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Central and Arctic Region
Canadian Science Advisory Secretariat
Science Advisory Report 2011/021

ADVICE REGARDING THE GENETIC STRUCTURE OF CANADIAN NARWHAL (*Monodon monoceros*)

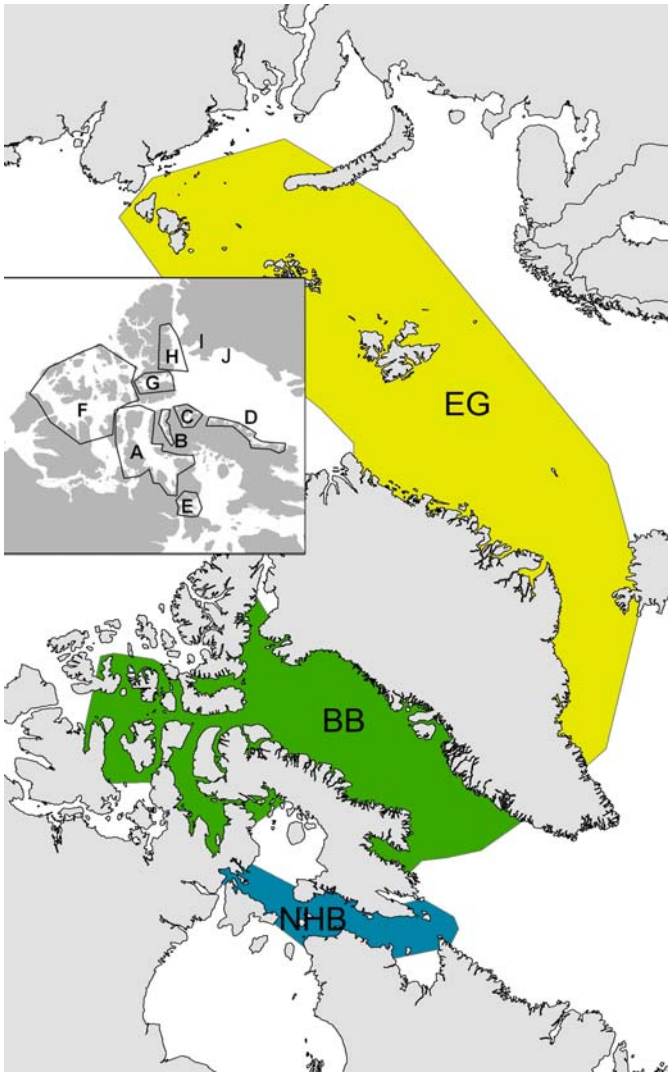
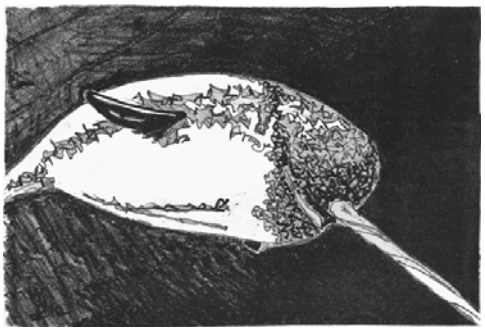


Figure 1. Approximate range of narwhal in the Arctic with three populations indicated: Baffin Bay (BB, green), Northern Hudson Bay (NHB, blue), and East Greenland (EG, yellow). Inset map indicates summering aggregation areas in Canada and West Greenland: A: Somerset Island; B: Admiralty Inlet; C: Eclipse Sound; D: East Baffin Island; E: Northern Hudson Bay; F: Parry Channel; G: Jones Sound; H: Smith Sound; I: Inglefield Bredning; J: Melville Bay.



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Context :

Narwhal (Monodon monoceros) is a key element of the eastern Canadian Arctic ecosystem and a culturally and economically important species for Inuit. Recent research has suggested that narwhal is vulnerable to habitat changes and hunting changes associated with global warming. Due to these pressures, it is important to actively address anthropogenic impacts and currently this is best approached with effective harvest management directed at summering stocks to reduce the potential for local depletions. Genetic identification of stock structure is needed to enable managers to determine the summering stock from which each harvested whale came from, especially where the harvests may be shared among Nunavut communities and between Canada and Greenland.

A number of avenues are being pursued to identify stock structure and to assign harvested whales to specific stocks including contaminant profiles, fatty acid signatures, and genetic profiles. This document summarizes the results of research initiated to identify stock structuring in narwhal using genetic data management purposes.

SUMMARY

- Narwhal samples from Canada and eastern and western Greenland were genetically profiled at 16 nuclear microsatellite markers.
- Conventional analysis which measures genetic differences (F_{ST}) among populations, detected a significant differentiation among the three populations (Baffin Bay, Northern Hudson Bay, and East Greenland).
- Genetic differences were evident between narwhals from Jones Sound and those from the Somerset Island summering stock.
- No other significant differences were observed however, a number of sampling issues limited the ability to differentiate among current summering stocks.
- Genetic profiling of narwhal coupled with new multivariate analyses show promise in distinguishing stocks but will require increased geographic sampling in the summer.

INTRODUCTION

Narwhals (*Monodon monoceros*) are mid-sized toothed whales that inhabit the Arctic seas north of 60^{o}N. This iconic species is an important resource for Inuit communities' annual food budgets, economic well-being, and cultural identity. Narwhal may be at increasing risk of mortality associated with climate change. In particular, it has been suggested that narwhal will be more vulnerable to ice entrapments (i.e., when animals are not able to reach open water because they are trapped under or behind forming ice) if patterns of sea ice formation become increasingly unpredictable. Pressure may also be increasing in the form of increased predation by killer whales (*Orcinus orca*) and changes in the timing and scale of harvests. Therefore, it is important to understand the stock structure of this species and to use that information to effectively manage this important resource.

In narwhal, several hierarchical levels of population structure have been proposed based on spatial segregation of animals during their annual migration cycle. At the coarsest scale, observational data, surveys, and tagging studies indicate that three populations occur throughout their range (Figure 1). These three populations consist of narwhal that move seasonally between: 1) northern Hudson Bay and Hudson Strait; 2) Baffin Bay and the high Arctic; and 3) eastern Greenland and the Greenland Sea. Mitochondrial sequence data from the control region have also supported the isolation of eastern Greenland narwhal from western Greenland and Canadian narwhal as well as the separation of northern Hudson Bay from Baffin Bay narwhal.

At a smaller spatial scale, the Baffin Bay population has been divided into a number of stocks based on the identification of summer concentrations of narwhal. The term 'stock' refers specifically to geographically segregated groups of animals subject to hunting and these may, or may not, correspond to actual genetic units (i.e., populations). Five stocks have been identified in the Canadian Arctic with up to three more hypothesised to exist in the High Arctic (Parry Channel, Jones Sound and Smith Sound) (DFO, 2010), and two stocks have been identified in northwest Greenland (Figure 1 inset). Although these stocks have been delineated using primarily non-genetic data sources, genetic data have been used to support some stock level groups. For example, de March et al. (2003) observed some evidence of differentiation between narwhal from Grise Fiord (Jones Sound) and other Baffin Bay stocks.

Genetic data have provided insight into the population and stock structure of a number of cetaceans, including beluga and killer whales.

ANALYSIS

We genetically profiled 877 narwhal samples, collected from the eastern Canadian Arctic and Greenland between 1982 and 2009, at 12 nuclear loci. For the stock level analysis this dataset was reduced so that only animals on their summering areas were used; this resulted in a dataset of 268 individuals. To ensure data quality, approximately 10% of the samples were extracted and genetically profiled in duplicate. In addition, each plate of samples included positive controls from two individuals.

Population Scale Differentiation

Significant genetic differentiation was detected among all populations with the greatest differentiation between Northern Hudson Bay and East Greenland (Figure 2). Inter-class principle components analysis (PCA) suggests some overlap in the allele frequencies of all populations (Figure 2).

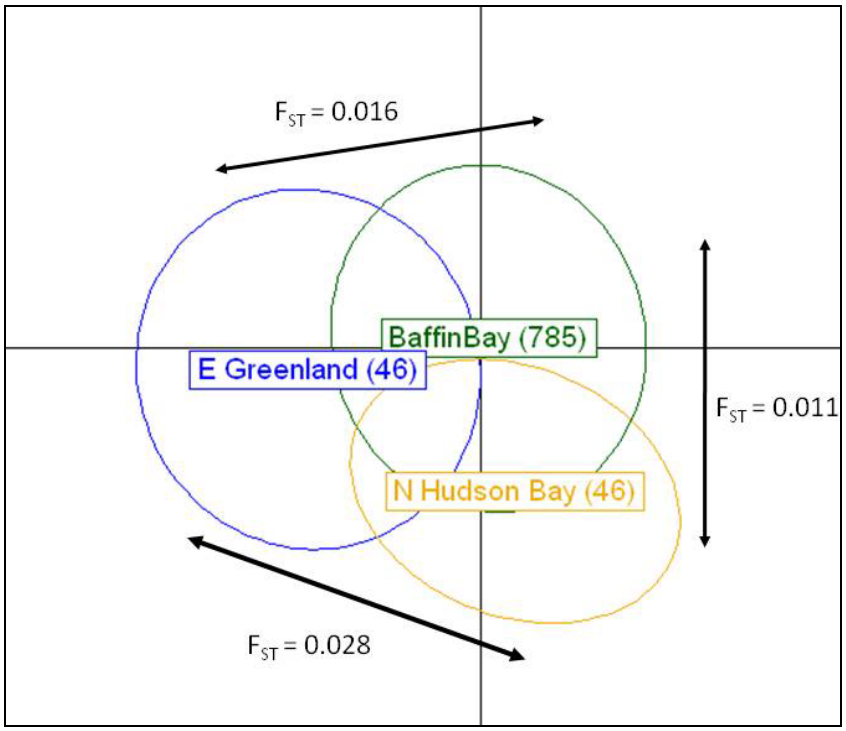

Figure 2. Visualization of the genetic differentiation among Narwhal populations derived from interclass PCA. Significant measures of genetic differentiation between the populations are included beside the arrows. Population labels are followed by the sample size used in brackets.

Stock Differentiation

Samples were grouped into stocks based on sampling location. Few groups showed significant differentiation (F_{ST}) outside of comparisons with the known populations of Northern Hudson Bay and East Greenland. Somerset Island stock was significantly differentiated from narwhal from Jones Sound.

Both PCA and correspondence analysis suggest that the Jones Sound animals are separate from other stocks and also separate from the Inglefield Bredning samples, which are

geographically close. Samples grouped into the Somerset Island stock also separate out in the multivariate analysis.

Sources of Uncertainty

Sources of uncertainty that may be contributing to the results:

1) Significant sampling gaps exist within the narwhal range (e.g., Smith Sound, Parry Channel, Somerset Island, and east Baffin Island). These areas may harbour unique groups or contribute to the overall genetic patterns.
2) A number of sampling issues limited the ability to differentiate among current summering stock designations.

CONCLUSIONS AND ADVICE

Overall the genetic data presented here have broadly supported the current population structure but are less clear in their support of the stock level designations. The application of novel multivariate methods to explore the differentiation among putative stocks is promising but a comprehensive sampling strategy needs to be implemented. The management of narwhal in Canada, and the joint management of stocks with Greenland, will certainly require increased effort to obtain samples – ideally in a designed (as opposed to an opportunistic) manner.

SOURCES OF INFORMATION

This Science Advisory Report results from the Fisheries and Oceans Canada, Canadian Science Advisory Secretariat, National Marine Mammal Peer Review Committee Meeting (NMMPRC) of November 22-26, 2010. Additional publications from this process will be posted as they become available on the DFO Science Advisory Schedule at http://www.dfo-mpo.gc.ca/csas-sccs/index-eng.htm.

de March, B.G.E., Tenkula, D.A. and Postma, L.D. 2003. Molecular genetics of narwhal (*Monodon monoceros*) from Canada and West Greenland (1982-2001). DFO Can. Sci. Advis. Sec. Res. Doc. 2003/080. 23 p.

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