). *Biological Journal of the Linnean Society*, 102(2), 420–439. <https://doi.org/10.1111/j.1095-8312.2010.01577.x>
- Autenrieth, M., Havenstein, K., De Cahsan, B., Canitz, J., Benke, H., Roos, A., Pampoulie, C., Sigurðsson, G. M., Siebert, U., Olsen, M. T., Biard, V., Heide-Jørgensen, M. P., Öztürk, A. A., Öztürk, B., Lawson, J. W., & Tiedemann, R. (2023). Genome-wide analysis of the harbour porpoise (*Phocoena phocoena*) indicates isolation-by-distance across the North Atlantic and potential local adaptation in adjacent waters. *Conservation Genetics*. <https://doi.org/10.1007/s10592-023-01589-0>
- Ball, R. J., Kitchiner, A., Davison, N. J., Brownlow, A., Berrow, S., McKeown, N. J., IJsseldijk, L. L., Geary, M., McDowall, I., & Muir, A. P. (2021). New haplotypes found in stranded long-finned pilot whales (*Globicephala melas*) in the eastern North Atlantic and adjacent waters. *Marine Mammal Science*, 38(3), 898–912. <https://doi.org/10.1111/mms.12893>
- Berta, A., & Churchill, M. (2011). Pinniped taxonomy: review of currently recognized species and subspecies, and evidence used for their description. *Mammal Review*, 42(3), 207–234. <https://doi.org/10.1111/j.1365-2907.2011.00193.x>
- Born, E., Andersen, L., Gjertz, I., & Wiig, Ø. (2001). A review of the genetic relationships of Atlantic walrus (*Odobenus rosmarus rosmarus*) east and west of Greenland. *Polar Biology*, 24(10), 713–718. <https://doi.org/10.1007/s003000100277>
- Boskovic, R., Kovacs, K. M., Hammill, M. O., & White, B. N. (1996). Geographic distribution of mitochondrial DNA haplotypes in grey seals (*Halichoerus grypus*). *Canadian Journal of Zoology*, 74(10), 1787–1796. <https://doi.org/10.1139/z96-199>
- Carroll, E. L., Hall, A., Olsen, M. T., Onoufriou, A. B., Gaggiotti, O. E., & Russell, D. J. (2020). Perturbation drives changing metapopulation dynamics in a top marine predator. *Proceedings of the Royal Society B Biological Sciences*, 287(1928), 20200318. <https://doi.org/10.1098/rspb.2020.0318>
- Celemín, E., Autenrieth, M., Roos, A., Pawliczka, I., Quintela, M., Lindstrøm, U., Benke, H., Siebert, U., Lockyer, C., Berggren, P., Öztürk, A. A., Öztürk, B., Lesage, V., & Tiedemann, R. (2023). Evolutionary history and seascape genomics of Harbour porpoises (*Phocoena phocoena*) across environmental gradients in the North Atlantic and adjacent waters. *Molecular Ecology Resources*. <https://doi.org/10.1111/1755-0998.13860>
- Chehida, Y. B., Loughnane, R., Thumloup, J., Kaschner, K., Garilao, C., Rosel, P., & Fontaine, M. C. (2021). No leading-edge effect in North Atlantic harbor porpoises: Evolutionary and conservation implications. *Evolutionary Applications*, 14(6), 1588–1611. <https://doi.org/10.1111/eva.13227>
- Cronin, M. A., Hills, S., Born, E. W., & Patton, J. C. (1994). Mitochondrial DNA variation in Atlantic and Pacific walruses. *Canadian Journal of Zoology*, 72(6), 1035–1043. <https://doi.org/10.1139/z94-140>

- De Greef, E., Müller, C., Thorstensen, M. J., Ferguson, S. H., Watt, C. A., Marcoux, M., Petersen, S. D., & Garroway, C. J. (2024). Unraveling the genetic legacy of commercial whaling and population dynamics in Arctic bowhead whales and narwhals. *Global Change Biology*, 30(10). <https://doi.org/10.1111/gcb.17528>
- Decker, C., Hassani, S., Jezequel, M., Rault, C., Dumas, C., Méheust, E., Alfonsi, E., & Jung, J. (2017). Mitochondrial DNA reveals historical maternal lineages and a postglacial expansion of the grey seal in European waters. *Marine Ecology Progress Series*, 566, 217–227. <https://doi.org/10.3354/meps12003>
- Fietz, K., Galatius, A., Teilmann, J., Dietz, R., Frie, A. K., Klimova, A., Palsbøll, P. J., Jensen, L. F., Graves, J. A., Hoffman, J. I., & Olsen, M. T. (2016). Shift of grey seal subspecies boundaries in response to climate, culling and conservation. *Molecular Ecology*, 25(17), 4097–4112. <https://doi.org/10.1111/mec.13748>
- Fietz, K., Graves, J. A., & Olsen, M. T. (2013). Control Control Control: A Reassessment and Comparison of GenBank and Chromatogram mtDNA Sequence Variation in Baltic Grey Seals (*Halichoerus grypus*). *PLoS ONE*, 8(8), e72853. <https://doi.org/10.1371/journal.pone.0072853>
- Fontaine, M. C., Baird, S. J., Piry, S., Ray, N., Tolley, K. A., Duke, S., Birkun, A., Ferreira, M., Jauniaux, T., Llavona, Á., Öztürk, B., Öztürk, A. A., Ridoux, V., Rogan, E., Sequeira, M., Siebert, U., Vikingsson, G. A., Bouquegneau, J., & Michaux, J. R. (2007). Rise of oceanographic barriers in continuous populations of a cetacean: the genetic structure of harbour porpoises in Old World waters. *BMC Biology*, 5(1). <https://doi.org/10.1186/1741-7007-5-30>
- Fontaine, M. C., Roland, K., Calves, I., Austerlitz, F., Palstra, F. P., Tolley, K. A., Ryan, S., Ferreira, M., Jauniaux, T., Llavona, A., Öztürk, B., Öztürk, A. A., Ridoux, V., Rogan, E., Sequeira, M., Siebert, U., Vikingsson, G. A., Borrell, A., Michaux, J. R., & Aguilar, A. (2014). Postglacial climate changes and rise of three ecotypes of harbour porpoises, *Phocoena phocoena*, in western Palearctic waters. *Molecular Ecology*, 23(13), 3306–3321. <https://doi.org/10.1111/mec.12817>
- Fontaine, M. C., Snirc, A., Frantzis, A., Koutrakis, E., Öztürk, B., Öztürk, A. A., & Austerlitz, F. (2012). History of expansion and anthropogenic collapse in a top marine predator of the Black Sea estimated from genetic data. *Proceedings of the National Academy of Sciences*, 109(38). <https://doi.org/10.1073/pnas.1201258109>
- Fontaine, M. C., Tolley, K. A., Michaux, J. R., Birkun, A., Ferreira, M., Jauniaux, T., Llavona, Á., Öztürk, B., Öztürk, A. A., Ridoux, V., Rogan, E., Sequeira, M., Bouquegneau, J., & Baird, S. J. E. (2010). Genetic and historic evidence for climate-driven population fragmentation in a top cetacean predator: the harbour porpoises in European water. *Proceedings of the Royal Society B Biological Sciences*, 277(1695), 2829–2837. <https://doi.org/10.1098/rspb.2010.0412>
- Fullard, K. J., Early, G., Heide-Jørgensen, M. P., Bloch, D., Rosing-Asvid, A., & Amos, W. (2000). Population structure of long-finned pilot whales in the North Atlantic: a correlation with sea surface temperature? *Molecular Ecology*, 9(7), 949–958. <https://doi.org/10.1046/j.1365-294x.2000.00957.x>

- Gaggiotti, O. E., Jones, F., Lee, W. M., Amos, W., Harwood, J., & Nichols, R. A. (2002). Patterns of colonization in a metapopulation of grey seals. *Nature*, 416(6879), 424–427. <https://doi.org/10.1038/416424a>
- Galatius, A., Svendsen, M. S., Messer, D., Valtonen, M., McGowen, M., Sabin, R., Dahl, V. A., Dahl, A. B., & Olsen, M. T. (2022). Range-wide variation in grey seal (*Halichoerus grypus*) skull morphology. *Zoology*, 153, 126023. <https://doi.org/10.1016/j.zool.2022.126023>
- Goodman, S. J. (1998). Patterns of extensive genetic differentiation and variation among European harbor seals (*Phoca vitulina vitulina*) revealed using microsatellite DNA polymorphisms. *Molecular Biology and Evolution*, 15(2), 104–118. <https://doi.org/10.1093/oxfordjournals.molbev.a025907>
- Gose, M., Humble, E., Brownlow, A., Mikkelsen, B., Loftus, C., Wall, D., Rogan, E., Doeschate, M. T., Davison, N., & Ogden, R. (2023). Stranding collections indicate broad-scale connectivity across the range of a pelagic marine predator, the Atlantic white-sided dolphin (*Lagenorhynchus acutus*). *ICES Journal of Marine Science*, 80(4), 1120–1128. <https://doi.org/10.1093/icesjms/fsad050>
- Gose, M., Humble, E., Brownlow, A., Wall, D., Rogan, E., Sigurðsson, G. M., Kiszka, J. J., Thøstesen, C. B., IJsseldijk, L. L., Doeschate, M. T., Davison, N. J., Øien, N., Deaville, R., Siebert, U., & Ogden, R. (2024). Population genomics of the white-beaked dolphin (*Lagenorhynchus albirostris*): Implications for conservation amid climate-driven range shifts. *Heredity*, 132(4), 192–201. <https://doi.org/10.1038/s41437-024-00672-7>
- Graves, J. A., Helyar, A., Biuw, M., Jüssi, M., Jüssi, I., & Karlsson, O. (2008). Microsatellite and mtDNA analysis of the population structure of grey seals (*Halichoerus grypus*) from three breeding areas in the Baltic Sea. *Conservation Genetics*, 10(1), 59–68. <https://doi.org/10.1007/s10592-008-9517-1>
- Hobbs, R. C., Reeves, R. R., Prewitt, J. S., Desportes, G., Breton-Honeyman, K., Christensen, T., Citta, J. J., Ferguson, S. H., Frost, K. J., Garde, E., Gavrilov, M., Ghazal, M., Glazov, D. M., Gosselin, J.-F., Hammill, M., Hansen, R. G., Harwood, L., Heide-Jørgensen, M. P., Inglangasuk, G., ... Watt, C. A. (2019). Global Review of the Conservation Status of Monodontid Stocks. *Marine Fisheries Review*, 81(3–4), 53. <https://doi.org/10.7755/MFR.81.3-4.1>
- Keighley, X., Pálsson, S., Einarsson, B. F., Petersen, A., Fernández-Coll, M., Jordan, P., Olsen, M. T., & Malmquist, H. J. (2019). Disappearance of Icelandic Walrus Coincided with Norse Settlement. *Molecular Biology and Evolution*, 36(12), 2656–2667. <https://doi.org/10.1093/molbev/msz196>
- Klimova, A., Phillips, C. D., Fietz, K., Olsen, M. T., Harwood, J., Amos, W., & Hoffman, J. I. (2014). Global population structure and demographic history of the grey seal. *Molecular Ecology*, 23(16), 3999–4017. <https://doi.org/10.1111/mec.12850>
- Kraft, S., Pérez-Álvarez, M., Olavarría, C., & Poulin, E. (2020). Global phylogeography and genetic diversity of the long-finned pilot whale *Globicephala melas*, with new data from the southeastern Pacific. *Scientific Reports*, 10(1). <https://doi.org/10.1038/s41598-020-58532-3>

- Lah, L., Trense, D., Benke, H., Berggren, P., Gunnlaugsson, P., Lockyer, C., Öztürk, A., Öztürk, B., Pawliczka, I., Roos, A., Siebert, U., Skóra, K., Víkingsson, G., & Tiedemann, R. (2016). Spatially explicit analysis of Genome-Wide SNPs detects subtle population structure in a mobile marine mammal, the harbor porpoise. *PLoS ONE*, 11(10), e0162792. <https://doi.org/10.1371/journal.pone.0162792>
- Liu, X., Schjøtt, S. R., Granquist, S. M., Rosing-Asvid, A., Dietz, R., Teilmann, J., Galatius, A., Cammen, K., O'Corry-Crowe, G., Harding, K., Härkönen, T., Hall, A., Carroll, E. L., Kobayashi, Y., Hammill, M., Stenson, G., Frie, A. K., Lydersen, C., Kovacs, K. M., . . . Olsen, M. T. (2022). Origin and expansion of the world's most widespread pinniped: Range-wide population genomics of the harbour seal (*Phoca vitulina*). *Molecular Ecology*, 31(6), 1682–1699. <https://doi.org/10.1111/mec.16365>
- McLeod, B. A., Frasier, T. R., & Lucas, Z. (2014). Assessment of the extirpated Maritimes walrus using morphological and ancient DNA analysis. *PLoS ONE*, 9(6), e99569. <https://doi.org/10.1371/journal.pone.0099569>
- Monteiro, S., Méndez-Fernandez, P., Piertney, S., Moffat, C., Ferreira, M., Vingada, J., López, A., Brownlow, A., Jepson, P., Mikkelsen, B., Niemeyer, M., Carvalho, J., & Pierce, G. (2015). Long-finned pilot whale population diversity and structure in Atlantic waters assessed through biogeochemical and genetic markers. *Marine Ecology Progress Series*, 536, 243–257. <https://doi.org/10.3354/meps11455>
- Olsen, M. T., Andersen, L. W., Dietz, R., Teilmann, J., Härkönen, T., & Siegismund, H. R. (2014). Integrating genetic data and population viability analyses for the identification of harbour seal (*Phoca vitulina*) populations and management units. *Molecular Ecology*, 23(4), 815–831. <https://doi.org/10.1111/mec.12644>
- Olsen, M. T., Galatius, A., Biard, V., Gregersen, K., & Kinze, C. C. (2016). The forgotten type specimen of the grey seal [*Halichoerus grypus*(Fabricius, 1791)] from the island of Amager, Denmark. *Zoological Journal of the Linnean Society*, 178(3), 713–720. <https://doi.org/10.1111/zoj.12426>
- Olsen, M. T., Islas, V., Graves, J. A., Onoufriou, A., Vincent, C., Brasseur, S., Frie, A. K., & Hall, A. J. (2017). Genetic population structure of harbour seals in the United Kingdom and neighbouring waters. *Aquatic Conservation Marine and Freshwater Ecosystems*, 27(4), 839–845. <https://doi.org/10.1002/aqc.2760>
- Olsen, M. T., Nielsen, N. H., Biard, V., Teilmann, J., Ngô, M. C., Víkingsson, G., Gunnlaugsson, T., Stenson, G., Lawson, J., Lah, L., Tiedemann, R., & Heide-Jørgensen, M. P. (2023). Genetic and behavioural data confirm the existence of a distinct harbour porpoise ecotype in West Greenland. *Ecological Genetics and Genomics*, 22, 100108. <https://doi.org/10.1016/j.egg.2021.100108>
- NAMMCO - North Atlantic Marine Mammal Commission (2023). Report of the Scientific Committee *Ad hoc* Working Group on Narwhal in East Greenland, December 2023, Copenhagen, Denmark.
- NAMMCO - North Atlantic Marine Mammal Commission (2024). Report of the 30th meeting of the NAMMCO Scientific Committee, January 2024, Hafnarfjörður, Iceland.

- Ramirez-Martinez, N. (2021). "Cetacean distribution and habitat use in the central and north-eastern North Atlantic". Ph.D. Thesis, University of St Andrews, Scotland.
- Rosing-Asvid, A., Teilmann, J., Dietz, R., & Olsen, M. T. (2010). First confirmed record of grey seals in Greenland. *ARCTIC*, 63(4). <https://doi.org/10.14430/arctic3336>
- Rosing-Asvid, A., Teilmann, J., Olsen, M. T., & Dietz, R. (2020). Deep diving harbor seals (*Phoca vitulina*) in South Greenland: movements, diving, haul-out and breeding activities described by telemetry. *Polar Biology*, 43(4), 359–368. <https://doi.org/10.1007/s00300-020-02639-w>
- Ruiz-Puerta, E. J., Keighley, X., Desjardins, S. P. A., Gotfredsen, A. B., Pan, S. E., Star, B., Boessenkool, S., Barrett, J. H., McCarthy, M. L., Andersen, L. W., Born, E. W., Howse, L. R., Szpak, P., Pálsson, S., Malmquist, H. J., Rufolo, S., Jordan, P. D., & Olsen, M. T. (2023). Holocene deglaciation drove rapid genetic diversification of Atlantic walrus. *Proceedings of the Royal Society B Biological Sciences*, 290(2007). <https://doi.org/10.1098/rspb.2023.1349>
- Shafer, A. B., Davis, C. S., Coltman, D. W., & Stewart, R. E. (2014). Microsatellite assessment of walrus (*Odobenus rosmarus rosmarus*) stocks in Canada. *NAMMCO Scientific Publications*, 9, 15. <https://doi.org/10.7557/3.2607>
- Shafer, A. B., Gattepaille, L. M., Stewart, R. E. A., & Wolf, J. B. W. (2015). Demographic inferences using short-read genomic data in an approximate Bayesian computation framework: in silico evaluation of power, biases and proof of concept in Atlantic walrus. *Molecular Ecology*, 24(2), 328–345. <https://doi.org/10.1111/mec.13034>
- Star, B., Barrett, J. H., Gondek, A. T., & Boessenkool, S. (2018). Ancient DNA reveals the chronology of walrus ivory trade from Norse Greenland. *Proceedings of the Royal Society B Biological Sciences*, 285(1884), 20180978. <https://doi.org/10.1098/rspb.2018.0978>
- Steinmetz, K., Murphy, S., Cadhla, O. Ó., Hoffman, J. I., Jung, J., Barnett, J., Cronin, M., Galatius, A., Hassani, S., Jessopp, M., Pomeroy, P., & Mirimin, L. (2024). Genetic analysis in aid of delineation of Management Units for a wide-ranging marine mammal, the grey seal (*Halichoerus grypus*), in European waters. *Research Square (Research Square)*. <https://doi.org/10.21203/rs.3.rs-4243253/v1>
- Steinmetz, K., Murphy, S., Cadhla, O. Ó., Carroll, E.L., Onoufriou, A.B., Russell, D.J.F. et al. (2023). Population structure and genetic connectivity reveals distinctiveness of Irish harbour seals (*Phoca vitulina*) and implications for conservation management. *Aquatic Conservation: Marine and Freshwater Ecosystems*, 33(2), 160–178. <https://doi.org/10.1002/aqc.3909>

APPENDIX 1: AGENDA

1. Welcome from the Chair

2. Adoption of agenda

3. Appointment of rapporteurs

4. Review of available meeting documents

5. Pilot whale

5.1 Population structure across the North Atlantic with specific focus on connectivity between different hunting areas (East Greenland, West Greenland, Faroe Islands, Iceland)

5.2 Information and guidance on analytical methods for Pilot Whale WG 2025, including the use of genetic data beyond stock delineation, e.g., for demographic modelling, pod composition, and assessment of vulnerability (see also point 9.1)

6. Narwhal

6.1 Genetic discreteness of putative small stocks in East Greenland

6.2 Population structure between Canada and Greenland

7. Beluga

7.1 Genetic provenance of animals occurring in East Greenland

7.2 Genetic relationship between West Greenland winter harvest and Southeast Baffin Island population

7.3 Stock structure in the High Arctic (North Water wintering, Qaanaaq hunt, West Greenland fall and winter hunt)

8. Dolphins

8.1 White-beaked and wide-sided dolphin population structure around Greenland in relation to the hunt

9. Genetics in stock assessments

Other applications of genetic data that NAMMCO should consider when assessing the health of stocks

10. Future focal points (WG meetings in 2026)

- 10.1 Harbour porpoise
- 10.2 Coastal seals (harbour and grey seal)
- 10.3 Walrus

11. Any other business

12. Adoption of report and meeting close

For information:

- **The Terms of Reference of this WG are:**
 - i. To review the genetic data that will be used in NAMMCO's species assessments.*
 - ii. To serve as a consultation body on topics related to genetics for NAMMCO's working groups.*
 - iii. To detect data and knowledge gaps needed for the assessment of specific species/stocks and provide NAMMCO with advice on how to move forward to fill such gaps.*
- **At its 30th meeting, the NAMMCO Scientific Committee prioritised the topics listed under items 5, 6, and 7 on this agenda.**

APPENDIX 2: LIST OF PARTICIPANTS

Áki Jarl Láruson

Marine and Freshwater Research Institute
Iceland
aki.jarl.laruson@hafogvatn.is

Maria Garagouni (Deputy Secretary)

NAMMCO Secretariat
maria@nammco.org

María Quintela Sánchez

Institute of Marine Research
Norway
maria.quintela.sanchez@hi.no

Marie Louis

Greenland Institute of Natural Resources
Greenland
marie.louis@natur.gl

Mikkel Skovrind

University of Copenhagen
Denmark
mikkel.skovrind@sund.ku.dk

Mioko Taguchi

Institute of Cetacean Research
Japan
taguchi@cetacean.jp

Morten Tange Olsen (Chair)

Globe Institute, University of Copenhagen
Denmark
morten.olsen@sund.ku.dk

Noor Elias (Intern)

NAMMCO Secretariat
intern@nammco.org

Rachel Ball

University of Chester
United Kingdom
racheljb2708@gmail.com

Sunnvør Klettskarð í Kongsstovu

University of the Faroe Islands
Faroe Islands
sunnvork@setur.fo

APPENDIX 3: LIST OF DOCUMENTS

Working Documents

Doc. No.	Title	Agenda item
SC/31/GENWG/01	Draft Agenda	2
SC/31/GENWG/02	Draft List of Participants	1
SC/31/GENWG/03	Draft List of Documents	Several
SC/31/GENWG/04	Fine-scale genetic structure of narwhals in East Greenland.	6
SC/31/GENWG/05	Genetic provenance of East Greenland belugas.	7
SC/31/GENWG/06	Genetics of long finned pilot whales in eastern North Atlantic	5

For Information Documents

Doc. No.	Title	Agenda item
SC/31/GENWG/FI01	ICES Meeting Etiquette (2022)	All
SC/31/GENWG/FI02	NAMMCO (2024). Report of the 30th meeting of the NAMMCO Scientific	Several
SC/31/GENWG/FI03	NAMMCO (2008). Report of the Scientific Committee Working Group on Pilot Whales.	5
SC/31/GENWG/FI04	NAMMCO (2022). Report of the Scientific Committee Working Group on Harbour Porpoise.	10.1
SC/31/GENWG/FI05	NAMMCO (2023). Report of the Scientific Committee Working Group on Dolphins.	8
SC/31/GENWG/FI06	Monteiro et al. (2015). Long-finned pilot whale population diversity and structure in Atlantic waters.	5
SC/31/GENWG/FI07	Ball et al. (2021). New haplotypes found in stranded long-finned pilot whales.	5
SC/31/GENWG/FI08	Kraft et al. (2020). Global phylogeography and genetic diversity of the long-finned pilot whale.	5
SC/31/GENWG/FI09	Marina et al. (2018). Long-finned pilot: Are there differences in their skulls?	5
SC/31/GENWG/FI10	Monteiro et al. (2016). Major Histocompatibility Complex (MHC) class II sequence polymorphism in long-finned pilot whale.	5
SC/31/GENWG/FI11	Fullard et al. (2000). Population structure of long-finned pilot whales.	5
SC/31/GENWG/FI12	Oremus et al. (2009). Worldwide mitochondrial DNA diversity and phylogeography of pilot whales.	5

SC/31/GENWG/FI13	Verborgh & Desportes (2023b). Long-Finned Pilot Whale, Mammals of Europe.	5
SC/31/GENWG/FI14	Desportes et al. (2023). IUCN Red List of Threatened Species: <i>Globicephala melas</i> . https://www.iucnredlist.org/species/9250/213293843	5
SC/31/GENWG/FI15	NAMMCO & IMR (2019). Report International Workshop on the Status of Harbour Porpoises in the North Atlantic.	10.1
SC/31/GENWG/FI16	Gose et al. (2023) Broad-scale connectivity of the Atlantic white-sided dolphin.	8
SC/31/GENWG/FI17	Gose et al. (2024) Population genomics of the white-beaked dolphin.	8
SC/31/GENWG/FI18	Thorne & Nye (2021) Long-finned pilot whales trait-mediated shifts.	5