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Population genomic assessment of white-beaked dolphins (*Lagenorhynchus albirostris*) and Atlantic white-sided dolphins (*Lagenorhynchus acutus*) for delineating management units for conservation

Marc-Alexander Gose, Emily Humble, Andrew Brownlow, Mariel ten Doeschate, Nicholas Davison, Rob Ogden



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Population genomic assessment of white-beaked dolphins (*Lagenorhynchus albirostris*) and Atlantic white-sided dolphins (*Lagenorhynchus acutus*) for delineating management units for conservation.

Marc-Alexander Gose¹, Emily Humble¹, Andrew Brownlow², Mariel ten Doeschate³, Nicholas Davison³, Rob Ogden¹

1. Royal (Dick) School of Veterinary Studies and the Roslin Institute, University of Edinburgh, Edinburgh, United Kingdom
2. College of Medical, Veterinary and Life Sciences, University of Glasgow, Glasgow, United Kingdom
3. Scottish Marine Animal Stranding Scheme, SRUC Veterinary Services, Inverness, United Kingdom

1. Introduction

White-beaked dolphins (*Lagenorhynchus albirostris*) and Atlantic white-sided dolphins (*Lagenorhynchus acutus*) are endemic to the North Atlantic and the North Sea. They inhabit cold, subpolar waters (≤ 12 °C) with low salinities. Although similar in appearance, both species exhibit different morphological features, prefer different habitats and feed on different prey species. White-beaked dolphins are mainly characterised by their white or greyish beak and coloration patterns on the saddle and flanks that change with increasing age¹. They are also slightly larger than *L. acutus* and generally live in smaller social units, feeding on different species of gadoid fish and primarily inhabiting shallower coastal waters². Atlantic white-sided dolphins are smaller with a characteristic white or yellow stripe on their flanks. They gather in larger groups and primarily inhabit deep pelagic waters where feeding on squid and fish species including rainbow smelt and mackerel^{3,4}.

The phylogenetic relationships among the species of the genus *Lagenorhynchus* were investigated in several studies during the past decade. Genetic evidence together with biogeographical and acoustic data led to an extensive revision of the genus in 2019, resulting in five new proposed genera^{5,6}. Under this proposed revision, *L. albirostris* would be the only species representing the genus *Lagenorhynchus*, while *L. acutus* is reclassified as *Leucopleurus acutus*. However, the new proposed taxonomy is not yet accepted by the Society for Marine Mammalogy's Committee on Taxonomy. Nevertheless, it is important to note that recent genetic evidence highlights that *L. albirostris* and *L. acutus* are not closely related to each other.

Abundance estimates of both species generally indicate high effective population sizes⁷⁻⁹, however, monitoring has been conducted irregularly and recent findings suggest that classical methodologies for abundance estimates are not precise and unable to detect large population declines¹⁰. Like most small cetaceans, *L. albirostris* and *L. acutus* face a variety of directly anthropogenically induced threats such as entanglement and bycatch¹¹, accumulation of contaminants¹² and noise pollution¹³, and depletion of prey stocks due to overfishing¹⁴. Moreover, warming sea surface temperatures (SST) potentially result in shifts of prey species and habitat partitioning¹⁵, the introduction of new zoonic diseases to their

habitat¹⁶, and increasing competition with warmer-water inhabiting species such as the common dolphin (*Delphinus delphis*)¹⁵.

Virtually none of the above-mentioned stressors and the effects they could have on the long-term survival of both species are well understood. Data deficiency remains a problem for the species and could lead to a dangerously optimistic assessment of their status. This has been recognised by marine management entities like the IWC and ASCOBANS¹⁷, which have both called for more detailed research in all broad areas of their ecology, population structure, distribution, abundance and conservation status. Nevertheless, research on these species currently remains scarce.

In this project, population genomic analyses of stranded white-beaked dolphins and Atlantic white-sided dolphins from European coastlines will be used to detect genetic structure present within their Northeast Atlantic range. Associated post-mortem data will be used to investigate evidence for prey shifts or the introduction of novel pathogens and contaminant load. Combining these findings with data on their population genetic structure will help to outline management units and inform conservation policy (Figure 1).

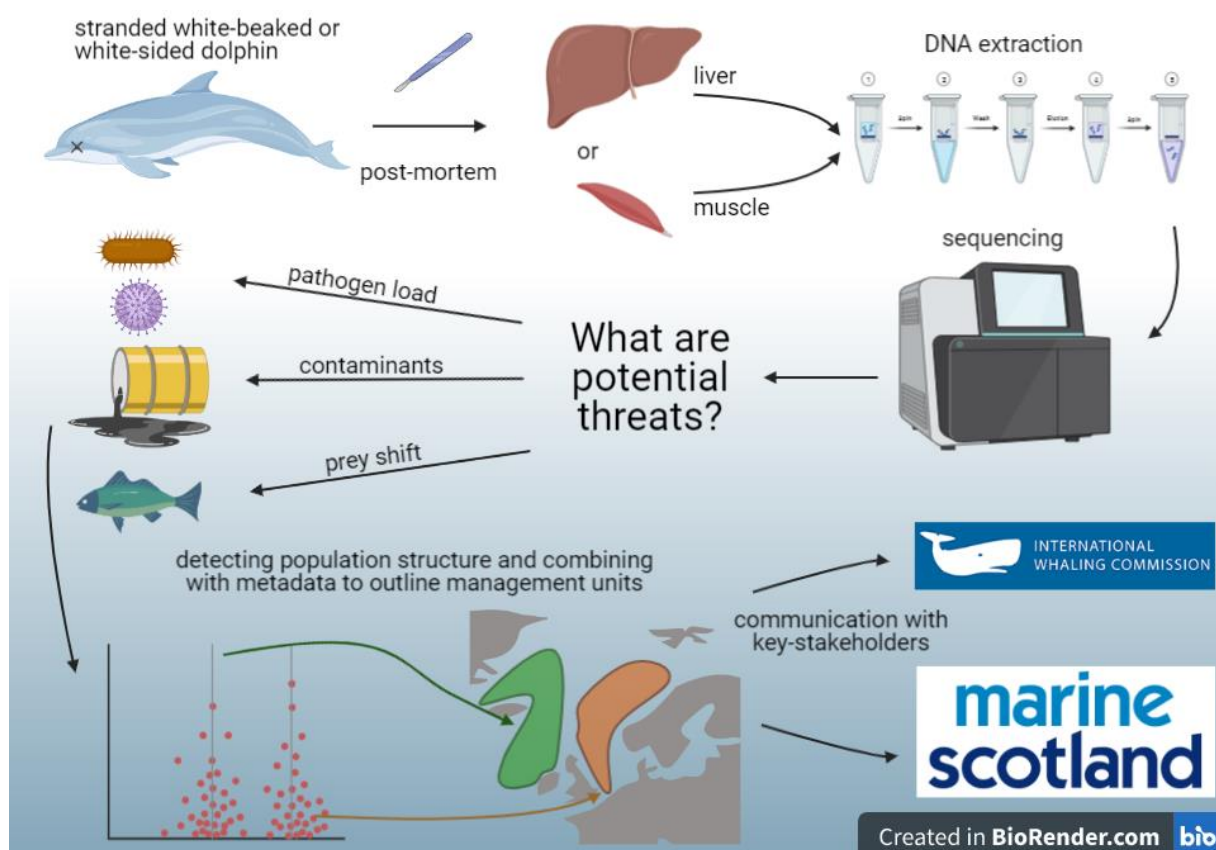


Figure 1: Graphical abstract visualising methodological approach and aims of the study.

2. Methodology

2.1 Samples

The majority of the sample set for this project comprises of tissue samples collected from deceased, stranded animals on the Scottish coast by the Scottish Marine Animal Stranding Scheme (SMASS), which includes approximately 90 samples for each target species. In addition, we acquired an additional ~50 white-beaked dolphin samples from Denmark, Iceland, Norway, France, Ireland, and Germany. We are continuing to gather samples from as many institutions as possible.

Altogether, the sample set is most likely going to be the largest current collection of tissue samples from both species and should be broadly representative of demographic and geographical differences throughout their entire Northeast Atlantic range.

2.2 DNA sequencing approach

Here, state-of-the-art population genomic approaches that measure variation at SNP (Single Nucleotide Polymorphism) DNA markers distributed throughout the genome will be used. Data will be generated through DArT-Sequencing (by Diversity Array Technologies, Australia), a method that is able to sequence multiple individuals simultaneously and is well suited for fragmented DNA, which is common in samples from stranded animals and has been successful in recovering high-quality data from a variety of difficult sample types¹⁸.

2.3 Statistical analyses and metadata

The University of Edinburgh houses a high-performance computer cluster that enables rapid population genomic analyses of big data sets. Established bioinformatic pipelines will be used to investigate the presence of population clusters within genetic data, using standard multi-variant statistical methods like Principal Component Analysis (PCA) and Discriminant Analysis of Principal Components (DAPC), as well as Bayesian clustering approaches (Structure).

The *L. acutus* genome is currently being sequenced by an international consortium and should be available in 2021. Access to this high-quality reference genome will improve the quality of the statistical analyses for this project by aligning the retained sequences to the assembly. It can also be used to identify chromosomal effects such as linkage equilibrium or enable identification of markers under selection that could have an evolutionary impact on the species in terms of adaptation to their specific ecological niche and/or environmental circumstances. Therefore, we are also actively seeking opportunities to sequence the *L. albirostris* genome.

Many of the samples are accompanied by valuable metadata about the individuals (sex, age class, cause of death) and the geographic location of the stranding (Figure 2). Further, ecological metadata such as stomach content data, contaminant load and records on pathogenic infections are available for part of the sample set. Thus, we will be able to map our genetic data against geographic, demographic, or other post-mortem data to examine spatial structuring and explore possible associations between population structure and individual biological data.

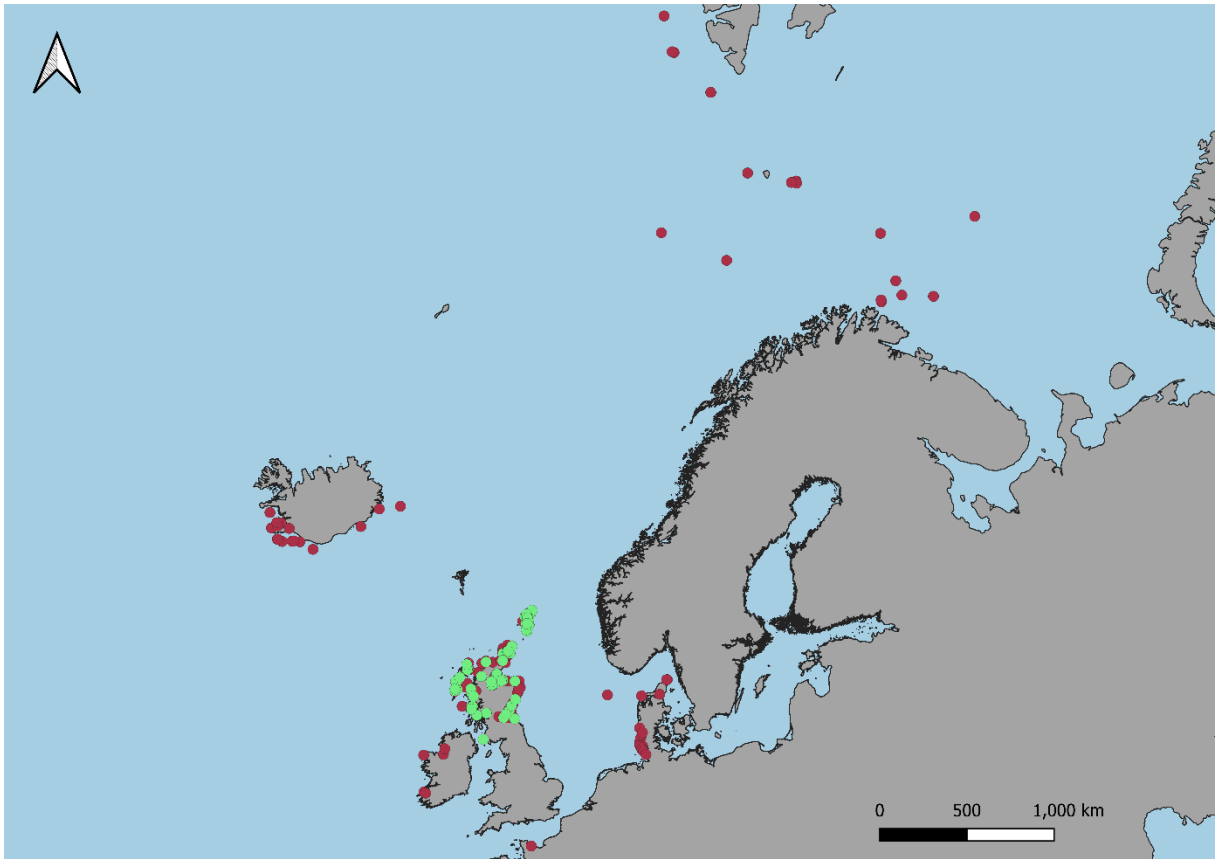


Figure 2: Distribution of the currently definite acquired sample set. Red dots represent white-beaked dolphins and green dots represent Atlantic white-sided dolphins.

3. Aims and potential outcomes

The project aims to:

- Assess population genomic structure in *L. acutus* and *L. albirostris* using state-of-the-art genomic tools
- Correlate population structure with available metadata (stomach content, contaminant load and pathogenic infections) to detect potential patterns that could be a threat for the long-term survival of the species or certain subgroups within the population
- Use our data as a basis to delineate potential management units and communicate our results to key stakeholders

Altogether, it is certain that this project will increase our overall understanding of the population structure, ecology, and conservation status of both species and therefore, contribute to a more detailed characterisation of *Lagenorhynchus* species as called for by the IWC and ASCOBANS. We aim to highlight the importance of international collaborations and multi-disciplinary approaches in marine mammal science to gain reliable results that ultimately fill data gaps and facilitate conservation of these vulnerable species.

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