

Agenda Item 4.1.1

Review of New Information on other Matters
Relevant for Small Cetacean Conservation

Population Size, Distribution, Structure and
Causes of Any Changes

Report and Recommendations of the joint
ACCOBAMS/ASCOBANS Workshop 2013

Document 4.1.1

**Report of the Joint
ECS/ACCOBAMS/ASCOBANS
Workshop on Cetacean Population
Structure**

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European Cetacean Society



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Report of the
Joint ECS-ACCOBAMS–ASCOBANS Workshop
on Cetacean Population Structure

Organising Committee: Stefania Gaspari, Peter Evans, and Camille Montiglio

Editors: Stefania Gaspari, University of Florence, Department of Biology, Florence, Italy
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1. INTRODUCTION

The workshop was held in Setúbal, Portugal, as part of the 27th European Cetacean Society's Annual Conference on the afternoon of Saturday 6 April 2013 between 12:00 and 19:00. It was attended by 50 registered participants, including 14 speakers (see Annexes A and B).

This workshop on cetacean population structure was organized following a decision of the ACCOBAMS Parties on the advice of its Scientific Committee (Report of the Scientific Committee of ACCOBAMS, 13-15 November 2012) to identify key research priorities within the ACCOBAMS area that would elucidate population structure of the major cetacean species in the region and support their conservation and management. The workshop was coordinated by Drs Stefania Gaspari (University of Florence, Italy) and Peter Evans (Sea Watch Foundation/University of Bangor, UK). The workshop was opened by Peter Evans who welcomed the participants and provided background to the workshop, summarising its objectives.

1.1 Rationale and Objectives

The principal aim of the workshop was to incorporate a multidisciplinary approach in an attempt to identify and highlight key issues and species within the ACCOBAMS area, through the following steps:

- (1) Summarise the available techniques for examining cetacean population structure, and their incorporation into conservation management plans;
- (2) Identify and prioritise information gaps and the means to address those gaps in the light of likely conservation needs;
- (3) Prioritise species in the relevant regions, based on the above and the potential relative ease to bridge those gaps (e.g. coastal species that have relatively high stranding rates);
- (4) Develop recommendations for future work, including analyses of existing data as well as the collection of new data.

1.2 Structure of the workshop

The workshop was structured into two sessions: the first session was devoted to providing an overview of the available methods for assessing cetacean population structure, while the second session examined study cases of different species present in the ACCOBAMS area.

A brief overview was given by Peter Evans of the main approaches currently applied to the study of cetacean population structure, in an attempt to define Management Units.

The methodologies that were examined in detail included: genetics (mitochondrial DNA, microsatellites, major histocompatibility complex, single nucleotide polymorphisms), skeletal variation, discontinuous distributions, photo identification, satellite tracking, stable isotope signatures, fatty acid profiles, life history parameters, parasite and chemical burdens.

The study cases investigated included seven species:

Fin whale *Balaenoptera physalus*, northern bottlenose whale *Hyperoodon ampullatus*, killer whale *Orcinus orca*, harbour porpoise *Phocoena phocoena*, short-beaked common dolphin *Delphinus delphis*, striped dolphin *Stenella coeruleoalba*, and bottlenose dolphin *Tursiops truncatus*,

2. FRAMEWORK FOR INVESTIGATION OF CETACEAN POPULATION STRUCTURE TO FACILITATE CONSERVATION AND MANAGEMENT IN THE ACCOBAMS AREA

The principal aim of the workshop was to identify and combine different approaches to investigate cetacean population structure, and to promote a multidisciplinary approach through the collaboration of different research groups in the ACCOBAMS Agreement area, to help identify management units for the different species that occur regularly.

It was agreed to share opinions and suggestions on which species should have priority for further investigation.

3. GENERAL PRINCIPLES

The workshop agreed on the benefit of combining multiple approaches in population structure assessments, and on the vital importance of identifying Management Units for conservation. It also agreed on the need to identify different types of data, and stressed the importance of consideration of their relative strengths and limitations as well as sampling issues that can affect interpretation of the results. Furthermore, it was underlined the important role that oceanographic features play on population structure processes and migratory routes.

4. PRELIMINARY CONCLUSIONS AND RECOMMENDATIONS

During the final discussion, several species and issues were identified for immediate attention with respect to investigating population structure. The participants underlined the importance to examine the status of short-beaked common dolphins particularly in Greek waters, following marked declines in the Eastern Mediterranean, and to investigate the possibility that the species has moved into different sea areas.

Risso's dolphin was another species highlighted as needing priority attention, given its relatively low abundance and patchy distribution, apparent strong site fidelity from photo-ID studies, suggesting that local clusters of animals may form separate management units. .

Killer whales in the Strait of Gibraltar and Gulf of Cadiz were considered a population in need of urgent conservation intervention due its small size and relatively high mortality rate. Further study of individuals from both Gibraltar and the Atlantic are important to elucidate population structure.

Harbour porpoises in the ACCOBAMS Agreement Area were also deemed in need of urgent attention. Evidence that the isolated Black Sea population had experienced a severe genetic bottleneck in the last 30 years correlated with an observed marked decline in abundance makes it all the more important to investigate the genetics of the small number of animals reported in recent times from the neighbouring Aegean Sea.

Cuvier's beaked whale is another Mediterranean species with localised distributions and distinct habitat preferences. At present, nothing is known of its population structure, and the workshop recommended that attention be paid to DNA sampling of individuals from within its various hotspots.

Finally, our knowledge of the genetic identity of fin whales within different regions of the Mediterranean remains equivocal, with some evidence indicating genetic isolation from the Atlantic and other evidence suggesting interchange between the two regions.

Annex A

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ANNEX B

Agenda

Introduction to the workshop

1. METHODS FOR ASSESSING POPULATION STRUCTURE

Chair: Peter Evans

- 1.1 Conservation genetic methods for more effective cetacean management
- 1.2 Review of North Atlantic minke whale population structure based on different markers
- 1.3 Stock identification using ecological markers and life history information
- 1.4 Use of Photo ID in understanding population structure
- 1.5 INTERCET: a Web-GIS platform supporting photo-ID investigations on a larger scale
- 1.6 Combining data from multiple approaches in population structure assessments

2. INSIGHTS INTO THE SPECIES

Chair: Rus Hoelzel

- 2.1 Population genetic structure of common bottlenose dolphins in the Adriatic Sea and contiguous regions
- 2.2 Bottlenose dolphin population structure in European waters correlated with well-described ecotypes and environmental differences
- 2.3 Investigating the structure of a wild bottlenose dolphin population using photo-ID techniques
- 2.4 Population genetic structure of striped dolphins in the Mediterranean Sea
- 2.5 Arda Tonay: Genetic status of the harbor porpoise in the Black Sea and adjacent waters
- 2.6 A reassessment of the genetic structure and demographic history of harbour porpoises along the entire Eastern North Atlantic distribution range and in the Black Sea
- 2.7 Satellite-tracking of fin whales in the Mediterranean - 2012
- 2.8 Common dolphin genetic studies in Europe reveal atypical panmixia in neutral markers contrasted by structuring at nuclear functional genes, while confirming a recent bottleneck in Eastern Mediterranean population
- 2.9 Seascape genetics of the short-beaked common dolphin (*Delphinus delphis*)
- 2.10 Using a multi-disciplinary approach to define and assess the conservation unit of killer whales (*Orcinus orca*) in Southern Spain
- 2.11 Northern Bottlenose whale Investigating population structure and demographic effects of whaling in the elusive northern bottlenose whale (*Hyperoodon ampullatus*) by use of modern and historic DNA

3. FINAL DISCUSSION

ANNEX C

Titles and Abstracts submitted

Conservation genetic methods for more effective cetacean management

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For conservation genetics key issues include retaining species diversity in support of natural ecosystems, retaining the potential for species to adapt to environmental change (preserving the raw material that allows adaptation), and avoiding the reduced individual fitness and demographic instability of small (endangered) populations. For cetaceans in particular, important issues include alpha taxonomy (the recognition of evolutionarily significant units for conservation at the 'species' level or above), intraspecific subdivision and the designation of units of conservation at the 'population' level, population trends (an indication of population recovery or decline), the identification of low diversity and the assessment of risk, and the identification of population structure that reflects functional genetic loci. Three methodologies have become especially important for addressing these questions – coalescent analysis to permit the assessment of effective population size dynamics and directional gene flow, Bayesian analyses to increase power to interpret genetic data in the context of connectivity, biogeography and environmental variables (including inference about loci under selection), and new technologies that increase the resolution of genetic data, and permit the assessment of both neutral and functional loci (genomics).

Review of North Atlantic minke whale population structure based on different markers

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Methods applied to determine stock structure in North Atlantic minke whales have included morphological, genetic and biochemical approaches, with different results depending on the specific markers used. Inferences from genetic methods alone have ranged from no population structure at all to 4 separate geographic populations, to mixed assemblages of two geographically independent populations on the summer feeding grounds. Four management areas, established in 1977 and based on catch and sightings distribution, sex and length distribution, as well as preliminary marking data, currently exist for minke whales in the North Atlantic. The migratory nature of the species means that samples have to be taken in the known summer feeding areas; winter breeding grounds are still unknown. Population structure for the species is still not resolved conclusively, and further studies should include evidence from satellite tracking data of individuals.

Stock identification using ecological markers and life history information

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Understanding stock structure in cetaceans can provide insights into the ecology and origins of animals living in an area as well as providing the basis for defining management units. Typically, management units are based on identification of reproductively isolated populations or stocks. However, ecological tracers can reveal (ecological) structuring within genetic stocks, providing insights into habitat use, migrations and trophic ecology which can also help inform management, especially in relation to understanding and mitigating effects of threats such as fishery by-catch. Techniques for studying stock structure range from those most suitable to reveal genetically distinct units (use of microsatellites or mitochondrial DNA, allozymes, and morphometrics) through the range of ecological tracers (stable isotopes, fatty acids, trace elements, persistent organic pollutants) which, depending of the tracer and tissue studied, can reveal segregation over time-scales ranging from days to years, to the (more speculative) interpretation of variation in life history parameters, or in diet as revealed by stomach contents.

Use of all these techniques requires understanding of their limitations, which in turn implies understanding the physiology and chemistry of isotopic fractionation, fatty acid deposition and contaminant bioaccumulation. Interpretation of tracers which have adverse health impacts (e.g. cadmium, mercury) requires particular caution, as does the drawing of inferences from samples obtained from stranded animals. Since these tracers originate almost exclusively from food organisms and some are bioaccumulated, information on the age, sex and maturity status of the studied animals is also essential to inform interpretation of results.

Microsatellite and mitochondrial DNA studies on Iberian bottlenose dolphins reveal evidence of two populations, one comprising resident animals from southern Galicia and the other possibly representing a more wide-ranging, oceanic group. The existence and interpretation of genetic differences are supported by stable (C and N) isotope data (Fernández *et al.*, 2011 a,b). The latter results also reveal the initially surprising decline in the proportion of ¹⁵N in tissues with increasing age. However, stomach contents data suggest this reflects increasing feeding on (the low trophic level) blue whiting (Santos *et al.*, in press).

Use of multivariate analysis of morphometric characters is exemplified by a recent study on skull shape in common dolphins, which suggested differences between dolphins from Portugal and those from elsewhere in the northeast Atlantic (Murphy *et al.*, 2006). Life history parameters which may be interpreted to suggest the existence of distinct genetic or ecological stocks include age at sexual maturity and asymptotic body size. The Iberian harbour porpoise reaches a higher maximum body size than porpoises from elsewhere

in the northeast Atlantic (López Fernandez, 2003; Learmonth, 2006), a finding consistent with more recent genetic findings (Fontaine *et al.*, 2007).

Fatty acid profiles of cetacean blubber show geographical variation, as seen in both harbour porpoises and common dolphins within the northeast Atlantic, although only in the latter species was clear geographical segregation evident (Pierce *et al.*, 2005; Learmonth, 2006). PCB concentrations in blubber also show geographic variation as well as variation between species. Among small cetaceans in the northeast Atlantic, highest concentrations tend to be seen in the bottlenose dolphin. In this species, highest concentrations have been recorded in the Iberian Peninsula, especially southern Spain (almost all above the proposed threshold for adverse effects on reproduction), and lowest values in Scotland, Ireland and the Canary Islands (Mendes-Fernández, 2012).

In conclusion, molecular genetics can give clear answers about population definition and, if we wish to understand population trends, the management unit should be the population. Life history characteristics and ecological markers differ between areas but these differences may be at least partly environmental in origin. While perhaps unsuitable as a basis for defining management units, ecological markers can undoubtedly help us understand the effects of specific threats to marine mammals.

Use of Photo ID in understanding population structure

Peter G.H. Evans

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The use of unique markings on the fin, back or tail of cetaceans has proved to be a cost-effective method for identifying different individuals of many species by photography. Recommended camera equipment includes a good digital single lens reflex camera with a capability to shoot at 5 frames per second or faster, one or more zoom lenses, a lens hood and reasonably sized set of memory cards. Photo-ID can provide information on abundance (through mark-recapture analysis), home range size and use, movements, social structure, and various life history parameters (e.g. birth rates, juvenile mortality rates). Some species are more amenable to photo-ID than others. Amongst Mediterranean species, it has been used most successfully on bottlenose dolphin, Risso's dolphin, killer whale, long-finned pilot whale, Cuvier's beaked whale, sperm whale and fin whale. It is important that markings are unique to a particular individual and can be readily identified (dorsal fin nicks for example are better than scratches), and if markings change over time (e.g. the accumulation of nicks, or healing of scars), that such variation is tracked. Studies of re-sighting rates, movements and home range all contribute to an understanding of population structure. It is important that surveys are conducted across the potential range of those individuals being studied, and that such surveys are repeated in different seasons to account for any seasonal variation in movements.

INTERCET: a Web-GIS platform supporting photo-ID investigations on a larger scale

Guido Gnone and Michela Bellingeri

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Photo-Identification techniques, in association with geo-referencing systems, can be used to gain important information from a wild population: movements and home ranges of single individuals and sub-groups, association patterns, population structure, demography data, abundance estimate and trends, etc. When applying this method on highly mobile animals like Cetaceans, often crossing the national borders within their normal displacements, it is fundamental to work on an appropriate scale in order to reach proper results. For this purpose modern Web and GIS technologies may be joined together with digital photographic techniques. INERCET is a Web-GIS platform planned to support collection, aggregation, visualization and integrated analysis of geo-referred and photographic data on a Mediterranean scale. It was developed by Acquario di Genova within GIONHA (Governance and Integrated Observation of marine Natural Habitat) a Cross Border Cooperation Project involving Italian and French regions facing the North Tyrrhenian and Ligurian Sea (Tuscany, Liguria, Sardinia and Corsica). The main objective of this platform is to connect researchers in a research network. The cross matching of the photographic catalogues uploaded by the network partners makes possible to track the movements of the animals between contiguous research areas, to identify local populations or subpopulations, to estimate their abundance and to investigate their structure.

Combining data from multiple approaches in population structure assessments

A. Viricel, P. Mendez-Fernandez, V. Ridoux, B. Simon-Bouhet, and F. Caurant

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Investigating habitat use and population structure using multiple approaches is beneficial to delineate management units as it provides an understanding of patterns of connectivity and habitat segregation at different time scales and thus also informs on the temporal dynamics of the structure observed. In this perspective, sampling schemes should aim at obtaining and storing tissue samples in a way that allows multiple analyses to be conducted (e.g. stable isotopes, genetics, trace elements) from each individual. We also emphasize the need to develop an analysis framework to integrate the different types of data. Such integration could provide a finer resolution of population structure, particularly in cases where signals from genetic markers are weak. We will illustrate the use of several approaches (ecological tracers and genetics) in two case studies. The first case study exemplifies how the combined analysis of stable isotopes and cadmium can provide information on ecological segregation among several odontocete species with close eco-biological requirements. The second case study is a pilot project on common dolphins, which aim is to explore the use of a next-generation sequencing approach (RAD seq) to discriminate between groups identified using ecological tracers.

Population genetic structure of common bottlenose dolphins in the Adriatic Sea and contiguous regions

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Levels of genetic differentiation and dispersal patterns of common bottlenose dolphins (*Tursiops truncatus*) were assessed in the northeast Mediterranean Sea, with a focus on the Adriatic Sea. This is a region characterised by diverse marine ecosystems and high levels of human-induced habitat degradation. Although this species seems almost uniformly distributed throughout the Adriatic basin, genetic evidence rejected the hypothesis of a single stock. Pairwise estimates of genetic differentiation at 12 microsatellite loci, and mitochondrial DNA (entire control region, 920bp), revealed diverse levels of genetic differentiation among five putative populations from the Tyrrhenian Sea to the Aegean Sea. A fine-scale genetic structure was recorded within the Adriatic Sea, where females appear to be the principal gene flow mediators. The assessment of recent migration rates indicates a relatively high level of gene flow from the north Adriatic towards adjacent areas. Indication of a fine-scale population structure across the Adriatic Sea is a factor to be carefully considered in the emerging marine management scenario set by the implementation of the EU Marine Strategy Framework Directive (2008/56/CE) and in relation to the designation of potential Adriatic Special Areas of Conservation for the bottlenose dolphin under the Habitats Directive (Council Directive 92/43/EEC).

Bottlenose dolphin population structure in European waters correlated with well described ecotypes and environmental differences

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The bottlenose dolphin (*Tursiops truncatus*) is found throughout Europe and the North Atlantic, both in coastal and pelagic waters. It is a widespread species globally, which is known for exhibiting strong local scale population structure, typically (but not exclusively) between pelagic and coastal ecotypes. Local scale studies on microsatellites sequences revealed the presence of 4 main clusters in European waters: Black Sea; Eastern Mediterranean; Western Mediterranean + North East Atlantic; Northern Scotland. mtDNA studies, using partial sequences from detailed sampling schemes, and full mitogenomic sequences focusing on the main population clusters, confirmed this separation but revealed a lack of reciprocal monophyly between regional clusters. This is most likely due to the recent origin of these clusters, as little sex biased dispersal has so far been detected. Further small-scale population sub-structure has been detected in Ireland, Iberian Peninsula and the British Isles, with estuarine communities in Sado (Portugal), Shannon (Ireland) and the Moray Firth (Scotland) also showing some level of differentiation from local coastal populations. However, sample availability and geographic representation is limited, and results should thus be considered preliminary. Identified genetic clusters correlate well with known ecotypes, namely the Black Sea sub-species and populations from pelagic waters. In coastal waters, genetic clusters

correspond well with local environmental differences, suggesting environmental adaptation as a potential driver. Differences in prey resource are commonly speculated as the most important environmental driver, but concrete data is unavailable. Data on functional regions of the genome is also at present unavailable.

Investigating the structure of a wild bottlenose dolphin population using photo-ID techniques

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This presentation refers to two main scientific papers produced within a fruitful collaborative research experience involving about 15 different groups collecting photographic data within the Pelagos Sanctuary borders from 1994 to 2011. Photo-identification was the main technique used to investigate the movements and the structure of a bottlenose dolphin population living in the Pelagos waters. Each research group independently selected the photo-ID data on the basis of the quality of the image, and the distinctiveness of the animals. All of the catalogues were then pooled and a further selection was implemented to normalize the photographic data before the matching process was performed. The cross-analysis of the photographic catalogues from the different sub-areas gave interesting and sometimes unexpected results. Bottlenose dolphins show a general sedentary behavior, with displacements usually within 80km (50km on average). Only a few dolphins exhibit more wide-ranging journeys, travelling up to 427km between sub-areas. A network analysis was performed to investigate the social structure of the same population, selecting those individuals with at least 4 captures in total (271 specimens in 414 schools). The Pelagos population resulted divided in two main sub-groups plus three minor sub-groups. These are located in distinct geographic areas, supporting the idea that the structure of the population is mainly shaped by the different ecological and physiographic traits of the residency areas; specialization in the foraging techniques, possibly including opportunistic feeding on local fishing activities, may have caused a (partial) separation between sub-groups. Genetic analysis should be used to test the actual isolation level of these.

Population genetic structure of striped dolphins in the Mediterranean Sea

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In this study we assess the level of genetic divergence and gene flow among striped dolphin population of the Mediterranean Sea. Striped dolphins genetic differentiations were assessed from Gibraltar to Greece and Israel. A total of 366 samples were analysed at 15 microsatellite DNA loci, and at the entire mitochondrial Control Region 919bp. Samples were collected from 1990 to 2007 from stranded and free ranging animals in different locations. The striped dolphin populations within the Mediterranean Sea show a phylogeographic genetic structure, such that population boundaries seem to limit gene flow. We found evidence for sex-biased dispersal, and that gene flow is females mediate,

though, gene flow boundaries are difficult to define. All population, except for the Western Ionian, seem to be demographically expanding, in particular the Ligurian Sea population seems to be genetically isolated and in rapid expansion.

Genetic Status of the Harbour Porpoises in the Black Sea and Adjacent Waters

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Black Sea harbour porpoises (*Phocoena phocoena relicta*) are morphologically and genetically differentiated from harbour porpoises in the other areas. The fragmentation of its distribution range in the Mediterranean Sea was triggered approximately 5000 years ago. They have been categorized as endangered since 2008 due to serious anthropogenic threats in the Black Sea, namely direct killing in the past, bycatch and depletion of prey. Based on all published and unpublished genetic studies, a total of 229 specimens from the Black Sea, nine from the Aegean Sea, and four from the Marmara Sea have been analysed. All nine Aegean Sea individuals originated from the Black Sea. All four individuals from the Marmara Sea shared the same unique haplotype. This haplotype was not observed in other individuals from the Black Sea or the Aegean Sea. This pattern supports the possibility of an isolated population in the Marmara Sea. Two genetic studies (in Ukraine and Turkey) are known to be ongoing at present. Our team is continuing stranding surveys on the western Black Sea coast on a monthly basis, and around the Marmara Sea seasonally. New samples currently being collected on three cetacean species in the Black Sea and adjacent waters will help to understand the genetic connectivity of these species in the area.

The Golden Age of small cetaceans in the Black Sea and their anthropogenic-driven collapse

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Two major ecological transitions marked the history of the Black Sea after the last Ice Age. The first was the postglacial transition from a brackish water to a marine ecosystem dominated by porpoises and dolphins once this basin was reconnected back to the Mediterranean Sea (ca. 8,000 y B.P.). The second occurred during the past decades, when overfishing and hunting activities brought these predators close to extinction, having a deep impact on the structure and dynamics of the ecosystem. Estimating the extent of this decimation is essential for characterizing this ecosystem's dynamics and for formulating restoration plans. However, this extent is poorly documented in historical records. We addressed this issue for one of the main Black Sea predators, the

harbor porpoise, using a population genetics approach. Analyzing its genetic diversity using an approximate Bayesian computation approach, we show that only a demographic expansion (at most 5,000 y ago) followed by a contemporaneous population collapse can explain the observed genetic data. We demonstrate that both the postglacial settlement of harbor porpoises in the Black Sea and the recent anthropogenic activities have left a clear footprint on their genetic diversity. Specifically, we infer a strong population reduction (<90%) that occurred within the past 5 decades, which can therefore clearly be related to the recent massive killing of small cetaceans and to the continuing incidental catches in commercial fisheries. Our study thus provides a quantitative assessment of these demographically catastrophic events, also showing that two separate historical events can be inferred from contemporary genetic data.

Satellite-tracking of fin whales in the Mediterranean - 2012

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In recent decades, several studies have been carried out to describe summer habitat use, behaviour, distribution and abundance of fin whales in the northwestern Mediterranean. However, knowledge of their distribution and movements during other seasons remains scarce. The present project was funded by the Italian Ministry of the Environment, to investigate post-summer fine scale habitat use, movements, and migration routes/destinations of fin whales. Location-only satellite transmitters (SPOT5, Wildlife Computers) were attached to eight individuals in the Pelagos Sanctuary (September 2012). Deployments occurred as late in the summer as possible, to maximise information outside known summer feeding grounds. Two different models using different attachment mechanisms were used ('LIMPET' n=3 and 'implantable' n=5), inter alia to examine potential differences in performance for future fin whales' studies. An important component of the project was to evaluate the strengths and weaknesses of tag designs and deployment to assist worldwide efforts to improve telemetry research programmes. At the time of writing, two implantables are still transmitting; LIMPET tags lasted max=35 days (mean=25) and implantables thus far max=83 days (mean=55.2). Fine scale associations with oceanographic features and potential feeding habitats within the Sanctuary are being investigated. Preliminary results indicate that tagged fin whales remained in the Pelagos Sanctuary feeding ground longer than expected, possibly due to the current particularly mild climate conditions which allowed prolonged feeding activities in the area. Two individuals left the Pelagos area and moved towards the Balearic Islands, remaining in a defined area (100x100 km) for approximately 20 days before moving towards the Gulf of Lions. Ongoing data collection, coupled with further deployments, could provide insights on small and large scale feeding behaviour and migratory routes. Alongside information on threats (e.g. vessel traffic), telemetry data are important for helping to develop focussed mitigation measures and providing baseline data to measure their effectiveness.

Common dolphin genetic studies in Europe reveal atypical panmixia in neutral markers contrasted by structuring at nuclear functional genes, while confirming a recent bottleneck in Eastern Mediterranean population

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The common dolphin (*Delphinus delphis*) is the most abundant cetacean species in the North East Atlantic within their distribution limits up to Southern Ireland and British Isles. In the Mediterranean, although once abundant, it has experienced a relatively well documented population decline, and is currently listed as endangered in the IUCN red list. Population structure within North Atlantic is very low, even between coastal areas on opposite sides of the ocean. Detailed information on local scale genetic structure in Europe is available for this species, from multiple studies using both microsatellites and mtDNA. These strongly suggest that the species is largely panmictic along the European coastline. The Eastern Mediterranean population appears to differentiate from populations elsewhere, but simulation studies suggest that loss of diversity and isolation due to a recent bottleneck is more likely than historical limitation of gene flow. Contrastingly, preliminary results on functional genetic variation reveal population differentiation between Irish, Atlantic and Mediterranean samples. Such differences may be related to local differences in prey energy contents, predatory pressure and pathogenic environments. This suggests that, although gene flow levels across Europe are high, different locally adapted populations might exist, perhaps explaining why no recolonisation of the Mediterranean has originated from the numerous Atlantic population. The few studies that have focused on the Black Sea population suggest some differentiation from the Mediterranean, but sample availability is extremely limited. More samples from the Black Sea population, and from other locations along the Mediterranean are needed for further assessment.

Seascape genetics of the short-beaked common dolphin (*Delphinus delphis*)

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Identifying which factors shape the distribution of intraspecific genetic diversity is central in evolutionary and conservation biology. In the marine realm, the absence of obvious barriers to dispersal can make this task more difficult. Nevertheless, recent studies have provided valuable insights into which factors may be shaping genetic structure in the world's oceans. Here, using a seascape genetics approach, we show that marine productivity and sea surface temperature are correlated with genetic structure in a highly mobile, widely distributed marine mammal species, the short-beaked common dolphin. We suggest that the relationship between environmental variables and population structure may be caused by prey behaviour, which is believed to determine common dolphins' movement patterns and preferred associations with certain oceanographic conditions. Our study highlights the role of oceanography in shaping genetic structure of a highly mobile and widely distributed top marine predator. Thus, seascape genetic studies can potentially track the biological effects of ongoing climate-change at oceanographic interfaces and also inform marine reserve design in

relation to the distribution and genetic connectivity of charismatic and ecologically important megafauna.

Using a multi-disciplinary approach to define and assess the conservation unit of killer whales (*Orcinus orca*) in Southern Spain

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Identifying discrete, demographically independent conservation units is a key goal for management. Previous genetic work assigned killer whales that are known to occur seasonally in the Strait of Gibraltar in a population with whales occasionally seen in the Canary Island. However, there was weak differentiation between the Canary Island and Strait of Gibraltar individuals. This could result from historic gene flow and an absence of contemporary gene flow or migration between the Canary Islands groups and the Strait of Gibraltar groups. Here we present new analyses of photo-identification and individual genotypes to assess the level of contemporary gene flow and migration between groups. A total of 26,430 dorsal fin images collected over 10 years were analyzed, showing the presence of 47 different individuals in the Strait of Gibraltar and 16 individuals in the Canary Islands, no matches were found between both areas. During the photo-id sessions, group structure was noted, and the catalogue was analysed with Socprog, resulting in the identification of a total of 5 pods in the Strait of Gibraltar and 2 pods in the Canary Islands. The temporal relationships were fitted to models calculating their lagged association rates resulting in a social system based on Rapid Dissociation and Constant Companions and Casual Acquaintances. Mitochondrial DNA haplotype was shared by all individuals sampled within each group (constant companions), but differed between the two Canaries groups and between groups within the Strait (casual acquaintances), suggesting that social structure was matrifocal and there was little or no migration between groups. Kinship analysis detected no close kin between Canaries and Gibraltar individuals, suggesting low or no contemporary gene flow. The results suggest that the individuals within the Strait of Gibraltar are a distinct 'conservation unit'. This study contributed to propose a Site of Community Importance (SCI) in the Strait of Gibraltar.

Investigating population structure and demographic effects of whaling in the elusive northern bottlenose whale (*Hyperoodon ampullatus*) by use of modern and historic DNA

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The northern bottlenose whale (*Hyperoodon ampullatus*) is a highly elusive and little-studied North Atlantic beaked whale occurring in offshore waters where it forages at large depths. Northern bottlenose whales were targets of intensive whaling with more than 65,000 animals harvested in the Northeast Atlantic from the 1880s to the 1920s. Its deepwater habitat and apparent regional scarcity implies that the general biology, conservation status and ecosystem role of the northern bottlenose whale is poorly understood.

Here we perform a genetic analysis of historic and modern material compiled from more than twenty research institutes, natural history museums, stranding networks and NGOs in Europe and North America to investigate population structure and potential effects of past whaling activities on the northern bottlenose whale. Thanks to this collaborative effort we were able to obtain a sample size of more than 300 animals spanning the entire known range of the species and covering the pre-whaling period, the intermediate period and the post-whaling period.

These animals were sequenced in two mitochondrial loci and additionally screened for genetic variation in nine nuclear loci. We found that although levels of genetic differentiation were low, northern bottlenose whales could be divided into at least four genetic units representing the Gully, the Labrador-Baffin Bay region, the waters around Iceland and the deep-water region west of Ireland. The observed levels of genetic diversity were among the lowest reported for a North Atlantic marine mammal. However, these levels could not be directly attributed to past whaling activities, perhaps because our sampling size from the former whaling grounds off Norway was too small for inference. Our results point to the existence of potential migration routes and admixture zones, and identify information gaps and areas of interest for further sampling.

Importantly, we show that even for highly elusive species where other modes of inference are difficult, baseline biological knowledge can be drawn from temporally and spatially spaced genetic data generated thanks to the combined effort of multiple international research institutes, natural history museums, stranding networks and NGOs.