COSEWIC Special Report

Designatable Units for Beluga Whales (*Delphinapterus leucas*) in Canada

COSEWIC
Committee on the Status
of Endangered Wildlife
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For additional copies contact:

COSEWIC Secretariat
c/o Canadian Wildlife Service
Environment Canada
Ottawa, ON
K1A 0H3

Tel: 819-938-4125
Fax: 819-938-3984
E-mail: ec.cosepac-cosewic.ec@canada.ca
http://www.cosewic.gc.ca

Beluga DU report

Preface

This report represents the Designatable Unit (DU) component of a Status Report on Beluga Whales (*Delphinapterus leucas;* hereafter, Belugas) in Canada. In preparation for upcoming assessments (and reassessments) of this species, a clear and consistent scheme for identifying DUs is needed. Due to the complexity of this species' population structure, the Marine Mammals Specialist Subcommittee (SSC) has elected to separate the designation and approval of the DUs from the status assessment process.

Similar to any COSEWIC Status Report, this report underwent two jurisdictional reviews and one review by COSEWIC. The report was also reviewed by a number of Beluga experts and other individuals familiar with application of the DU concept.

The DU structure proposed in this report was accepted by COSEWIC in Novemer 2016.

Executive Summary

Over their circumpolar distribution in Arctic and sub-Arctic environments, Belugas (*Delphinapterus leucas*) exhibit variation in ecology (*e.g.,* diet, habitat selection), genetics, behaviour (*e.g.,* migration patterns), and morphology (*e.g.,* body size). A significant portion of the global range of this medium-sized toothed whale is in Canada. Most management units (variously defined as stocks, populations, etc.) are shared by multiple jurisdictions, both within Canada (*e.g.*, Nunavut, Quebec, Manitoba) and between Canada and other countries (Greenland, United States, Russian Federation).

Only one species of Beluga is recognized worldwide, with no recognized subspecies. Populations are generally defined based on non-overlapping summer distributions informed by variation in migratory pattern and timing, genetics, and environmental chemicals. COSEWIC's Designatable Units (DUs) are recognized as both discrete and significant units that constitute irreplaceable components of Canada's biodiversity. Canada's *Species at Risk Act* (SARA) recognizes that entities below the species level require conservation, and provides COSEWIC the mandate to assess them.

The last COSEWIC assessments for most Belugas were conducted in 2004, when seven recognized DUs (covering all Canadian populations) were assessed with status ranks ranging from Not at Risk to Endangered. The St. Lawrence Estuary DU was reassessed as Endangered in 2014.

COSEWIC's DUs are defined as "discrete and evolutionarily significant units of the taxonomic species", where "significant" means that the unit is important to the evolutionary legacy of the species as a whole and if lost would likely not be replaced through natural dispersion (COSEWIC 2012). COSEWIC recognizes 3 different lines of evidence for "discreteness" and 4 different lines of evidence for "evolutionary significance", at least one line of evidence from each must be met to justify a DU designation:

Discreteness:

1. Genetic distinctiveness including inherited traits (including life history or behaviour) and or neutral genetic markers (including DNA microsatellites);
2. Natural disjunction in geographic range (such that local adaptation is likely);
3. Occupation of differing eco-geographic regions relevant to the species, reflecting historical or genetic distinction.

Evolutionary Significance:

1. Evidence that the discrete population differs markedly from others in genetic characteristics thought to reflect relatively deep phylogenetic divergence, *e.g.,* based on relatively slow-evolving markers;
2. Persistence of the discrete population in a unique ecological setting that is likely or known to have given rise to local adaptations;
3. Evidence that the discrete population is the only surviving natural occurrence of a species that is only found elsewhere as an introduced species;
4. Evidence that loss of the discrete population would result in an extensive gap in the range of the species in Canada.

We used five principal lines of evidence to identify DUs for Belugas, based on COSEWIC guidelines. We examined available evidence on phylogenetics; genetic diversity and structure; morphology; movements, behavior, and life history strategies; and distribution for each grouping. Aboriginal Traditional Knowledge (ATK) (summarized in Cardinal 2013) was applied to each type of evidence where available. Little documented ATK was available regarding Ungava Bay Belugas, a possibly extirpated DU, and there was virtually no ATK for Belugas in the St. Lawrence Estuary.

All studies of sources of variation (*e.g.*, genetics) have been limited in geographical scope or sample size, making it difficult to undertake comprehensive comparisons across the entire range of the species in Canada. Because some criteria for both discreteness and significance offered stronger evidence than others, DU decisions were generally made on multiple lines of evidence.

Based on the COSEWIC DU criteria for discreteness and significance we propose eight (8) DUs for Belugas in Canada. These are: DU1: Eastern Beaufort Sea (EBS), DU2: Eastern High Arctic – Baffin Bay (EHA-BB), DU3: Cumberland Sound (CS), DU4: Ungava Bay (UB), DU5: Western Hudson Bay (WHB) (or Western-Northern-Southern Hudson Bay, see Richard 2010), DU6: Eastern Hudson Bay (EHB), DU7: St. Lawrence Estuary (STL), and DU8: James Bay (JB) (or Hudson Bay-James Bay, see Cardinal 2013). This list includes seven recognized DUs from the 2004 assessment, plus a new DU recognized for JB on the basis of both scientific information and Aboriginal Traditional Knowledge (ATK). ATK described two populations in the EHA-BB DU, one centred in the Lancaster Sound region and another in Jones Sound. Further information may result in splitting this unit into two DUs. ATK also indicated that range overlap of WHB, EHB, and UB DUs was likely in Hudson Strait; and that the WHB, EHB, and JB DUs likely mix in the region of the Belcher Islands in southeast Hudson Bay. There is some interbreeding between animals from different DUs on wintering grounds, but culturally transmitted or learned migration routes may prevent substantial genetic exchange between partially (seasonally) sympatric DUs.

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Introduction

Effective conservation and management of Canadian wildlife requires consideration of species as a whole and of the diversity within each species. Across a species' range, individuals can display considerable morphological, genetic, and behavioural variability that reflects both their plasticity in these traits and their ability to adapt to local environmental conditions. Units below the population level can be critical components of the species and of diversity as a whole. This intraspecific heterogeneity has been long recognized as important but the scale at which to provide protection can be difficult to define.

The approach used to identify putative beluga designatable units (DUs) is based upon COSEWIC guidelines ("*Appendix F5: Guidelines for Recognizing Designatable Units*"). The identification of such DUs can be challenging given the range of traits that exist within a species and level of existing knowledge of those traits, particularly for species with extensive ranges. Designation of DUs must therefore consider all sources of taxonomic, phylogenetic, genetic, morphological, life history, and behavioural information available, in addition to biogeographical information such as range disjunction. Information sources include both scientific knowledge and Aboriginal Traditional Knowledge (ATK), which is increasingly being applied to resource management and conservation in northern regions (Usher 2000).

The Beluga (*Delphinapterus leucas*) is a medium-sized toothed whale (odontocetes) and one of only two species in the Family Monodontidae (along with the Narwhal, *Monodon monoceros*). Belugas have a circumpolar distribution in Arctic and sub-Arctic waters and are widely distributed in Canada. They occur in the coastal waters and estuaries of most territories and provinces that border the Arctic and/or Atlantic oceans including the Yukon, Northwest Territories, Nunavut, Manitoba, Ontario, Quebec (including the St. Lawrence estuary), and Newfoundland and Labrador (Figure 1). Although widely distributed, Belugas show strong fidelity and consistently return to the same coastal regions in the summer. Less is known about winter distribution, which might vary depending on ice conditions. Belugas are important to the subsistence economy and culture of coastal Aboriginal people across the north, and as such there is a significant body of ATK for this species (Cardinal 2013).

To establish the long-term biological foundations of Beluga Whale conservation and management in Canada, COSEWIC undertook a special project to define the DUs for upcoming status assessments and reassessments. Seven populations (DUs) were recognized by COSEWIC in 2004. One of these (St. Lawrence Estuary) was reassessed in 2014. The others will soon require reassessment. Recent formalization of the DU concept by COSEWIC (2014) makes it appropriate and necessary to reconsider the DU scheme for Belugas to ensure that it is consistent with the current guidelines.

Beluga Biology, Ecology, and Distribution in Canada

Belugas, or White Whales, inhabit Arctic and sub-Arctic waters throughout Canada. They lack a dorsal fin, which is generally believed to be an adaptation to living in ice-filled waters. Newborn calves are grey at birth and *ca.* 150 cm in length (Doidge *et al.* 2002), less than half the length of their mothers. Yearling calves are 60-65% of their mother's length (Caron and Smith 1990). As they age, juveniles gradually become paler and are almost pure white upon, or shortly after, reaching sexual maturity (Sergeant 1973;

Heide-Jørgensen and Teilmann 1994). The common name is derived from the Russian word *belukha*, for white. Adult Belugas range in total length from about 2.6 to 4.5 metres and can weigh up to 1,900 kg. Adult females reach ca. 80% of the length of adult males (Brodie 1989; Doidge 1990a). Belugas are gregarious animals often seen in groups of a few to 15 and sometimes in groups of several hundred (Sergeant and Brodie 1975).

The age of Belugas is determined by counting annual growth layer groups (GLGs) in the dentinal or cemental tissues of their teeth. There was debate about whether one or two GLGs represent a year of growth (Sergeant 1973; Perrin and Myrick 1980; Brodie 1989). The most recent COSEWIC (2004) assessment of the species considered the two GLGs per year hypothesis to be best supported. Most recent research, however, supports the one GLG hypothesis (Stewart *et al*. 2006; but see Brodie *et al*. 2013) and this means that the age estimates (*e.g.*, longevity, age at physical or sexual maturity) reported in COSEWIC (2004) need to be approximately doubled. Belugas are long-lived mammals, with mean longevities of 30-60 years and maximum ages of over 100 (Harwood *et al*. 2002, but see Luque and Ferguson 2006, 2010 for potential biases introduced by having different people read tooth layers). A deposition rate of one GLG annually means females and males become sexually mature at 8-14 and 12-14 years of age, respectively (Brodie 1971; Sergeant 1973; Burns and Seaman 1985; Doidge 1990b; Heide-Jørgensen and Teilmann 1994; Stewart *et al*. 2006).

Mating is thought to occur in offshore areas during late winter to early spring (Burns and Seaman 1985), and most calves are born between June and September (Brodie 1971; Sergeant 1973; Cardinal 2013). Gestation lasts 12.8 to 14.5 months (Brodie 1971; Sergeant 1973; Doidge 1990b) and lactation from 20 to 32 months (Brodie 1971; Sergeant 1973; Burns and Seaman 1985; Doidge 1990b; Heide-Jørgensen and Teilmann 1994; Matthews and Ferguson 2015). Scientific data suggest a three-year reproductive cycle (Sergeant 1973; Burns and Seaman 1985) although some ATK holders believe Belugas give birth annually (Cardinal 2013).

Although the season of major feeding likely varies between Beluga populations, Belugas tend to have their lowest blubber depth while in the estuaries in the summer (Doidge 1990c). In summer they begin to feed intensively, often in deep areas that can be far from their centres of summer distribution (Smith and Martin 1994; Richard *et al*. 2001a,b). Belugas feed mainly on fishes including Greenland Halibut (*Reinhardtius hippoglossoides*), Arctic Cod (*Boreogadus saida*), Capelin (*Mallotus villosus*), Saffron Cod (*Eleginus novaga*), Pacific Herring (*Clupea pallasii*), and Least Cisco (*Coregonus sardinella*) (Byers and Roberts 1995; McDonald *et al*. 1997; Kilabuk 1998; Loseto *et al*. 2009; Kelley *et al*. 2010; Cuerrier *et al*. 2012). Various species of invertebrates are also consumed (Sergeant 1962, 1973; Watts and Draper 1986; Loseto *et al.* 2009). McLeod *et al*. (2008) have compiled a field guide of potential and reported prey species of Canadian Belugas.

Belugas are distributed throughout the northern circumpolar region and occur in much of Canada’s northern waters, including the Beaufort Sea, channels and sounds of the Arctic Archipelago, Baffin Bay, Hudson Bay, and the Gulf of St Lawrence (Figure 1). Beluga habitat use varies seasonally and includes both deep offshore areas and shallow coastal waters. During summer, Belugas are often associated with coastal bays and estuaries (Sergeant 1973; Smith and Martin 1994), and they show strong fidelity to these areas from one year to the next (Caron and Smith 1990; Smith *et al*. 1994). There is uncertainty as to whether Belugas use these summering areas primarily for epidermal moulting (St. Aubin *et al*. 1990), feeding, or calving (Stewart and Stewart 1989). ATK holders indicate that Belugas use these shallow, warmer coastal waters to feed, moult, calve, and take refuge from predators (Kilabuk 1998; Brown and Fast 2012; Cardinal 2013). Primary activities in estuaries likely vary by geographical location and time of year.

Most, but not all, Beluga populations follow a similar annual pattern, migrating long distances between summering and wintering areas. Related individuals tend to follow the same routes (Colbeck *et al*. 2013). In late summer the whales begin to move away from their estuarine summering areas. Some populations, such as the High Arctic-Baffin Bay and the Eastern Beaufort Sea populations, make long journeys to deep offshore areas where they spend several weeks diving to the ocean bottom and feeding intensively (Smith and Martin 1994; Richard *et al.* 2001a,b). Belugas overwinter in partially ice-covered areas away from the coast, and aerial surveys in late winter and spring indicate that Belugas are found in loose to moderate pack ice (4/10 to 8/10) or in polynyas (Jonkel 1969; Koski and Davis 1979; Finley and Renaud 1980; Asselin *et al.* 2011; Hornby *et al*. 2016). In general terms, some wintering areas are shared by more than one population but details of winter behaviour (*e.g*., potential for mating) and distribution (*i.e.*, spatial and temporal overlap between DUs) are mostly lacking. In spring Belugas are often seen migrating along the floe edge, following traditional migration routes to their summering grounds (Stirling 1980; Brown and Fast 2012). During spring migrations along the ice edges or in leads they may be seen in aggregations of several hundred animals (Sergeant and Brodie 1975).

Current Taxonomy

The family Monodontidae is thought to have arisen in the middle to late Miocene, based on analyses of full mitogenome sequences (Hassanin *et al.* 2012). The earliest known monodontid (*Denebola brachycephala*) fossil dates from the late Miocene (10.4-6.7 million years ago (mya); location: Baja California) (Rice 1998; Harington 2008). Beluga fossil remains from the Pleistocene have been discovered in Ontario, Quebec, and Vermont suggesting distribution in the Champlain Sea during this epoch (Harington 1977).

Three Beluga subspecies have been named: *D. l. leucas* (Pallas, 1776); *D. l. freimani* Tomilin, 1962; and *D. l. marisalbi* Ostroumov, 1935, but all are considered *nomina dubia* (“doubtful names”) and are not accepted subspecies (Perrin 2014). These subspecies were described by Russian authors (*D. l. marisabli* Ostroumov, 1935 [= *D. l. freimani* Klumov, 1935]; *D. l. dorofeevi* Klumov and Barabash, 1935; and *D. l. leucas* [Pallas, 1776]) based on slight differences in cranial morphology and body size. These divisions of *Delphinapterus leucas* have not been supported by subsequent research (Rice 1998: 97).

The deepest phylogenetic divergence within Canadian Beluga populations has been the identification of two clades, one of which is hypothesized to have descended from Belugas inhabiting a northwest Atlantic refugium and the other derived from a Pacific refugium (Brown Gladden *et al*. 1997; de March and Maiers 2001). Fossil evidence suggests the Atlantic refugium whales were present in the Champlain Sea and reached eastern Hudson Bay by 4320 BP (Harington 2003). Mitochondrial haplotypes diagnostic for this clade are regularly present in the St. Lawrence Estuary (STL) and eastern Hudson Bay (EHB) but are not found in high frequencies in other eastern Arctic regions (Brown Gladden *et al.* 1997; de March and Maiers 2001; Turgeon *et al*. 2012) and are absent in the western Arctic and Bering Sea (O'Corry-Crowe *et al*. 2010; Meschersky *et al*. 2013). The clade representing the Pacific refugium consists of numerous closely related haplotypes that are distributed throughout the circumpolar Arctic (Brown Gladden *et al*. 1997; de March and Maiers 2001; O'Corry-Crowe *et al*. 2010; Meschersky *et al*. 2013). In general, Belugas show more genetic structuring between sub-Arctic and Arctic waters than they do across the circumpolar Arctic (O'Corry-Crowe *et al*. 2010).

Up to 29 Beluga management stocks have been identified across the species' circumpolar range, with between five and seven assigned to whales in Canadian waters (International Whaling Commission 1992, 2000). These stocks are generally based on the locations of summer aggregations.

Current DU Structure of Belugas in Canada

The most recent assessment of Belugas in Canada recognized seven DUs (COSEWIC 2004). These are: (1) the Eastern Beaufort Sea (EBS) population; (2) the Eastern High Arctic - Baffin Bay (EHA-BB) population;(3) the Cumberland Sound (CS) population; (4) the Ungava Bay (UB) population; (5) the Western Hudson Bay (WHB) population; (6) the Eastern Hudson Bay (EHB) population; and (7) the St. Lawrence Estuary (STL) population (Figure 1, Table 1). These populations had already been recognized by the Department of Fisheries and Oceans (DFO) Canada for management purposes, and COSEWIC assessments for several of the populations date to the early or mid-1980s (*e.g.,* Pippard 1983 for the STL population; Finley *et al*. 1985, 1987 for the EBS population). The Cumberland Sound population had previously been designated by COSEWIC as the Southeast Baffin Island/Cumberland Sound population. In 2004, the structure of this population was redefined and the southeast Baffin Island component included as part of the western Hudson Bay population (COSEWIC 2004).

Methods

Sub-units of a species are variously defined as "populations" and "stocks" among many other terms. There is considerable debate as to how these sub-units can or should be differentiated (Stewart 2008). In this report, DUs are identified based on the guidelines provided by COSEWIC (2014) wherein: "*Designatable Units should be discrete and evolutionarily significant units of the taxonomic species, where "significant" means that the unit is important to the evolutionary legacy of the species as a whole and if lost would likely not be replaced through natural dispersion.*"

Since the last Beluga assessment in 2004, COSEWIC has refined the definition of Designatable Units and its guidelines for recognizing them (COSEWIC 2014a). DUs can be recognized if they are named subspecies or varieties or through a two-step process of evaluation. In this evaluation, potential DUs are evaluated as to their discreteness from other DUs and then as to their evolutionary significance relative to other DUs. Discreteness can refer to distinctiveness in genetic characteristics including inherited traits, natural disjunction between large portions of the species range, or ecological isolation. Discreteness is meant to encompass existing genetic differentiation and the circumstances and processes that could lead to local adaptations. Once discreteness has been established, significance is examined. Evolutionary significance may apply when there is evidence: 1) of deep intraspecific phylogenetic divergence, 2) that the population or group of populations persists in an ecological setting that is unusual or unique for the species and is known or likely to have given rise to local adaptations, 3) it is the only surviving natural occurrence when other populations exist as introduced species outside of the natural range, or 4) that the loss of the discrete population would result in an extensive gap in the range of the species in Canada that is unlikely to be re-inhabited by natural dispersal. The guidelines also recognize that some criteria may provide more compelling evidence of “discreteness” and “significance” than others. Therefore, we have endeavored to present the best available evidence for all criteria that are met.

Determining Putative Designatable Units

The guidelines explicitly allow subspecies to be considered as DUs, but no Beluga subspecies are recognized so this criterion is not relevant.

Beluga populations (as defined by COSEWIC 2004) and stocks (as defined by DFO 2010) are generally identified on the basis of their estuarine centres of aggregation during the summer open-water season. In most cases the summer distribution of one population is separate from other populations. In many cases, however, the winter range and migratory route(s) are contiguous with or overlap those of other populations. Although Belugas from discrete summering areas may mix at other times, the evidence from estuaries where they have been over-exploited suggests that once Belugas have been hunted out (extirpated) from a summering area, recolonization is likely to take a very long time, i.e. a significant gap is created in the species’ distribution and that gap is likely to persist indefinitely.

We evaluate five lines of evidence for discreteness and significance as listed in the COSEWIC DU guidelines (COSEWIC 2014a), modeled after a recent report that used the same lines of evidence to determine DUs for caribou (*Rangifer tarandus*) in Canada (COSEWIC 2011). Aboriginal Traditional Knowledge (ATK) (Cardinal 2013), which often overlaps science-based criteria (*e.g.*, Inuit knowledge of morphological differences and of spatiotemporal segregation), was included in the different lines of evidence as appropriate.

We began by considering the known groupings that were recognized as DUs in 2004 by COSEWIC (2004). We examined available evidence for each defined population, evaluating whether or not such units were discrete and significant with respect to other units, with a focus on neighbouring units. We also examined this evidence to determine whether any sub-units within the described populations merited separate DU status. In this manner, we evaluated units and their neighbours systematically, ultimately ensuring that all known geographical populations or areas with Belugas in Canada had been included in our analysis. Recognition of each DU was made in the context of the best available science and ATK as interpreted by the writers of this report, the Marine Mammals Specialist Subcommittee of COSEWIC, and independent and jurisdictional reviewers.

Belugas present a challenge for evaluating DUs due to the vast area occupied by the species and overlapping migration routes and wintering areas for geographically separated summer aggregations. Gene flow may result if this overlap occurs during the breeding season. In Canada, Beluga populations are, or were before being overhunted (in some cases to severe depletion), quite large. This, when coupled with long life-spans and overlapping generations, tends to preclude genetic differentiation even in the presence of strong barriers to gene flow. In addition, the amount of data available on which to base the designations is limited in geographical scope, which makes it difficult to undertake comprehensive comparisons across the entire range of the species in Canada.

The location and extent of putative DUs are shown in Figure 1, and summaries of the extent and strength of the evidence for the putative DUs are presented in Tables 3-7.

Lines of Evidence used to Evaluate Discreteness and Significance Criteria for DU Recognition

Two recent compilations summarize information related to the identification of DUs for Belugas, and both were referred to extensively when examining the existing COSEWIC (2004) DUs. The information they contain was examined in light of the five lines of evidence detailed below.

The first compilation is a Fisheries and Oceans Canada (DFO) Research Document that provides information relevant to the definition of Beluga stocks in Nunavut. It was prepared in response to a request from the Nunavut Wildlife Management Board (NWMB) for clarification on the rationale for providing science advice on the basis of summering stock aggregations rather than at the population level (Richard 2010; also see DFO 2010). Summer stock definitions were derived from various sources, including: (1) studies of the seasonal range of the species in Nunavut and adjacent waters (both local observations and written reports), (2) differences in appearance and behaviour of animals from different areas, (3) studies of genetic and contaminant differences of animals from different areas, and (4) satellite-tracking of animals to estimate their seasonal range and delimit areas of aggregations (Richard 2010; DFO 2010). Using all available data, DFO and its co-management partners identified six Beluga summer stocks in Nunavut. Further definition of these stock definitions was complicated by overlap in their migrations and wintering areas. Consequently, these summer stocks were considered provisional management stocks, on the understanding that new information would be taken into consideration to revise the list if needed. Using summering stocks as management units is considered precautionary by DFO, as otherwise harvesting could cause local depletions or extirpations (Cope and Punt 2009).

The second compilation is the Aboriginal Traditional Knowledge (ATK) Beluga DU report prepared for the ATK Subcommittee of COSEWIC (Cardinal 2013). COSEWIC defines ATK as including but not limited to “the knowledge Aboriginal Peoples have accumulated about wildlife species and their environment” (COSEWIC 2012). ATK is amassed through generations and exists at both the community and individual levels. Belugas are an important socio-economic and cultural resource for Aboriginal people across the north, and have been harvested by northern Aboriginal people for many generations (*e.g.*, McGhee 1974; Tremblay 1993). A substantial body of ATK is therefore available for most Beluga populations in Canada. The ATK compiled by Cardinal (2013) was combined with available scientific knowledge to conduct a comprehensive assessment of DU structure for beluga whales in Canada. Eight different DUs were identified for Canadian Belugas on the basis of ATK (including the seven recognized by COSEWIC 2004). Identification of DUs was largely based on distinct migration routes and summer distributions for each DU. The Beluga population aggregations identified by the three studies (COSEWIC 2004; Richard 2010; Cardinal 2013) are summarized and compared in Table 2.

1. Phylogenetics

Phylogenetic lines of evidence are derived from genetic markers that reveal divergences between clades over long time scales (100s to 1000s of generations). Phylogenetic patterns are generally inferred from comparisons of nucleotide sequences, but deeper divergences can be inferred from other sources such as gene order (Sankoff *et al*. 1992). Phylogeographic patterns in Belugas have been inferred only using data from the mitochondrial genome (Brennin *et al*. 1997; Brown Gladden *et al*. 1997). Mitochondria are cellular organelles that carry a separate genome that is passed from mother to offspring without recombination (maternally inherited). Portions of the mitochondrial genome are widely used in studies of wildlife because they are easy to sequence and the maternal inheritance pattern reduces the effective population size and increases the rate of lineage sorting (Harrison 1989; Avise 1994; Moritz 1994). These traits have allowed for the differentiation of unique groups on faster time scales than other portions of the genome.

To date, all phylogenetic studies of Belugas have used partial mitochondrial control region sequences to infer evolutionary history. This region is pseudo-neutrally evolving in that it is not under direct selection because its function is a result of its conformational shape rather than its sequence of nucleotides (Shadel and Clayton 1993; Sbisà *et al*. 1997). It is, however, linked to a number of other genes on the mitochondrial genome and therefore can be influenced by selective sweeps (Charlesworth 1992; Galtier *et al.* 2000).

While there are several large and presumably longstanding barriers to gene flow in the species' range (*e.g.*, ice cover in the central Arctic), only one deep phylogenetic divergence has been observed. This genetic split in mitochondrial control region sequences separates Belugas into two clades and is hypothesized to be the result of isolation of Belugas in either Pacific or northwest Atlantic refugia (western and eastern haplotype assemblages, respectively) during the Wisconsinian Glaciations (Brennin *et al*. 1997; Brown Gladden *et al*. 1997). Haplotypes from the Atlantic refugial group are primarily found in animals sampled from the St. Lawrence Estuary (STL) and eastern Hudson Bay (EHB) (Brennin *et al*. 1997; Brown Gladden *et al*. 1997; de March and Postma 2003; Turgeon *et al*. 2012). Pacific refugium haplotypes are found in animals throughout the rest of the species' circumpolar distribution (O'Corry-Crowe *et al*. 2010; Turgeon *et al*. 2012; Meschersky *et al*. 2013), but not in the St Lawrence estuary (Figure 3).

The phylogenetic split formed by these two refugia creates two monophyletic groups but the current distribution of animals that carry the haplotypes is more complex. Atlantic refugium haplotypes are found occasionally, and in small numbers, in whales taken in Hudson Bay communities outside the EHB summer range (Brown Gladden *et al*. 1999; Turgeon *et al*. 2009, 2012). Similarly, Pacific refugium haplotypes are observed in animals harvested in EHB communities.

2. Genetic Diversity and Structure

Recent (10s of generations) and contemporary gene flow in wild populations can be used to develop hypothetical DUs where the inferred barriers to gene flow either support the discreteness of a unit as an evolutionarily significant unit with local adaptations or suggest that a loss of that unit would produce a gap in the range. Barriers to dispersal (natural or anthropogenic) and subsequent reduced gene flow can be a result of physical formations (*e.g.,* land masses, ice masses) or behavioural patterns (*e.g.*, natal fidelity).

In Belugas, and many other species, the primary markers to examine DU structure on contemporary time scales have been mitochondrial control region haplotype frequencies (reduced unique sequences) and nuclear microsatellite loci (neutral markers). These genetic markers are discussed below in addition to a third class of markers that has been applied to the DU question in Belugas - nuclear genes that are under selection.

Haplotype frequencies

The natural history of Belugas coupled with the maternal inheritance pattern of mitochondria is such that natal fidelity to estuaries can be detected using haplotypes and haplotype frequencies (Brown Gladden *et al*. 1997; O'Corry-Crowe *et al*. 1997). Belugas learn the locations of summer aggregations and wintering areas and the routes between them from their mothers (Colbeck *et al*. 2013; see also ATK summarized by Cardinal 2013). Female Belugas and their female offspring form maternal lineages that are detected using haplotype frequencies. Turgeon *et al*. (2012: 424) observed that summer locations explained a higher proportion of the genetic variance for females than for males.

A number of the current DUs are identified by unique mixtures of haplotypes. For example, EHB Belugas primarily carry one of the following haplotypes: hap 7, 17, or 18 (de March and Postma 2003; Turgeon *et al*. 2012). Analyses conducted on samples taken from locations along migration routes in the spring and autumn typically are more difficult to interpret, although there is evidence of fidelity to these routes as well (Colbeck *et al*. 2013). In the early years of using genetics as a management tool, DU structure was confounded by the inadvertent sampling of related pods of animals where yearly variation in sampling of maternal lineages and small sample sizes suggested higher degrees of differentiation among locations than are now considered plausible (Palsbøll *et al*. 2002). Subsequent to the realization that this was leading to spurious results, studies have used larger samples, collected over multiple years, and/or the samples have been checked for closely related individuals (de March and Postma 2003).

Microsatellites

Complementing the analysis of mitochondrial DNA (mtDNA) in most wildlife population genetics studies is the use of neutral markers, called microsatellites, found within the nuclear genome and representing both the male and female contributions to gene flow. These genetic markers are used primarily to detect contemporary gene flow although long standing barriers may also be detected. Of significance to wildlife population studies, microsatellite markers are a measure of total gene flow but can also be used to infer male-mediated gene flow when they show a contradictory pattern to mtDNA, which is maternally inherited.

Microsatellite data have often been used to examine population structure in Belugas (Brown Gladden *et al*. 1997; Brennin *et al*. 1997; de March and Postma 2003; Meschersky *et al*. 2008; O'Corry-Crowe *et al*. 2010; Postma *et al*. 2012; Turgeon *et al*. 2012; Colbeck *et al*. 2013; Meschersky *et al*. 2013). Unfortunately, no study to date has analyzed samples from across the entire species' range and only three have used Bayesian methods, which have become the standard for population genetics investigations (O'Corry-Crowe *et al*. 2010; Postma *et al*. 2012; Turgeon *et al*. 2012). Individual-based Bayesian analysis allows the data to dictate the number of genetic clusters based on population genetics theory. Bayesian analysis has an advantage compared to frequency-based methods in that the data, not the researcher, determine the groups. This is especially important in Belugas, where significant numbers of samples come from outside the mating season and/or from mixed-stock harvests.

O'Corry-Crowe *et al*. (2010) examined Beluga samples from the circumpolar Arctic excluding Canada using Bayesian methods and suggested that two genetic clusters could be identified corresponding to the Arctic (represented by samples from Svalbard, White Sea, Greenland, and Beaufort Sea) and sub-Arctic (represented by samples from the Gulf of Alaska). They suggest that EBS and Svalbard have experienced recurring periods of gene flow, likely occurring along the Siberian coast. Turgeon *et al*. (2012) used a Bayesian analysis and found no genetic clusters corresponding to CS and Hudson Bay groups. This suggests that Bayesian analysis of Canadian samples from across the entire range (but excluding STL) may show very little or no genetic differentiation in spite of some presumed long standing barriers to gene flow such as the multi-year ice between breeding areas in the eastern and western Canadian Arctic. This may be the result of low but constant levels of gene flow among DUs or could be due to the combination of high population sizes coupled with life history characteristics (long life span, overlapping generations) that limit genetic drift and population differentiation.

Brown Gladden *et al*. (1999) analyzed microsatellite frequencies (not using Bayesian analysis) in Beluga samples within the Canadian range and observed differentiation between the western Canadian Arctic (represented by samples from the Beaufort and Bering Seas) and eastern Canadian Arctic[1] (represented by samples from the Canadian Arctic Archipelago and Hudson Bay) and West Greenland. Frequency analysis of microsatellite markers has revealed differentiation among some DUs in eastern Canada, although most studies to date have taken a regional approach and have not examined samples from the entire range.

Other markers

Genes that are under selection, in particular two genes in the Major Histocompatability Complex (MHC), have been used to examine DU structure in Belugas. This gene complex is thought to be involved in immune response so groups of animals that have experienced similar selective pressures from disease may share MHC alleles. In general, genes under selection may show local adaptation and be useful for determining DU structure. In practice, patterns of allelic similarity or differences in genes associated with immune function, like MHC, can be difficult to interpret in an evolutionary context. Murray *et al*. (1995) examined Belugas from across the Canadian range and found those in High Arctic (Grise Fiord, Creswell Bay, and Cunningham Inlet) to be differentiated from all other regions.

3. Morphology

Geographical variation in body size between Belugas collected in different parts of the Arctic was the first evidence used to discriminate among populations (Sergeant and Brodie 1969; Brodie 1971). Additional examination of the data and methods of analysis confirmed that minor differences do occur, for example Doidge (1990a) found that Belugas from eastern Hudson Bay tend to be smaller than those from most other eastern Canadian Arctic locations. Stewart (1994) used samples from additional locations and concluded that Belugas from western Hudson Bay were smaller than those from the High Arctic and Southeast Baffin, but were as large as those from eastern Hudson Bay. Harwood *et al*. (2002) presented asymptotic lengths of male Belugas from the eastern Beaufort Sea, which were similar to those from Cumberland Sound and Alaska (Doidge 1990a). Stewart (1994) suggested that body size differences were of waning importance to population identity issues when considered in light of new genetic population discrimination techniques, and Doidge (1990a) noted that differences did not occur to a degree that they might offer practical criteria to differentiate adjacent Beluga populations.

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[1] In Canada, the eastern and western Arctic has been divided roughly by the division between the Northwest Territories and Nunavut. This division also follows the area of permanent, multi-year ice that historically divided the Canadian Arctic Region.

Luque and Ferguson (2006, 2010) compared age structure and body-length distribution (both sexes separately) among five Beluga populations in the Canadian Arctic: eastern Beaufort Sea, Baffin Bay, Cumberland Sound, western Hudson Bay, and eastern Hudson Bay. Growth showed a significant positive relationship with latitude: EBS Belugas were significantly longer and their growth rate differed, relative to eastern Arctic populations, revealing a geographical gradient in a south to north-northwest direction, so that EHB Belugas were the smallest. Age distributions of harvested animals also differed among populations in their shape. Latitudinal variation in growth and adult body size supported the hypothesis that environmental seasonality imposes stronger constraints on life-history traits of Belugas with increasing latitude (Luque and Ferguson 2006, 2010).

Care must be exercised when using morphological features to support the discreteness or significance of a specific DU. Differences in morphological features, which are summarized in Table 3, may represent inherited traits that are locally adapted but alternatively they can represent normal variation in plastic traits over an environmental gradient. Differentiating between developmental plasticity and local adaptation requires large sample sizes to capture as much variation as possible. Most research correlates morphological differences with environmental variables (*e.g.*, see Luque and Ferguson 2006, 2010 above). Common garden experiments (*e.g.*, taking Belugas from one area to another area and seeing if they grow up to look like animals in the source or the destination population) would be needed to establish what proportion of the physical differences are genetically based. Such experiments are not feasible but genomic methods that are being developed may provide an alternative in the future. A recent study by Harwood *et al.* (2014) found changes in eastern Beaufort Sea Belugas over a period of only a few decades, suggesting that growth (age at length at least) is plastic, and likely related to environmental factors.

Size and internal differences have been noted by Arctic hunters who harvest and consume Belugas (Thomsen 1993; Kilabuk 1998). Size, colour, taste, and blubber thickness are differences identified by hunters as indicative of morphological differences (Cardinal 2013). These differences may be linked to fundamental differences in habitat and prey consumption that distinguish sets of animals with shared ecology.

4. Movement, Behaviour, and Life History Strategies

During summer, Belugas are found in both coastal and offshore areas, with the distribution of most DUs centred on estuaries (Sergeant 1973; Sergeant and Brodie 1975; Smith and Martin 1994; Smith *et al*. 1985). While in estuaries Belugas are moulting, feeding and/or calving (Stewart and Stewart 1989; St. Aubin et al. 1990; Cardinal 2013), but the primary reason(s) for their use of estuaries in the summer is not fully understood and might vary from one area to another (COSEWIC 2004). Shallow-water estuaries might provide protection from Killer Whale (*Orcinus orca*) predation (Brodie 1971), but also increase vulnerability to disturbance, Polar Bear (*Ursus maritimus*) predation, and human harvesting, especially considering the strong philopatric behaviour of Belugas (Caron and Smith 1990; Smith *et al.* 1994).

The preference of Belugas for specific summer aggregation sites has long been known. The Hudson's Bay Company (HBC) and later commercial whalers took advantage of this knowledge to harvest Belugas in Hudson Bay, beginning in 1668 and continuing until 1970 (Reeves and Mitchell 1989a). They exploited Belugas in numerous areas, including the Mucalic Estuary in Ungava Bay (Finley *et al.* 1982; Reeves and Mitchell 1987c, 1989b), the Great Whale River in eastern Hudson Bay (Francis 1977; Reeves and

Mitchell 1987b, 1989b), Clearwater Fiord in Cumberland Sound (Reeves and Mitchell 1981; Stewart 2004), the Churchill River estuary in Manitoba (Doan and Douglas 1953; Reeves and Mitchell 1989a), the high Arctic (Reeves and Mitchell 1987a), the Mackenzie River Delta (Flyger 1965; Nuligak 1966; McGhee 1974) and the St. Lawrence Estuary (Reeves and Mitchell 1984, 1987d). Intensive commercial harvesting may have extirpated at least one population (Ungava Bay) and left others depleted (CS, EHB) (COSEWIC 2004). ATK holders have substantial knowledge of Beluga summer aggregation areas (Cardinal 2013) and their ancestors were harvesting Belugas long before the first Europeans arrived in the St. Lawrence (Reeves and Mitchell 1987d) and in the Arctic (*e.g.*, McGhee 1974; Savelle 1994).

Prior to autumn migration, whales begin to move out of the estuaries and begin to exhibit migratory behaviour (Sergeant 1973; Smith 2007). During this time some individuals in some populations (*e.g.*, EHA-BB, EBS) make long-distance trips to offshore deep-water areas where they spend several weeks diving intensively to the bottom and presumably foraging (Smith and Martin 1994; Richard *et al.* 2001a). The whales then begin to move toward their wintering areas in the autumn. Belugas often overwinter in open water away from coastal regions, in polynyas, or loose pack ice (*ca.* 4-10/10s) (Jonkel 1969; Finley and Renaud 1980; McDonald *et al.* 1997; Lewis *et al.* 2009). In the spring Belugas are often seen migrating along the floe edge on their traditional migration routes to summer aggregation areas (Cardinal 2013).

Migration routes and overwintering areas are less well characterized than the summer aggregation areas. A number of studies present data on movements determined using satellite telemetry, although many are limited by small sample sizes and short tag durations. Movement data were used, when available, to assess the discreteness of putative DUs by evaluating the extent of overlap in areas used during migration and winter. The tags are affixed at summer aggregation sites and transmit for a limited period before failing, often during migration, although the transmission life and length of attachment time for whale tags has increased over time. Extensive ATK is also available on Beluga migration timing and migration routes, albeit often limited to coastal regions (Cardinal 2013).

Belugas in most DUs have a similar annual pattern, with well-defined summer and winter ranges and movement routes between the two. While there is variation in migration timing and distance (*e.g.*, EBS Belugas travel much longer distances than do CS, JB, or STL Belugas), life-history strategies are generally similar across the Canadian range. Movement patterns can be used to indicate the extent to which a DU is spatially and temporally separated from other DUs. Movement data were used here to assess the discreteness of Beluga DUs by evaluating the extent of movement across the range of other DUs (*i.e.*, overlap in space and time) (see also next section below).

5. Distribution

Evidence of disjunction between substantial portions of the species' geographic range is an important consideration for the identification of DUs. Summer aggregation patterns, along with genetic divergence, were major determinants of the DU structure for the previous assessment (COSEWIC 2004) and also for the "summer stocks" currently recognized by DFO (Richard 2010).

Delineation of geographical populations based on summer distributions has a long history (Sergeant and Brodie 1975; Smith *et al.* 1985) and is supported by behavioural studies in estuaries, which showed that Belugas are philopatric and strongly site tenacious (Caron and Smith 1990; Smith *et al*. 1994). Genetic and telemetry studies also support the distinctiveness of the summer aggregations (Brown Gladden *et al.* 1997, 1999; Richard *et al*. 2001a,b; de March *et al*. 2002; de March and Postma 2003; Loseto *et al.* 2006; Lewis *et al.* 2009; Bailleul *et al.* 2012). The DUs assessed previously by COSEWIC (2004) all have coastal/estuarine centres of aggregation during the summer open-water season. In most cases their summer coastal and offshore distributions are separate from other populations, although autumn, winter, and spring ranges are often contiguous or overlapping.

Numerous ATK studies (*e.g*., Read and Stephansson 1976; Remnant and Thomas 1992; Byers and Roberts 1995; Stewart *et al*. 1995; McDonald *et al*. 1997; Kilabuk 1998) describe the separate and discrete movements of Belugas in different areas of the Canadian Arctic, which provides an indication of range disjunction between units when examined regionally (see also Stewart 2001). Genetic evidence suggests that Beluga groups may intermix in offshore wintering areas (*e.g.*, Turgeon *et al*. 2012), and special consideration was given to winter distribution and the timing and location of migration routes. However, with respect to ATK, there is significant information regarding summer distribution and migration patterns, but much less is known about distribution patterns during winter months. As noted above, movement data collected using scientific approaches (*e.g.,* satellite-tagging) are also deficient outside the summer period. This stems from a general lack of winter aerial surveys in comparison to summer, in part due to logistical difficulties with surveys during the darkness of winter, and satellite transmitters not lasting long enough to provide data through the migration and/or winter periods.

Table 4 shows pairwise comparisons of the extent of overlap between the various DUs for three different seasons: summer, winter, and migration (spring and fall). In most cases, summer distribution (both coastal and offshore regions) is separate from other populations (DUs), but winter ranges and migration routes are sometimes contiguous or overlapping (COSEWIC 2004).

Other information sources considered

Vocalization patterns (*e.g*., dialects) have proven useful for differentiating population groupings of cetaceans (*e.g.*, Filatova *et al*. 2012; Garland *et al*. 2015a) and could be useful in the future for differentiating beluga populations. Historically, Belugas were referred to as the “canaries of the sea” because they are highly social, extremely vocal, and produce a broad repertoire of sounds. Their vocalizations have been well-studied in both captive and wild individuals and their vocal repertoire has been classified for populations across the species’ range, including some Canadian DUs: STL (Faucher 1988; Lesage *et al*. 1999), EHA-BB (Sjare and Smith 1986), WHB (Chmelnitsky 2010; Chmelnitsky and Ferguson 2012), and EHB (Garland *et al*. 2015b). Many similarities exist in the call types of animals from different regions, but there are also novel call types that suggest geographical differences exist among distant populations (Karlsen *et al*. 2002). Vocal classifications are often done in a subjective manner that makes comparisons difficult (Chmelnitsky and Ferguson 2012), and Belugas have a graded call system with a continuum of call types that adds difficulty to classification approaches (Garland *et al*. 2015b). Studies to date have primarily been descriptive in nature, with no major efforts to provide a functional analysis of calls (Vergara *et al*. 2010). At present there are no comparable data to inform an assessment of Canadian DUs. But Garland *et al*. (2015b) recently established a robust and repeatable methodology that could be used to compare call repertoires of different Beluga DUs in a structured manner.

Dietary markers (fatty acids and stable isotopes) provide other possible lines of evidence for DU structure. There has been research on Beluga dietary markers for some Canadian DUs including: STL (Lesage 2014), EHA-BB (Matley *et al*. 2015), WHB (Kelly *et al*. 2010); EBS (Loseto *et al*. 2009), EHB (Rioux *et al*. 2012) and CS (Marcoux *et al*. 2012), but there are no comparisons across different DUs. These dietary markers are therefore not discussed any further in the report. Future comparison and interpretation of dietary markers will be confounded by the extent of the Belugas' seasonal migrations and their sometimes-overlapping distributions, both of which affect dietary exposure.

Disease and contaminant data were also reviewed to assess their value in identifying DUs. Neither of these information sources proved to be particularly informative and they are summarized here in a general manner rather than in detailed sections for the individual DUs. Where relevant, brief mention is provided in the individual DU descriptions.

Diseases

Disease information (*e.g.*, Nielsen *et al.* 2000, 2001a,b, 2004; Phillipa *et al.* 2004; Maggi *et al.* 2008) was examined to determine if animals in one area have been exposed to a virus, bacterium, or other pathogen (*i.e.*, have antibodies) while those in other areas have not, thus providing possible evidence of discreteness. DFO has conducted disease surveillance projects across the Canadian Arctic since the mid-1990s in response to Inuit concerns about subsistence food safety (reviewed in Nielsen *et al.* 2004), but there has been no consistent effort to monitor a suite of diseases across the full range of Belugas. Sample sizes for disease-related studies are typically small when considered on a population-by-population basis. Serological surveys for antibodies to morbillivirus, *Brucella* spp., and influenza A have been conducted for Belugas across the Canadian Arctic and in the Gulf of St. Lawrence (Nielsen *et al.* 2000, 2001a,b).

None of the 445 hunter-harvested Belugas from Arctic waters (covering four of the populations considered in COSEWIC 2004) had antibodies to dolphin morbillivirus (DMV) above the threshold serum dilution, and none of the 18 beach-cast Beluga carcasses from the Gulf of St. Lawrence were positive for antibodies to DMV (Nielsen *et al.* 2000; see also Phillipa *et al.* 2004).

A serological survey of antibodies to *Brucella* spp. (Nielsen *et al.* 2001a) included samples from 463 hunter-harvested Belugas from 18 Arctic locations plus 25 beach-cast whales from the St. Lawrence Estuary. Five of the COSEWIC (2004) Beluga populations were sampled, and samples from all five tested positive (28 of 488 samples (5.7%) overall) (Nielsen *et al.* 2001a). There was no significant difference in antibody prevalence related to sex, but juvenile Belugas were significantly more likely to have antibodies to *Brucella* spp. than adults.

Samples from many of the same whales (n = 418 total, sampled in NT and NU including populations from four of the DUs covered in COSEWIC 2004) were used in a serological survey of influenza A antibodies (Nielsen *et al.* 2001b). Only five of 418 (1.2%) Belugas were serologically positive, and all positive samples were identified from communities on southeast Baffin Island (Cape Dorset, Kimmirut and Iqaluit). Nielsen *et al.* (2001b) considered influenza A infection in Arctic marine mammals to be sporadic and probably self-limiting.

Other infectious agents that have been identified in Belugas include phocine herpes, dolphin rhabdovirus, and canine adenovirus (Nielsen *et al.* 2004; Phillipa *et al.* 2004). The pathogenic bacterium *Bartonella henselae* was detected in two of three samples from hunter-harvested Belugas in the Mackenzie Delta (Maggi *et al.* 2008), but has not been surveyed for in other regions.

Disease monitoring by DFO has continued since 2004 but more recent studies have not been published. Ultimately there is little value of disease monitoring for stock discrimination, as the same diseases (or absence thereof) are found from the Gulf of St. Lawrence to Alaska (O. Nielsen, DFO Winnipeg, pers. comm.).

Contaminants

Contaminant information (*e.g.*, Tomy *et al.* 2000; Innes *et al.* 2002a; de March *et al.* 2004; Braune *et al.* 2005; Lockhart *et al.* 2005; Stern *et al.* 2005; Martineau 2012) was examined, where available, to compare putative DUs. A difficulty with these data is getting comparable information given differences in animal age, sampling years, monitoring intensity, etc. Contaminant studies generally provide information that demonstrates differences in dietary exposure to contaminants but are of limited value for determining discreteness (summarized in Table 5).

Levels of C10−C13 polychloro-n-alkanes (sPCAs) from the blubber of Belugas from West Greenland were similar to those in Belugas from the Mackenzie Delta (Tomy *et al.* 2000). sPCA levels were 6-8 times higher in blubber from St. Lawrence Belugas, with higher proportions of the less volatile sPCA congeners compared to the predominance of the shorter chain length lower percent chlorinated PCA congeners in the Arctic samples. These observations were consistent with long-range atmospheric transport of sPCAs to the Arctic and local source contamination in the St. Lawrence River estuary (Tomy *et al.* 2000; Braune *et al.* 2005). Mean polychlorinated biphenyl (PCB) levels (ng/g) in blubber of male Belugas were largely similar across different regions, with the exception of the St. Lawrence River where levels were and are elevated (Martineau 2012). With respect to total mercury, early analyses suggested that Belugas in the western Canadian Arctic had higher levels than those in the eastern Canadian Arctic, but these regional differences have diminished over time and are no longer statistically significant (Lockhart *et al.* 2005).

Innes *et al.* (2002a) used concentrations of organochlorine contaminants (OC) in Beluga blubber to discriminate between stocks. Blubber samples were obtained from Belugas harvested by hunters from seven locations and from biopsies of live-captured Belugas near Churchill, MB. A Canonical Discriminant Analysis was able to separate all seven sampling locations from each other, with over 90% successful sample classification. de March *et al.* (2004) extended the work of Innes *et al.* (2002a) and examined putative stock differences in Belugas harvested by hunters from the southeast Baffin Island communities of Kimmirut, Iqaluit, and Pangnirtung using OC profiles and molecular genetics. OC concentrations were generally lower in Belugas from Pangnirtung than those hunted in the other two communities. A Canonical Discriminant Function analysis separated whales from Pangnirtung from those in Iqaluit and Kimmirut, and the results were in agreement with findings from molecular genetic analyses (de March *et al.* 2002). In a combined analysis that used both OC profiles and genetics, many whales were slightly more strongly associated with a particular community than they were in the original studies (de March *et al.* 2004). The relative tissue levels of several OC compounds were similar in Belugas over large spatial areas, but there were some distinct compounds that allowed populations to be differentiated (*e.g.,* Beaufort Sea compared to Hudson Bay) (Stern *et al.* 2005).

Three studies (Innes *et al.* 2002a; de March *et al.* 2004; Stern *et al.* 2005) demonstrate the value of organochlorine contaminant concentrations for examining stock structure in Belugas, and generally agree with the results of genetic and movement and distribution studies which are discussed in greater detail below.

Beluga Designatable Units

Eight Beluga DUs can be identified on the basis of the COSEWIC DU criteria for discreteness and significance. These are:

- DU1: Eastern Beaufort Sea (EBS),
- DU2: Eastern High Arctic – Baffin Bay (EHA-BB),
- DU3: Cumberland Sound (CS),
- DU4: Ungava Bay (UB),
- DU5: Western Hudson Bay (WHB) (now referred to as the Western-Northern-Southern Hudson Bay summer stock by DFO, Richard 2010),
- DU6: Eastern Hudson Bay (EHB),
- DU7: St. Lawrence Estuary (STL), and
- DU8: James Bay (JB).

This includes the seven DUs assessed in 2004, plus a new James Bay DU (formerly considered part of WHB).

DU1: Eastern Beaufort Sea (EBS)

Belugas comprising the EBS DU have an extensive Canadian range, with an extent of occurrence (EO) of *ca.* 591,000 km², and area of occupancy (AO) of 445,000 km² (COSEWIC 2004). Whales in this DU leave Canadian waters for much of the year. Genetic samples from this region have been collected primarily from animals in the Mackenzie Delta, Husky Lakes, and waters near Paulatuk, Northwest Territories.

Lines of Evidence

1. Phylogenetics

Haplotype sequences of EBS Belugas place them in the Pacific clade (Brown Gladden *et al.* 1997, who called it the 'Western' clade). In recent history (~1000s of years), sea ice has limited or prevented dispersal between the eastern and western Canadian Arctic but this has not been sufficient to create a monophyletic split between the two regions (Brown Gladden *et al.* 1997). O'Corry Crowe *et al.* (2010) examined samples from several locations across the Arctic, but excluding Canada, and found greater genetic structure between Arctic and sub-Arctic samples than among circumpolar Arctic samples. Therefore, it seems that currently there is no phylogenetic (deep divergence) evidence for distinguishing this DU from others in Canada with the exception of EHB and STL, which are part of the Atlantic clade (Brown Gladden *et al.* 1997).

2. Genetic Diversity and Structure

Genetic evidence from haplotype frequencies and microsatellite differentiation among locations (measured in F_{ST} or its analogs) has generally supported the separation of eastern and western Arctic Belugas (Brown Gladden *et al.* 1999). Early work on Beluga genetics compared EBS to EHB or STL and, not surprisingly, found significant differentiation between east and west (Helbig *et al.* 1989; Cummings 1990; Brennin *et al.* 1997; Brown Gladden *et al.* 1997). Unfortunately, subsequent research has focused on eastern or western Belugas and has not included available samples from all Canadian locations. Recent work by L. Postma (unpublished) combines all Canadian samples and highlights mitochondrial haplotype frequency differences (Figure 2). The similarity of the colouration of the different pie charts in Figure 2 indicates mtDNA relatedness among DUs and sites, but there is deeper structure which is not revealed by the pie charts. For instance the Eastern Hudson Bay and St Lawrence Estuary haplotype distributions show no overlap in haplotype frequencies, but they are more related than either is to any of the other DUs.

Bayesian analysis found evidence for two genetic clusters corresponding to Arctic and sub-Arctic groups (O'Corry-Crowe *et al.* 2010). Within the Arctic Ocean there was "low" genetic structure between samples from Svalbard and the Eastern Beaufort Sea and "moderate" structure between samples from West Greenland and Svalbard/ EBS (O'Corry-Crowe *et al*. 2010). These results suggest recurring periods of gene flow between the EBS and Svalbard along the Russian coast rather than through the Canadian Arctic. Similar to other regions, mtDNA haplotype frequencies showed significant differences among summering populations in the eastern Beaufort, Chukchi and Bering seas (O'Corry-Crowe *et al.* 1997, 2002). Belugas from the western Bering Sea exhibit significant mtDNA differentiation among some summering areas and between Russia and the USA and between Russia and the EBS (Meschersky *et al.* 2013). In general, summering aggregations in the sub-Arctic (Bering Sea) are more differentiated than those in the Russian, Alaskan, and Canadian Arctic including the Beaufort Sea (O'Corry-Crowe *et al.* 2010; Meschersky *et al.* 2013).

Some research has suggested intra-region structure in the EBS (Brown Gladden *et al.* 1997). This is a current (2015) area of research and may represent maternally transmitted social structure along lines of extended family groups (L. Postma, DFO Winnipeg, pers. comm.). ATK has not identified different kinds of Belugas in the EBS (Cardinal 2013).

3. Morphology

Harwood *et al.* (2002) found that asymptotic lengths of male EBS Belugas were similar to those from Cumberland Sound and Alaska (see Table 3). Luque and Ferguson (2006, 2010), however, found that EBS Belugas were significantly longer and their growth rate differed relative to eastern Arctic populations (including Cumberland Sound). Biases introduced to age estimates by having different people read tooth GLGs may have contributed to these differences (Luque and Ferguson 2006, 2010). However, a new assessment by Harwood *et al.* (2014) indicates a linear decline in size-at-age of 0.08% (SE 0.038%) per year or 1.75% over the 19-yr time series, which they suggest is a result of ecosystem changes that have negatively affected food availability or quality (see also Loseto *et al*. 2009). Hunters in the region did not describe any morphological differences among the Belugas in the eastern Beaufort Sea (Cardinal 2013).

4. Movement, Behaviour, and Life History Strategies

In summer, Belugas are found throughout the southeastern Beaufort Sea, aggregating in and near the Mackenzie River Estuary (Fraker *et al.* 1979; Harwood *et al.* 1996; DFO 2000; Richard *et al.* 2001a; Harwood and Kingsley 2013; Cardinal 2013). They are first seen along the coast in late April or early May, depending on ice conditions, as they migrate eastward from Alaskan waters (Cardinal 2013). The whales aggregate in the shallow waters of the delta from June to early July and are thought to use coastal waters primarily to calve, moult, and gain protection from predators.

Both tagging studies and ATK indicate that whales travel into areas such as Amundsen Gulf, Viscount Melville Sound, and Prince of Wales Strait in the summer (Byers and Roberts 1995; DFO 2000, 2011; Richard *et al.* 2001a; Loseto *et al.* 2006; Brown and Fast 2012; Cardinal 2013; Hauser *et al.* 2104). Belugas tagged in the Mackenzie River Estuary between late June and early August began migrating westward to the Chukchi Sea in September, continuing on to the Bering Strait area before the tags all stopped transmitting by late November (DFO 2000; Richard *et al.* 2001a; Loseto *et al.* 2006; Hauser *et al.* 2014).

5. Distribution

EBS Belugas occupy a distinct geographic region in the summer and they are essentially separate from all other Canadian Belugas in all seasons (Table 4). This may change as reduced ice cover (Parkinson 2014) allows contact with EHA-BB Belugas (see Heide-Jørgensen *et al.* 2011). The overlap in range would occur during the summer season, however, and differing migration patterns (west and south to wintering grounds for EBS, east and south to wintering grounds for EHA-BB) may keep them separate during the breeding season. The summering range of EBS Belugas is also separate from those of other Pacific populations, and the timing of autumn migration is staggered for EBS and Eastern Chukchi Sea Belugas (Hauser *et al.* 2014). Overlap with adjacent Alaskan populations in the winter (Brown Gladden *et al.* 1997) creates the potential for interbreeding with them (COSEWIC 2004). Available ATK further supports the idea that EBS Belugas are geographically discrete from other Canadian DUs (Cardinal 2013).

Discreteness and Significance

This DU is currently discrete from other Canadian stocks although this has the potential to change (*i.e.*, become connected with other DUs) with reduced ice cover in the Canadian Arctic Archipelago, as observed recently with Bowhead Whales, *Balaena mysticetus,* (Heide-Jørgensen *et al.* 2011). Animals from this DU are also discrete from summering aggregations in the Chukchi and Bering seas.

Belugas in the EBS DU can be considered significant as the animals in this region have unique migratory direction and timing compared to the other DUs considered in this report. Although haplotype and microsatellite frequencies differentiate these animals from other Canadian DUs, the sequences and alleles observed are also observed in other DUs (Figure 2). This could suggest that local adaptations have not occurred and that loss of this DU would not reduce the genetic diversity of the species. However, current genetic analyses have only limited coverage of the full Beluga genome, which limits the ability to detect differences. New methods and analyses that focus on a greater portion of the genome will likely resolve whether the Belugas that summer in the Beaufort Sea are locally adapted or diverging in relative isolation from eastern Arctic DUs. The unit is important to the evolutionary legacy of the species in Canada, and if lost would likely not be replaced through natural dispersion. Loss of this DU would create a significant distributional gap not only in Canada but also in the circumpolar range of the species.

DU2: Eastern High Arctic – Baffin Bay (EHA-BB)

This DU includes animals summering in the Canadian Arctic Archipelago and along the northeastern coast of Baffin Island. It has an EO of *ca.* 250,000 km^2 and an AO of 49,000 km^2 (COSEWIC 2004). Information on the distribution and movements of the Belugas in the EHA and BB comes from aerial surveys (Smith *et al.* 1985; Innes *et al.* 2002b), satellite-tagging (Smith and Martin 1994; Richard *et al.* 2001b; Heide-Jørgensen *et al.* 2003), and ATK (Cardinal 2013 and references therein). Genetic sampling has been carried out in Grise Fiord, Arctic Bay, Creswell Bay, Croker Bay, Cunningham Inlet, Elwin Bay, and Coningham Bay (Brown Gladden *et al.* 1997, 1999; de March *et al.* 2002; Turgeon *et al.* 2012). Whales sampled at Kimmirut (Hudson Strait, SE Baffin) have historically been assigned to this DU (de March *et al.* 2002) although Turgeon *et al.* (2012) considered the samples obtained from Kimmirut to represent multiple (mixed) stocks and DFO (2010; Richard 2010) considers these animals to belong to the large Western-Northern-Southern Hudson Bay (aka WHB) summer stock (see also discussion on CS DU below). COSEWIC (2004) noted that there was increasing evidence of substructure in the EHA-BB population (see also Cardinal 2013), but concluded that the available data were insufficient to justify splitting into more than one DU. No additional research has been conducted since the 2004 assessment so this question remains unresolved and these animals are still treated as a single DU in this report.

Lines of Evidence

1. Phylogenetics

No phylogenetic separation is evident that would distinguish this DU from adjacent units in Canada or Greenland. Brown Gladden *et al.* (1997) found that haplotypes observed in Belugas from this region are part of the Pacific clade (*i.e.*, “Western haplotype assemblage”) and are common to Belugas in all Canadian populations other than those in the St. Lawrence Estuary and eastern Hudson Bay.

2. Genetic Diversity, and Structure

In the northern and central portions of this DUs range there are few samples and sampling locations from which to draw conclusions. Brown Gladden *et al.* (1997, 1999) did not observe significant differences between Belugas sampled in Grise Fiord and those from West Greenland. However, subsequent analysis with larger sample sizes from more locations did detect significant mtDNA haplotype differences between Lancaster Sound samples (6 locations) and West Greenland/Grise Fiord samples (de March *et al.* 2002) (Table 6). Confounding these results was the observation that samples from Creswell Bay (Lancaster Sound) obtained in 1993 were more similar to West Greenland/Grise Fiord than to other Lancaster Sound samples (de March *et al.* 2002). This may indicate that there are subdivisions within the current Eastern High Arctic –Baffin Bay DU although this has not been well explored. Heide-Jørgensen *et al.* (2003) argued that the differentiation between Canadian and Greenland samples is a sampling artifact and cited satellite tag data showing that whales move across the Canada-Greenland border as support for the hypothesis of a single, shared stock. de March *et al.* (2002) pointed out that differentiation among locations depends to a large degree on whether or not annual collections are pooled for the analysis and suggested that without a firm understanding of the social structure of Belugas, inferring population structure would be challenging.

In the southern portion of this DUs range there has been some confusion related to Cumberland Sound samples. Pangnirtung (Cumberland Sound) animals cluster with those from Iqaluit and Kimmirut when samples from multiple years are pooled but some samples collected in a given year do not follow this pattern (Brown Gladden *et al.* 1997: 9). Over the sampling history, hunters from Pangnirtung took Belugas belonging to at least two stocks and closure of the Clearwater Fiord hunt skewed the genetic results (Brown Gladden *et al.* 1997, 1999). Similar confusion and changes have occurred with respect to samples from communities south of Pangnirtung (*i.e.*, Iqaluit and Kimmirut).

Brown Gladden *et al.* (1997, 1999) grouped Belugas from the southern Baffin region (Iqaluit, Kimmirut, and Pangnirtung in part) with western Hudson Bay samples.

There has yet to be a Bayesian-type analysis of microsatellite data fully representative of this DU and adjacent DUs. Frequency analysis of microsatellite markers detected significant differences between sampling locations in the EHA-BB DU and both EHB and STL (Brown Gladden *et al.* 1999). There were few significant differences between locations in DUs thought to overwinter in Baffin Bay and Hudson Strait (EHA-BB, WHB, EHB) (Brown Gladden *et al.* 1999). This could stem from gene flow while animals are at wintering areas in Hudson Strait, Davis Strait, and Baffin Bay (Brown Gladden *et al.* 1999; Turgeon *et al.* 2012). The occasional presence of haplotypes characteristic of EHB in other locations suggests that some animals temporarily disperse among summering areas; however, the presence of maternal genetic structure suggests they return to natal regions to mate (Turgeon *et al.* 2012). Examination of haplotype frequencies across Canada suggest similarities with CS and WHB (shared most common haplotype) but also differences (second and third most common haplotypes in EHA-BB are low frequency in other DUs) (Figure 2; L. Postma, unpublished). Large population size coupled with high mobility, overlapping generations, and long life spans make genetic differentiation within the EHA-BB DU or between the EHA-BB and other DUs likely to go undetected even with significant barriers to gene flow (Petersen *et al.* 2010). Overall, the EHA-BB DU is under-sampled, especially in the high and central Arctic regions, and therefore the genetic relationships within the DU and between this and adjacent DUs in Canada and Greenland are poorly understood.

3. Morphology

The asymptotic length of whales (for both sexes) harvested by Inuit at Grise Fiord (Jones Sound) was significantly greater than that of whales harvested at Arviat (WHB), but it was not significantly different than that of whales harvested at Pangnirtung (CS) (Stewart 1994). The asymptotic length of whales harvested in West Greenland was significantly greater than that of whales from Alaska and western and eastern Hudson Bay (Heide-Jørgensen and Teilmann 1994). Body lengths of male Belugas harvested by Baffin Bay communities were significantly greater than those of whales from WHB and EHB but were indistinguishable from those of EBS and CS Belugas (Luque and Ferguson 2006, 2010). The authors were unable to include Baffin Bay animals in growth analyses due to small sample size for length at age. ATK indicates some morphological differences. For example, whales from the Grise Fiord area are said to be smaller than those in Cumberland Sound, and knowledge holders have described differences in melon shape between the whales at Clyde River and those around Ellesmere Island (see below re: distribution) (Cardinal 2013).

4. Movement, Behaviour, and Life History Strategies

The whales assigned to this DU are widely distributed throughout the Canadian Arctic Archipelago and along the eastern coast of Baffin Island during summer. They are not concentrated around river estuaries in summer to the same extent as whales in some other regions, but they do aggregate in Creswell Bay, Cunningham Inlet, and Elwin Bay off Somerset Island (Smith *et al.* 1985; Richard *et al.* 2001b; Innes *et al.* 2002b).

ATK suggests that there are two groups, one that occupies Lancaster Sound and eastern and northern Baffin Island, and another centred around Ellesmere Island (Cardinal 2013). ATK holders report a general northern and western migration of whales from eastern Baffin Island and Baffin Bay into Lancaster Sound (Read and Stephansson 1976;

Remnant and Thomas 1992; Cardinal 2013). Some whales continue westward as breakup occurs in late spring, moving into Barrow Strait and south into Peel Sound (see also aerial survey results in Smith *et al.* 1985 and Innes *et al.* 2002b), and others travel south into the Gulf of Boothia and northern Foxe Basin (Remnant and Thomas 1992; Stewart *et al.* 1995). In autumn, the whales migrate away from coastal areas as sea ice forms, back into Lancaster Sound (Remnant and Thomas 1992; Stewart 2001). ATK on winter distribution is sparse, but some Inuit think that the whales likely overwinter in Davis Strait or in open water in Baffin Bay (Remnant and Thomas 1992). Hunters from Greenland believe that Belugas that overwinter south of Disko Bay in West Greenland are from Canadian summer populations (Thomsen 1993). Five Belugas were satellite tracked from Creswell Bay, Somerset Island, in autumn 2001 (Heide-Jørgensen *et al.* 2003). Three stayed in the North Water Polynya while the other two moved to West Greenland for the winter. That study estimated that *ca.* 15% of the Belugas that summer in the Canadian High Arctic migrate to West Greenland for the winter.

The second putative group of EHA-BB Belugas is found around Ellesmere Island (Cardinal 2013), where they occur year round. Inuit living in Grise Fiord see Belugas throughout the winter along the floe edge at the mouth of Jones Sound (Stewart 2001). Animals are also thought to overwinter in waters between Ellesmere Island and Baffin Island and Greenland (*i.e.*, the North Water Polynya) (Cardinal 2013; Heide-Jørgensen *et al.* 2013). As the land fast ice begins to break up in spring, some Belugas move to areas along eastern and northern Baffin Island; others migrate northward east of Ellesmere Island or westward into Jones Sound (Remnant and Thomas 1992; Stewart *et al.* 1995; Stewart 2001). During summer Belugas occur in coastal areas of both Smith Sound and Jones Sound (Reeves and Mitchell 1987a; Stewart 2001). In the fall, Belugas migrate out of coastal areas.

5. Distribution

Animals in this DU summer throughout much of the Canadian Arctic Archipelago (Smith and Martin 1994; Richard *et al.* 2001b). Their core summer habitat is located in the Lancaster Sound region, including Peel Sound and the coastal waters of Somerset and Prince of Wales Islands, northern Baffin Island, and Jones Sound (Cardinal 2013). This region is not used by other Canadian Beluga populations in summer (Table 4). The migration and distribution patterns of this DU separate it from the neighbouring EBS DU to the west (see above). At least some portion of the population migrates to West Greenland for the winter, and other animals overwinter in the North Water Polynya. Some ATK indicates potential mixing with whales of the WHB DU in northern Foxe Basin in the spring, summer, and fall (Remnant and Thomas 1992; McDonald *et al.* 1997; Stewart 2001; Cardinal 2013). Finally, Cardinal (2013) notes the possibility of mixing with the CS DU in winter although this would likely require EHA-BB whales to overwinter along the southern coast of Baffin Island (see CS DU below).

Discreteness and Significance

There are numerous uncertainties relating to this DU, especially with respect to sub-structure and relationships to adjacent DUs in Canada and to West Greenland Belugas. Both scientific sources (Richard *et al.* 1998; Heide-Jørgensen *et al.* 2003; de March and Postma 2003) and ATK (Cardinal 2013) point to the possibility that more than one DU should be recognized, but evidence as to where boundaries should be drawn is not conclusive (see Figure 3). Until sampling in high and central Canadian Arctic locations (*e.g.*, aggregations in Elwin Bay and Cunningham Inlet) has increased substantially, there is no way to determine whether there is important genetic structure.

Although uncertainties exist, genetic and telemetry evidence for wintering grounds in the North Water Polynya and in West Greenland suggests that these animals are discrete from those in the Eastern Beaufort Sea and those further south in the eastern Canadian Arctic and sub-Arctic. High Arctic Belugas may be evolutionarily significant due to the fact that they spend comparatively long portions of the year in ice-covered waters and due to their apparent flexibility in using different summering areas in response to seasonally and annually variable ice conditions. Loss of this large and widely distributed population would create a significant gap in the distribution of the species within Canada and more generally, and reduce overall genetic diversity (see Figure 2).

DU3: Cumberland Sound (CS)

Belugas in Cumberland Sound were identified as a distinct population in the 1970s (Sergeant and Brodie 1975). They were initially considered part of a Southeast Baffin Island stock (Brown Gladden *et al.* 1997, 1999) but in 2004 were recognized as a separate DU (COSEWIC 2004). This DU encompasses all of Cumberland Sound (EO = *ca.* 27,000 km², AO = 9,000 km²) although Belugas from other DUs may be harvested within this area. ATK identifies three distinct CS Beluga populations, all separate from those found along eastern Baffin Island (Kilabuk 1998). One population summers on the west side of Cumberland Sound; a second population inhabits Clearwater Fiord; and a third population exists at the floe edge. Cardinal (2013) grouped the three putative populations together in the same designatable unit, noting that there was little knowledge regarding wintering distributions and that all occupy a relatively small area. Whales from this DU have been sampled from harvests by Pangnirtung Inuit and the location of the harvest has shifted over time (see genetic diversity below).

Lines of Evidence

1. Phylogenetics

Cumberland Sound Belugas can be differentiated from those of other DUs using mitochondrial haplotype frequencies, including a haplotype almost unique to the region (Turgeon *et al.* 2012). However, this haplotype is not monophyletic and occurs with other common haplotypes. This suggests that sufficient time has not passed or the Belugas are not isolated strongly enough for lineage sorting to occur.

2. Genetic Diversity, and Structure

Cumberland Sound has been identified as a discrete unit although this is most strongly supported by mtDNA haplotype frequency analysis, which may be an indication of maternal fidelity (Figure 2, Table 6). Haplotype frequencies and genetic mixture analysis suggest CS is a unique genetic entity (Turgeon *et al.* 2012).

Individual- based Bayesian clustering analysis of nuclear genetic markers did not identify a unique CS cluster (Turgeon *et al.* 2012). However, low levels of nuclear DNA differentiation were observed between samples from CS and other regions using frequency analysis. This suggests that CS Belugas do not migrate to Hudson Strait, the purported wintering/breeding area for adjacent DUs, and that this is enough to create low but detectable genetic differentiation. A combined genetics and organochlorine contaminants study also supports the uniqueness of Belugas harvested in Clearwater Fiord (Innes *et al.* 2002a; de March *et al.* 2004) (see Table 5).

Brown Gladden *et al.* (1999) observed significant temporal heterogeneity in the samples collected from Pangnirtung and attributed the change to differences in harvests between the 1980s and the 1990s, corresponding to a shift in hunting away from Clearwater Fiord that occurred in the 1990s (Brown Gladden *et al.* 1997: 1040). The consensus on the part of ATK and science is that the harvest by Pangnirtung Inuit has been primarily directed at Belugas from two DUs, CS and another as yet unknown, but likely WHB (see Turgeon *et al.* 2012) DU.

3. Morphology

Sergeant and Brodie (1969) reported that adult male and female Beluga whales in CS were larger than those from WHB, and Stewart and Walker (1987) concluded that WHB whales could be distinguished from those in CS and Jones Sound based on their growth curves. Doidge (1990a) found that Belugas from a number of regions, including CS, tended to be longer than those from Hudson Bay, but differences were too small to accurately classify individuals to a population strictly on the basis of size. In contrast, Stewart (1994) found that adult Belugas from CS were significantly larger than those from WHB and EHB, but not significantly different from those harvested in Grise Fiord (Jones Sound, EHA-BB). The asymptotic lengths of whales from EBS presented by Harwood *et al.* (2002) were similar to those from CS shown by Doidge (1990a), but Luque and Ferguson (2006) found that CS whales were significantly smaller than those from EBS. The latter authors compared five Beluga populations (DUs), and found that both sexes followed a general pattern with the smallest animals in EHB, progressively larger animals in WHB, CS, and EHA-BB, and the largest in EBS. Whales from CS were significantly larger than those from EHB and WHB, significantly smaller than those from EBS, and not significantly different from those in EHA-BB. Growth analysis using a Gompertz model, with EHA-BB removed due to small sample sizes, found the highest asymptotic lengths in CS male Belugas, but standard error of parameter estimates indicated relatively large uncertainties in these comparisons (Luque and Ferguson 2006, 2010). Since these studies were conducted, Harwood *et al.* (2014) have observed a declining linear trend in size-at-age in EBS Belugas, which suggests that size-at-age varies over time within populations and that size-at-age relationships among populations also change, thereby weakening the value of morphology as a tool for differentiating populations.

ATK holders recognize some morphological differences distinguishing the three putative CS sub-units (Kilabuk 1998; DFO 2002; Brown and Fast 2012; Cardinal 2013) - the whales found at the floe edge in spring are smaller, thinner and very white while those that summer in Clearwater Fiord are the largest and have a yellow colouration (*i.e.*, showing signs of epidermal moult; COSEWIC 2004). Belugas that summer along the west side of Cumberland Sound are smaller than those in Clearwater Fiord and have thicker, stronger-tasting muktuk. Some hunters note that whales that appear at the floe edge and those that summer in western CS are similar in size and have similar-tasting muktuk (Kilabuk 1998).

4. Movement, Behaviour, and Life History Strategies

CS Belugas are relatively sedentary in comparison to other DUs (other than JB). They inhabit Cumberland Sound on a year-round basis and make short migrations between summering (*e.g.*, Clearwater Fiord) and wintering areas near the mouth of Cumberland Sound (Richard and Stewart 2008).

Aerial surveys in CS and along the southeast Baffin coast show that the major summer aggregation of Belugas in this DU is limited to the Clearwater Fiord area, where they occupy the Ranger River estuary from mid-July to mid-September (Richard and Stewart 2008). Whales are highly aggregated in Clearwater Fiord in August, with reduced abundance in other areas of CS and in a diminishing gradient from north to south.

Satellite telemetry results show that whales ranged from Nettilling Fiord to Clearwater Fiord, where most locations were estimated, in late July, and were almost entirely limited to Clearwater Fiord in August. In September, tagged whales were still concentrated in the Clearwater Fiord area but many ranged far south down the western side of CS. Locations were further south again in October and further to the east by December, to the southeast side of the Sound along Cumberland Peninsula (Richard and Stewart 2008). ATK observations (Kilabuk 1998) support the summer and autumn ranges of Belugas that have been inferred from tagging studies.

ATK holders suggest that there are three Beluga populations in CS, with distinct migration and distribution patterns (Cardinal 2013). Belugas are first seen at the CS floe edge in April, and these belong to the population of whales that resides at the floe edge (Kilabuk 1998). The two other putative sub-populations arrive at the floe edge later in the spring (April-May) and move into CS later in the summer (Kilabuk 1998; DFO 2011). The main population then uses ice leads to move to the summer calving area in Clearwater Fiord, while the other population summers along the west side of CS (Kilabuk 1998). Belugas start to migrate from their coastal summering areas in early fall (Remnant and Thomas 1992), and there are some differences in migration timing among the putative sub-units (Kilabuk 1998).

Two satellite tags affixed in August to whales in Cumberland Sound continued to work into January and one into February. The tag transmissions showed that these whales remained in the same area they were in during December. Richard and Stewart (2008) suggested that the wintering range of CS Belugas is likely centred in that area because sightings were also made there during March aerial surveys. ATK holders had little information on the winter distribution of whales from the CS DU (Cardinal 2013): some felt that whales overwintered at the mouth of Frobisher Bay (Kilabuk 1998) and others stated that they overwintered in a polynya at the mouth of CS (Brown and Fast 2012).

5. Distribution

Data on CS Beluga distribution come from satellite tracking (14 whales tagged in 1998-1999 and 2006-2007; Richard and Stewart 2008), aerial surveys (Richard and Stewart 2008; Richard 2013), and ATK (Kilabuk 1998; Brown and Fast 2012). Previous studies assumed that Belugas summering in Frobisher Bay and along the Hudson Strait coast near Kimmirut came from the CS DU, which was at that time considered part of the South East Baffin population (Richard and Orr 1986). More recent aerial surveys and satellite-tagging work indicate that Belugas remain in CS throughout the year (Richard and Stewart 2008). Belugas that summer around southeastern Baffin Island outside CS are now considered to be animals from the WHB (or W-N-S HB, Richard 2010) group that do not migrate into Hudson Bay.

Discreteness and Significance

Mitochondrial genetic evidence and to a lesser degree nuclear markers support the discreteness of Cumberland Sound as it applies to animals that are sampled in Clearwater Fiord. Whales in the CS DU have distinct migration and distribution patterns that separate them from whales of other adjacent DUs, including those of the EHA-BB DU and those of the southeast Baffin Island region (*i.e.*, WHB DU) (Cardinal 2013). The CS DU is also somewhat unusual among Belugas of the high Arctic in having a juxtaposition of habitats that enables them to follow a relatively sedentary lifestyle and avoid long-distance migrations.

The loss of this DU would not create a large gap in the species range in Canada, when considered as a whole, but it would result in the loss of a unique group of Belugas. The Belugas that summer in Clearwater Fiord are genetically distinct (*e.g*., low but significant F_{ST} differences between CS and EHB and CS and WHB [Turgeon *et al*. 2012]) and have a relatively sedentary life-history that sets them apart and may include locally adapted traits. The loss of this DU would likely result in the elimination of Beluga use of Clearwater Fiord.

DU4: Ungava Bay (UB)

Belugas in this putative DU were defined by a summer aggregation centred near the Mucalic River estuary, with other smaller estuarine concentrations at the George, Soak, Leaf, and Whale rivers (Finley *et al.* 1982; Reeves and Mitchell 1989b; Cardinal 2013) (EO = *ca.* 51,000 km², AO = 12,000 km²; COSEWIC 2004). The historical population was small in relation to other DUs and was reduced by commercial hunting (Reeves and Mitchell 1987c, 1989b). The Mucalic River no longer supports any significant numbers of Belugas, and the main centres of aggregation are now almost unoccupied (COSEWIC 2004). Information from aerial surveys and limited genetic analyses indicates that this population is at undetectably low levels or has been extirpated. Intensive systematic aerial surveys of Ungava Bay (25% coverage) were flown in 1985, 1993, 2001, and 2008 (Smith and Hammill 1986; Kingsley 2000; Gosselin *et al.* 2002, 2009) without any on-transect sightings. Concurrent reconnaissance flights in some years also failed to find more than a few whales - sometimes none. Kingsley (2000) estimated that a minimum of 200 Belugas would have to be present in Ungava Bay for them to be detectable on survey transects. Finley *et al.* (1982) observed small numbers on non-systematic aerial surveys and ground-based observation points in August 1980, and concluded that the summer-resident stock in UB was much reduced from historical levels, to less than 100 animals. Kingsley (2000) estimated a population possibly as large as 50 animals from off-transect sightings, with an imprecise upper 90% confidence limit of 150 individuals that was not corrected for availability bias.

The most recent assessment used a Bayesian approach that included all four surveys with zero-counts and yielded a mean (corrected) estimate of the current population size as 32 individuals (95% CI 0–94) (Doniol-Valcroze and Hammill 2012). ATK also indicates the population is much reduced compared to the historical population that summered in UB, while noting the presence of large number of migrating whales (Lee *et al.* 2002; Breton-Honeyman *et al.* 2013; Cardinal 2013). The most recent status assessment (COSEWIC 2004) concluded that the resident Beluga population of UB was very low if, in fact, it did still exist. No significant estuarine aggregations were known and observations made at the principal estuaries in the 1980s had not revealed any important concentrations of Belugas during the summer months. There has been no subsequent evidence to change these conclusions.

Lines of Evidence

1. Phylogenetics

Samples for genetic analysis have been collected from five locations within Ungava Bay (de March and Maiers 2001; Turgeon *et al.* 2009). These samples were not collected from a summer aggregation and likely originate from Belugas that were migrating through the bay from other DUs. Of the samples obtained, there are haplotypes from both the Atlantic and Pacific lineages so no predictions can be made about the lineage(s) of Belugas that have occupied UB in summer if they are among the sampled animals.

Therefore, phylogenetics cannot provide evidence for or against the discreteness of Belugas that were historically found in this region.

2. Genetic Diversity, and Structure

Genetic samples are not available from a summer aggregation of Belugas in UB but it is possible that animals from this DU have been sampled during migration. Genetic samples that have been collected in Ungava Bay and analyzed (*e.g.*, Mancuso 1995 in COSEWIC 2004; de March and Maiers 2001) have likely come from other DUs (WHB, EHB) that enter in Ungava Bay at certain times of the year (*e.g.*, Smith 2007; Lewis *et al.* 2009). A genetic mixture analysis (GMA), that theoretically should identify unknown stock in mixtures of animals, found no evidence for the endangered UB stock (Turgeon *et al.* 2009, 2012). As evidence that the power to detect an unknown stock is inherent in the analysis, the GMA did suggest an unknown stock that is likely the James Bay stock. Ungava Bay animals could be present but at such low density during the sampling period that they have not been sampled and therefore go undetected by this method. In addition, individual-based Bayesian analysis did not detect a genetic cluster that could indicate a separate UB population (Turgeon *et al.* 2012).

3. Morphology

Finley *et al.* (1982) could not distinguish among whales sampled in eastern Hudson Bay, Ungava Bay (summer harvests) and Hudson Strait (fall harvests). There is little ATK regarding morphological differences (Cardinal 2013). One hunter from Clyde River noted that the Belugas there are larger than those in UB (DFO 2011). Inuit in Kangiqsualujjuaq note that the whales observed there are smaller than those near Pangnirtung, which in turn are smaller than those from Greenland (Breton-Honeyman *et al.* 2013). Belugas that summer around Quaqtaq are larger than those that migrate through the area in the spring (Breton-Honeyman *et al.* 2013). Overall, ATK suggests that Belugas of the Ungava Bay DU are smaller than those found in Cumberland Sound and the High Arctic (Cardinal 2013) (Table 3).

4. Movement, Behaviour, and Life History Strategies

Little is directly known of the seasonal movements of Belugas in Ungava Bay (COSEWIC 2004). Knowledge holders from Quaqtaq noted that Belugas are seen in small numbers throughout the summer, most notably in rivers to the east of Kangiqsujjuaq; some hunters believe these whales belong to the Ungava DU, though others believe they belong to a migrating group (Breton-Honeyman *et al.* 2013). ATK holders in Kangiqsualujjuaq note that whales will enter rivers between Kuujjuaq and the Killiniq area to moult, and then move back towards Hudson Strait and Killiniq (Cuerrier *et al.* 2012).

Belugas were fairly common along the northern Labrador coast in summer until the 1950s, but have been very scarce since (Brice-Bennett 1978). They are still seen sporadically but in low numbers (COSEWIC 2004). The affinities of these whales and their relation to the UB DU are unknown.

Ungava Bay Inuit report ATK on migration and distribution patterns (Breton-Honeyman *et al.* 2013), but much of this may relate to observations of migrating whales from other DUs (*e.g.*, WHB, EHB) (Cardinal 2013). Both scientific information and ATK indicate that many of the Belugas seen in the region are migratory and may belong to other DUs. Some of the early spring and late fall Belugas harvested in Ungava Bay are probably from a mixed wintering population of EHB and WHB whales (Lee *et al.* 2002; de March and Postma 2003; Smith 2007; Lewis *et al.* 2009; Doniol-Valcroze and Hammill 2012; Cuerrier *et al.* 2012; Breton-Honeyman *et al.* 2013).

Available ATK suggests that whales of the UB DU leave the Bay and overwinter in Hudson Strait or further offshore, including off the Labrador coast (Cuerrier *et al.* 2012; Breton-Honeyman *et al.* 2013).

5. Distribution

Historically, whales aggregated in river estuaries in Ungava Bay in the summer, mainly the Mucalic River, and others (*e.g.*, Soak and Leaf rivers) to a lesser extent (Finley *et al.* 1982). Belugas are still seen in George River in early summer (Cuerrier *et al.* 2012; Breton-Honeyman *et al.* 2013). COSEWIC (2004) includes the Ungava Bay area as the complete range for this DU but ATK suggests these animals leave the bay during the winter.

Discreteness and Significance

The recognition of the UB DU is based primarily on ATK and the historical harvest record. Compared to Beluga populations in Nunavut, there is little ATK available on Belugas in Ungava Bay (Cardinal 2013). From a genetic evidence view-point there are no data to support or refute the discreteness or significance of this DU. Similarly, morphological differences (*i.e*., body size) are not readily apparent due to lack of samples. Most DUs are defined by their summer estuarine aggregation areas. Historically, Belugas in the UB DU aggregated at rivers in southern Ungava Bay, where they are now rare or absent. Despite the paucity of current distributional information, this historical presence suggests these Belugas represent or represented a discrete DU.

Migrating whales from other DUs in Hudson Strait (WHB, EHB) occur in Ungava Bay in spring, fall and winter but not summer (Lewis *et al.* 2009; Cuerrier *et al.* 2012; Cardinal 2013). Hence, if the UB DU were to become extirpated, or has been already, much of southern Ungava Bay would remain unoccupied by Belugas, creating a significant gap in the species' summer range. The whales that are observed there during migrations are not there during the summer season, suggesting that recovery potential is limited.

DU5: Western Hudson Bay (WHB)

The WHB DU is a large population (> 60,000 animals; Richard 2005, 2010) that summers in the river estuaries of western Hudson Bay (primarily the Seal, Churchill and Nelson rivers) and migrates to Hudson Strait during the winter. It has a large range in comparison to most other DUs (EO = *ca.* 770,000 km^2; AO = 51,000 km^2; COSEWIC 2004 - but note that this EO calculation includes James Bay, which is now considered a separate DU). Numerous Inuit communities harvest Belugas from the WHB DU at different times of the year, and there is a significant volume of ATK supporting the existence of multiple DUs in Hudson Bay (McDonald *et al.* 1997; Gislason 2007; Lewis *et al.* 2009; DFO 2011; Brown and Fast 2012; Breton-Honeyman *et al.* 2013). Genetic samples have come from numerous locations within Hudson Bay and from Foxe Basin, Hudson Strait, and Frobisher Bay.

Lines of Evidence

1. Phylogenetics

The mtDNA haplotypes observed in samples from Belugas harvested in the WHB DU are primarily derived from the Pacific refugium (Western clade) (Brown Gladden *et al.* 1997). This provides evidence of phylogenetic divergence from the EHB DU and STL DU, which are primarily made up of Atlantic refugial haplotypes, but does not provide evidence of phylogenetic divergence from the other Canadian DUs.

2. Genetic Diversity, and Structure

This DU can be separated from other DUs using mitochondrial haplotype frequencies (Table 6) although there is some evidence of mixing (Figure 2). Turgeon *et al.* (2012) compared Belugas from EHB, WHB, and CS and found strong evidence that these areas were differentiated, with EHB having the most distinct haplotype set. One haplotype (H20) found in WHB at a high frequency (8%) was not found elsewhere. A genetic mixture analysis (GMA) of harvests divided by season suggests that WHB animals are harvested by communities in northern Hudson Bay, Foxe Basin, Hudson Strait, and Frobisher Bay (Turgeon *et al.* 2012).

Nuclear genetic markers have not identified genetic clusters that suggest reduced gene flow between WHB and other eastern Arctic DUs (Turgeon *et al.* 2012; Postma *et al.* 2012). This is consistent with male-mediated gene flow or gene flow occurring during the mating season when individuals from several DUs may co-occur. Gene flow likely occurs in the spring while animals are wintering in, or migrating through, Davis and Hudson straits. Alternatively, there may be separation of animals in this DU from others but the large population size, long lifespan, and overlapping generations prevent genetic drift from occurring at a detectable rate.

Within the area defined to encompass the WHB DU there has been the suggestion of some substructure (see Figure 3). de March and Postma (2003) indicated that Churchill River Belugas are primarily one haplotype and suggested that they may constitute a stock. Churchill was the focal point for the Hudson Bay Company (HBC) whaling activities in WHB (Doan and Douglas 1953; Reeves and Mitchell 1989a). Beginning in 1688 and continuing until *ca.* 1930 the HBC harvested Belugas from the estuaries of the Seal and Churchill rivers for their oil, skins and meat. Over 500 Belugas were taken at the Seal River in some decades (1820s, 1840s, and 1850s) and during the peak decade of harvest the HBC hunt at Churchill took over 1,300 whales (1880s). The commercial hunt was reestablished in 1949 and pursued through 1968 by a Manitoba company, which caught an average of 370 Belugas per year over the two decades (Sergeant 1981).

There is potential for estuary specific maternal lineages (*e.g.*, Seal, Churchill, and Nelson rivers) in WHB but currently few samples are available to examine this hypothesis.

3. Morphology

Sergeant and Brodie (1969) reported that adult male Belugas from WHB were smaller than those from CS. Doidge (1990a) found that Belugas from WHB were similar to those from EHB and smaller than those from most other eastern Canadian Arctic locations, although differences were slight (Table 3). Stewart (1994) (also Stewart and Walker 1987) determined that whales from WHB were significantly smaller than those from EHA-BB and CS. Luque and Ferguson (2006, 2010) determined that WHB males were significantly larger than those from EHB and significantly smaller than those from CS.

ATK holders have also noted some morphological differences amongst the three DUs in Hudson Bay (Cardinal 2013). The Belugas in the WHB DU were described by some Inuit as larger, longer, and thinner (skinnier) than those that migrate to EHB (Breton-Honeyman *et al.* 2013). In a different study, one Nunavik ATK holder described WHB Belugas as being larger than those from EHB (Gislason 2007). Others have noted that EHB Belugas are larger in size (Tyrrell 2008). When comparisons are made to whales outside the Hudson Bay region, WHB and EHB Belugas are described as being similar to each other but smaller than those from CS and EHA-BB (Richard 2010). The

Belugas that are seen in Frobisher Bay are similar in appearance to those that migrate past Kimmirut (Kilabuk 1998).

4. Movement, Behaviour, and Life History Strategies

During the summer WHB Belugas are found in coastal waters from the Winisk River in Ontario west and north to Lyon Inlet in Nunavut but are most concentrated in the estuaries of the Churchill, Nelson, and Seal rivers (Sergeant 1973; Richard 1993, 2005, 2010; McDonald *et al.* 1997; Breton-Honeyman *et al.* 2013). The entire region from Churchill to Rankin Inlet is considered by ATK holders to be an important area for Belugas (DFO 2011). These whales begin arriving at the estuaries in mid-June and build in numbers until late July or early August, when they begin to shift to migratory behaviour (Sergeant 1973; McDonald *et al.* 1997; Smith 2007). Belugas tagged at the Churchill estuary in 1992-1993 (n = 8) spent the summer months in shallow coastal waters prior to migrating through deeper waters (Martin *et al.* 2001). Whales tagged at the Nelson River estuary in July and August 2002–2005 (n = 14) had all departed the local area by late September (Smith 2007). Not all whales from this DU migrate into western Hudson Bay; some remain in Hudson Strait and Frobisher Bay throughout the summer months (Priest and Usher 2004; Richard 2010).

In early September of 1993, whales tagged in the Churchill River estuary started an easterly migration marked by diving in deep water (and assumed foraging) (Martin *et al.* 2001). Tags stopped transmitting by late September and yielded no information about late autumn migration patterns. After departing the local area by late September, whales tagged at the Nelson River estuary moved north along the west coast of Hudson Bay or east to the area around the Belcher Islands (Smith 2007). The six whales tagged at the Seal River estuary in July 2012 all migrated north along the Hudson Bay coast and were near Rankin Inlet from the end of August to the end of September (K. Westdal, Oceans North Canada, pers. comm., 19 June 2014). All tagged whales moved north through Roes Welcome Sound. Some of the whales went into Repulse Bay and/or Lyon Inlet, and all spent time in the Frozen Strait area north of Southampton Island. ATK provides similar information on Beluga migration routes and timing (McDonald *et al.* 1997). Rankin Inlet is considered to be an important area for Belugas, and local Inuit say the whales enter the Inlet in late September to early October but historically arrived there in August (Brown and Fast 2012).

After departing the local area by late September, whales tagged at the Nelson River estuary moved north along the west coast of Hudson Bay or east to the area around the Belcher Islands or across the middle of the Bay (Smith 2007). Individuals that migrated east across Hudson Bay and up the Nunavik coast tended to travel slower, spending time near the Belcher Islands and arriving in Hudson Strait later. By mid-November all the study whales with working satellite tags had reached Hudson Strait, and pooled relative-use patterns remained similar for *ca.* five weeks until the last satellite tag stopped transmitting. Movements during this timeframe suggested possible foraging behaviour (Smith 2007). One whale went north into Foxe Basin during the fall and was north of Southampton Island when the tag failed in late December. Belugas leave the Southampton Island area to migrate past Cape Dorset in October and winter near Kimmirut, although some whales also stay and are seen overwintering there (McDonald *et al.* 1997). Hunters from Kimmirut also see Belugas migrating eastward in the fall (Kilabuk 1998). ATK holders in Quaqtaq and Ivujivik see both WHB and EHB Belugas migrating past their region in autumn (Breton-Honeyman *et al.* 2013).

Throughout the winter period (November-March), whales tagged at the Nelson River estuary were mostly in eastern Hudson Strait and northern Ungava Bay, with some individuals located off the coast of northern Labrador or in western Hudson Strait (*i.e.*, a whale that had migrated east to the Belcher Islands area after departing the Nelson River) (Smith 2007). The Belugas tagged at the Seal River estuary overwintered in western Hudson Strait, near Nottingham and Salisbury Islands (K. Westdal, Oceans North Canada, pers. comm., 19 June 2014). Belugas of the WHB DU are thought by ATK holders to mainly overwinter in Hudson Strait and off the Labrador coast (Brice-Bennett 1978; McDonald *et al.* 1997; DFO 2011). Inuit in Cape Dorset note that whales overwinter between Mill and Salisbury Islands (DFO 2011). Belugas are seen arriving at the floe edge near Kimmirut in spring as they migrate westward towards Cape Dorset (Kilabuk 1998).

5. Distribution

Data on WHB Beluga distribution come from satellite tracking (*e.g*., Smith 2007), aerial surveys (Sergeant 1973; Richard 1993, 2005), and ATK (McDonald *et al.* 1997; Kilabuk 1998; DFO 2011; Brown and Fast 2012; Breton-Honeyman *et al.* 2013). Throughout the year, WHB Beluga whales are widely distributed, ranging from south and west Hudson Bay to eastern Hudson Strait. During summer, whales are concentrated in southwestern Hudson Bay but occur in smaller numbers throughout the region (Richard 2010). Some whales overwinter in northwest Hudson Bay (McDonald *et al.* 1997), but most are concentrated in Hudson Strait at this time. The summering aggregation areas are separate from other Beluga DUs, but there is overlap during fall and spring migrations and during winter (see below).

Discreteness and Significance

Genetic evidence supports the discreteness of this DU when mitochondrial haplotypes of summer areas are analyzed. There does however, seem to be gene flow among Hudson Bay Belugas as suggested by the lack of clustering observed in Bayesian analyses. The WHB DU has a distinct summer aggregation area, but migration routes and wintering areas overlap with those used by whales from the EHB DU and possibly the JB (southeastern Hudson Bay), UB (Hudson Strait), and EHA-BB (Foxe Basin) DUs. Some morphological differences between WHB and EHB whales have been observed but as mentioned previously cannot be relied upon to support the discreteness of a DU.

The fidelity that Belugas show to summering estuaries (Sergeant and Brodie 1969) coupled with their loss from certain estuaries (UB) suggests that these areas are of learned importance. However, it is also possible that there are local adaptations associated with these habitats. Therefore, they should be treated as evolutionarily significant. The loss of this DU would result in a significant gap in the species range (all of western Hudson Bay, Foxe Basin, and Frobisher Bay).

DU6: Eastern Hudson Bay (EHB)

The Beluga population in the EHB DU is centred in the arc of eastern Hudson Bay during summer and winters in the Labrador Sea (EO = *ca.* 221,000 km²; AO = 41,000 km²; COSEWIC 2004). This DU was depleted by intensive commercial hunting (Reeves and Mitchell 1987b, 1989b; Hammill *et al.* 2004; Doniol-Valcroze *et al.* 2011). Systematic visual aerial surveys were flown by DFO in 1985, 1993, 2001, 2004, 2008, and 2011(Smith and Hammill 1986; Kingsley 2000; Hammill *et al.* 2004; Gosselin *et al.* 2009, 2013) and satellite tagging has also been conducted between 1993-2004 (n=37) (Kingsley *et al.* 2001; Lewis *et al.* 2009; Bailleul *et al.* 2012). As noted previously, there is a large amount of ATK on the Beluga DUs found in Hudson Bay (McDonald *et al.* 1997; Gislason 2007; Lewis *et al.* 2009; DFO 2011; Brown and Fast 2012; Breton-Honeyman *et al.* 2013), including the EHB DU. Genetic samples have been collected in the main estuaries of the eastern Hudson Bay Arc, and along the migration route in Hudson Strait.

Lines of Evidence

1. Phylogenetics

Several haplotypes that occur at high frequency in the EHB group with haplotypes from STL and form a distinct phylogenetic lineage (clade) that is hypothesized to have originated in an Atlantic refugium (Brown Gladden *et al.* 1997). This eastern clade of haplotypes may have been isolated in the Atlantic Ocean or the glacial Champlain Sea (Harington *et al.* 2006). Several diagnostic haplotypes have been used to differentiate animals from this DU for management purposes.

2. Genetic Diversity, and Structure

Significant differentiation of haplotype frequencies has been observed between EHB and other DUs (Figure 2; Brown Gladden *et al.* 1997; de March and Maiers 2001; de March and Postma 2003; Postma *et al.* 2012; Turgeon *et al.* 2012). In the most recent analysis, Turgeon *et al.* (2012) observed that three haplotypes made up 78% of the EHB samples and these haplotypes were rare or absent in WHB and CS - the two other summer areas studied. Summer areas along the eastern arc of Hudson Bay are not differentiated from one another within this DU (de March and Postma 2003). Mixture analysis indicates that animals from this DU are harvested along their seasonal migration routes along with WHB animals (de March and Maiers 2001; de March and Postma 2003).

Nuclear genetic markers provide weak or no support for the discreteness of this DU (Brown Gladden *et al.* 1999; Postma *et al.* 2012; Turgeon *et al.* 2012). Individual-based Bayesian analysis did not detect multiple clusters that might differentiate EHB from other DUs (Turgeon *et al.* 2012). These results are consistent with the hypothesis that gene flow is occurring when animals from several DUs are together during the winter/ spring (mating season) but then return to maternal natal areas.

3. Morphology

Finley *et al.* (1982) found no differences in body length between whales sampled in EHB, UB and Hudson Strait. Doidge (1990a) found that Belugas from WHB were similar in length-at-age to those from EHB. However, Luque and Ferguson (2006, 2010) determined that EHB males were significantly smaller than those from WHB, CS, and EBS. ATK holders note some morphological differences amongst the different Hudson Bay DUs, but the information is equivocal in some cases (Cardinal 2013). Some knowledge holders in Nunavik reported EHB Belugas to be larger and travel in smaller groups (Tyrrell 2008). However others have described EHB Belugas as smaller, shorter and fatter than WHB Belugas (Gislason 2007; Breton-Honeyman *et al.* 2013). Some ATK sources consider EHB whales to be smaller than those from James Bay (Doidge *et al.* 2002), although informants in a different study indicate that JB Belugas are shorter and fatter (Breton-Honeyman *et al.* 2013). When comparisons are made to DUs outside Hudson Bay, both WHB and EHB Belugas are described as being similar to each other but smaller than those from CS and EHA-BB (Richard 2010).

4. Movement, Behaviour, and Life History Strategies

ATK holders note differences in spring migratory behaviour between EHB and WHB whales (Cardinal 2013). EHB Belugas migrate in late winter/early spring a few weeks later, traveling westward along the southern shore of Hudson Strait into eastern Hudson Bay. They are observed traveling past Quaqtaq and Ivujivik in May and June (Breton-Honeyman *et al.* 2013).

This population is defined by its centres of estuarine concentration at the Nastapoka and Little Whale rivers, with the main area of summer coastal occupation extending from Kujjuarapik to Inukjuak. Aerial surveys, which started in 1983, showed that there was an offshore distribution of animals throughout this area as far offshore as the Belcher Islands (Smith and Hammill 1986; Kingsley 2000; Gosselin *et al.* 2002, 2009, 2013). The Nastapoka and Little Whale rivers are the main estuarine areas where EHB whales aggregate, and they are frequented by Belugas from mid-July to the end of August (Breton-Provencher 1979; Caron and Smith 1990; Doidge 1994; McDonald *et al.* 1997; Doidge and Lesage 2001; Tyrrell 2008; Lewis *et al.* 2009; Breton-Honeyman *et al.* 2013). They are also present at the Little Whale River, Richmond Gulf, and around Long Island, but few if any whales are seen around Ivujivik in August (Breton-Honeyman *et al.* 2013). Thirty-seven Belugas were equipped with satellite transmitters between 1993 and 2004 (July or August) in the Hudson Bay Arc and tracked throughout the summer, fall and winter (as tag life allowed) (Lewis *et al.* 2009; Bailleul *et al.* 2012). During the summer (July-September) animals remain concentrated near the coast, and most individuals performed repeated inshore-offshore movements extending out to the Belcher Islands (Bailleul *et al.* 2012) but returning repeatedly to their estuarine tagging site (Doniol-Valcroze *et al*. 2012).

In the fall EHB Belugas leave coastal areas and migrate north along the eastern Hudson Bay coastline. ATK holders report that most migrate past Ivujivik into Hudson Strait in September and October (McDonald *et al.* 1997; Breton-Honeyman *et al.* 2013). Inuit in Quaqtaq and Ivujivik observe whales from both the EHB and WHB DUs on their migrations, and note that both groups will migrate at the same time but stay in separate groups (Breton-Honeyman *et al.* 2013). Tagged Belugas departed the EHB area between mid-September and late November, depending on the individual (mean ± SD: 16 October ± 18 d) (Bailleul *et al.* 2012). Diving activity increased markedly when Belugas were located to the north of the Belcher Islands for the several-month period prior to migration, indicating possible foraging activity. By mid-November all the whales with working transmitters had migrated out of Hudson Bay and moved to the Ivujuvik and Hudson Strait area (Bailleul *et al.* 2012). The animals then continued eastward through Hudson Strait and entered UB, where they spent time in the southeastern part of the bay (Lewis *et al.* 2009; Bailleul *et al.* 2012).

ATK holders from Ivujivik report that Belugas overwinter in open waters in the region from January to April, mainly around Digges Island in southern Hudson Strait (Lewis *et al.* 2009; Breton-Honeyman *et al.* 2013). This is the same area where some satellite-tagged whales from the WHB DU have overwintered (see above). The satellite-tagged EHB whales stayed in UB for part of the winter, up until late February for one individual. Other whales departed UB in December, after spending on average 40 ± 17 d there (range: 6 to 55 d) (Bailleul *et al.* 2012, also see Lewis *et al.* 2009). These whales then travelled over 500 km along the coast to an area of deep troughs in the Labrador Sea, arriving in January and remaining there until tag failure (all tags had ceased functioning by early March) (Bailleul *et al.* 2012). Belugas that are seen off northern Labrador in the winter and spring (Brice-Bennett 1978) are likely from the EHB population.

5. Distribution

The EHB population summers on the east coast of Hudson Bay and the majority of individuals overwinter in Hudson Strait. While in their summer aggregation sites these whales are mostly discrete from other DUs, although there may be some late-summer overlap with whales from the WHB and JB DUs. Overlap may increase during migration and overwintering (and also with the UB DU). Inuit along the Hudson Strait and eastern Hudson Bay coasts have observed that many of the rivers formerly frequented are no longer used by Belugas, and most believe that anthropogenic noise has caused them to shift offshore (Doidge *et al.* 2002; McDonald *et al.* 1997; COSEWIC 2004).

Discreteness and Significance

Based on mitochondrial sequences and haplotype frequencies, this DU is discrete, although EHB haplotypes are occasionally observed in samples from WHB and CS (Turgeon *et al.* 2012). The whales in this DU are mostly separated from other DUs during the summer, with some possible overlap with migrating whales from WHB in late summer, or with JB whales. Overlap and potential for genetic mixing would be highest during the winter but the distribution of tagged whales suggests some separation. In winter, satellite tagged EHB whales spent more time in southern Ungava Bay (Lewis *et al.* 2009; Bailleul *et al.* 2012), while WHB whales tended to stay to the northern end of Ungava Bay or in Hudson Strait (Smith 2007). In addition, EHB whales migrated down the Labrador coast (Bailleul *et al.* 2012) whereas whales from WHB did not travel further than the northern tip of Labrador (Smith 2007). This may serve to keep the two DUs largely separate during the mating period.

The EHB DU has a distinct summer aggregation in the Hudson Bay Arc. It does mix with other DUs (WHB, JB) around the Belcher islands but these other DUs do not aggregate at the estuaries along the Nunavik coast (Nastapoka, Great Whale River, etc.). Loss of the EHB DU would therefore result in the loss of Belugas from a significant portion of eastern Hudson Bay. Historical commercial harvests greatly reduced the number of Belugas in this DU (Reeves and Mitchell 1987b); estuary use has also changed and numbers have not recovered.

The evidence for evolutionary significance of this DU is very strong as the haplotypes and some haplotypes frequencies are observed only in one other DU (STL). Often with the divergence of mtDNA lineages there is also the inference that other parts of the genome have also evolved along unique evolutionary pathways. It is likely that isolation in the Atlantic refugium that gave rise to the unique haplotypes also conferred adaptations that have enabled these Belugas to persist and not be replaced with the more common Pacific refugium haplotypes. Loss of this DU would create a gap in the distribution and remove most of the Belugas with these important lineages.

DU7: St. Lawrence Estuary (STL)

The St. Lawrence Estuary Beluga population, long presumed to be a relict Arctic population, is at the southernmost limit of the species' global range. Its current range is small compared to its historical distribution, and is centred near the mouth of the Saguenay River (EO = *ca.* 36,000 km²; IAO = 20,628 km²; COSEWIC 2014b). The summer range of these animals is well known as, since 1973, it has been entirely covered by numerous aerial surveys (visual and photographic) (COSEWIC 2004). Less is known of the population’s winter distribution. No satellite-tagging has been conducted but Lemieux Lefebvre *et al.* (2012) studied fine-scale movement patterns using VHF-TDR suction-cup tags. Beluga numbers in the Gulf of St. Lawrence were significantly reduced by hunting (Vladykov 1944; Reeves and Mitchell 1984, 1987d) and also possibly by the loss of certain estuarine habitats (Kingsley 2002). No ATK is available for this DU but there is archaeological and historical evidence of harvests by Iroquois hunters (Reeves and Mitchell 1984, 1987d; Tremblay 1993). Fewer than 20 genetic samples from this DU have been reported in the literature and specific locations are not identified as the samples are from beach cast whales that have drifted an unknown distance. The results of recent biopsy sampling are not yet published (L. Postma, DFO Winnipeg, pers. comm.).

Lines of Evidence

1. Phylogenetics

Animals in the STL DU are by far the most genetically divergent group of Belugas in Canada. Mitochondrial haplotypes observed in this DU are part of an eastern clade thought to be derived from an Atlantic Refugium (Brown Gladden *et al.* 1997).

2. Genetic Diversity, and Structure

Mitochondrial haplotype diversity is very low in this DU. Of the three haplotypes observed two appear to be rare or absent in other DUs (Brown Gladden *et al.* 1997; de March and Maiers 2001; de March and Postma 2003) (Figure 2). The third haplotype has been found in animals from WHB (rare) and EHB (more common) (de March and Postma 2003). This low diversity could be due to bottlenecks in the past or from a more recent and prolonged genetic bottleneck.

Frequency-based analysis of nuclear genetic data indicates significant differentiation between STL and all other DUs (Brown Gladden *et al.* 1999). Given these early results, there has been no Bayesian-based analysis to determine if migrants occur. There may be potential for migrants from the north but the low genetic diversity suggests that this is uncommon.

3. Morphology

Data on the body size of St. Lawrence Belugas are limited (*e.g.*, Vladykov 1944; Sergeant 1986). Sergeant and Brodie (1969) examined differences in extrapolated body weight and concluded that three different Beluga populations were found in eastern North America, with small Belugas in WHB, medium-sized Belugas in the Canadian Arctic and St. Lawrence River, and large Belugas along the West Greenland coast. A re-analysis of the data showed that these differences were generally too small to classify individuals to region on the basis of size (Doidge 1990a). Earlier analyses were likely influenced by biases in historical measurements (versus current standard measurements) (Doidge 1990a; also see Vladykov 1943). Weight at length did not vary significantly between Belugas from EHB, WHB and STL. Both male and female Belugas from the St. Lawrence River were slightly longer than those from Hudson Bay of the same age, but statistical interpretation was limited by small sample sizes. Length at age comparisons of northern Quebec and St. Lawrence animals showed similar slight differences between sites. The differences were generally too small to classify individuals to region on the basis of size (Doidge 1990a). There is no ATK available on the morphological characteristics of animals in this DU (Cardinal 2013).

4. Movement, Behaviour, and Life History Strategies

Belugas of the STL DU summer in the region influenced by the outflow of the Saguenay River, and this well-known distribution has not changed appreciably in recent decades (Michaud *et al.* 1990; Michaud 1993; Lesage and Kingsley 1995; Mosnier *et al.* 2010;

Lemieux Lefebvre *et al.* 2012; Gosselin *et al.* 2014). The population's historical range was much larger and extended further downstream and upstream in the St Lawrence estuary (Vladykov 1944; Reeves and Mitchell 1984).

The whales are year-round residents of the St. Lawrence River system and undertake only short seasonal migrations (Lemieux Lefebvre *et al.* 2012). A general movement east during the fall, and west during the spring, was documented in the 1930s (Mosnier *et al.* 2010). Visual aerial surveys conducted in 1989 and 1990 (and reviewed by Mosnier *et al.* 2010) recorded fall movements (mid-October and November) to the Lower Estuary east to Baie-Comeau (north shore) and Rimouski (south shore). These observations of eastward fall movements were consistent with those of Vladykov (1944), but that study also documented a migration of large adults west of Île-aux-Coudres to Quebec City and upstream in the Saguenay River to Anse-Saint-Jean. These whales were presumably seeking migrating eels but this observation cannot be confirmed with the information available (Mosnier *et al.* 2010).

Little is known of the STL Belugas current winter distribution. Knowledge of their winter distribution is mostly based on ten visual aerial surveys, with variable coverage, conducted from December to March 1989-1990 (Mosnier *et al.* 2010). Belugas were observed near the Saguenay River mouth/Les Escoumins area, with most observations being made in December and March (also see Vladykov 1944). There appears to be a slight increase in the use of areas a little further downstream during the winter months (Kingsley 1998). During winter, Belugas are largely absent in the Upper Estuary and present in the Lower Estuary (Mosnier *et al.* 2010). In March, most Belugas were seen along the south shore of the Estuary between Île Verte and Les Méchins, and in the Gulf (Michaud *et al.* 1990). During mid-winter surveys (end of January to beginning of March 1990), most whales were observed in the northern part of the Gulf of St. Lawrence, particularly around Sept-Îles, with no Beluga seen along the south shore (Mosnier *et al.* 2010). Belugas do occur during winter (December to March) off the Saguenay River and Les Escoumins (Mosnier *et al.* 2010), as well as off Godbout where there is only partial ice coverage (Saucier *et al.* 2003).

5. Distribution

The STL DU is restricted to the Gulf of St. Lawrence area of eastern Canada. The range of this DU has remained stable in recent decades but is much reduced from the historical (pre-exploitation) range. The Belugas inhabit a relatively restricted zone of a highly populated, industrialized region that is a heavily used maritime shipping corridor (COSEWIC 2004). Habitat use by and behaviour of this DU are influenced by vessel traffic (Lesage *et al.* 1999, 2014; Ménard *et al.* 2014) and by long-term changes in environmental conditions in the Gulf of St. Lawrence (Plourde *et al.* 2013). Lemieux Lefebvre *et al.* (2012) reported the summer range to cover *ca.* 2,790 km^2 in the St. Lawrence Estuary and Saguenay River. This is a much smaller area than the AO reported in COSEWIC (2004). This population is listed as threatened under the Canadian *Species at Risk Act* (SARA) and Critical Habitat has been identified, corresponding to the summer area occupied by females accompanied by calves and juveniles (DFO 2014).

Additional information is needed to identify areas of winter concentration and assess the proportion of the population using the Lower Estuary versus Gulf during winter (Mosnier *et al.* 2010).

Occasional extralimital sightings of Belugas are reported either along the Labrador coast or south of the St. Lawrence Estuary (Curren and Lien 1998). Genetic analysis of an extralimital animal from Labrador indicated that it belonged to an Arctic population (COSEWIC 2004). However, some of these animals could be strays from the STL DU, particularly those seen to the south.

Discreteness and Significance

This is the most genetically divergent group of Belugas in Canada and it is significantly differentiated from other DUs. Genetic diversity of this population is the lowest of all Canadian populations. There has been no Bayesian-based analysis to determine if migrants occur; a larger, more recent sample from this population would be valuable for genetic analyses. There may be the potential for migrants from northern DUs however low diversity suggests that this is not common. Of potential evolutionary significance is the fact that this DU is the farthest south and could harbour local adaptations to both a year-round riverine habitat existence and to a warmer southern location.

This DU is widely separated from other DUs and there is an absence of any significant numbers of Belugas in the areas contiguous to their location. Given the significant distance between the St. Lawrence Belugas and the Arctic DUs, these animals can be considered a discrete DU. However, the occurrence of large numbers of Belugas off St. Anthony, Newfoundland in 2009 (CBC 2009), while distant and unusual, suggests potential for genetic exchange.

Historically, there might have been two populations of Belugas in the St. Lawrence, one centred on the Saguenay River and the other on the Manicouagan River (Kingsley 2002). The latter was heavily exploited (Laurin 1982) and the damming of the river might have resulted in the disappearance of this population. It is not possible to determine if two different DUs originally resided in this area. The loss of this DU would result in the loss of Belugas from the Gulf of St. Lawrence area and the loss of the most-southerly distributed Beluga population in the world.

DU8: James Bay (JB)

This is a new DU that was not recognized in the last status assessment (COSEWIC 2004) and therefore has no measures of EO or AO. The 2004 assessment included whales found in James Bay with the WHB population but noted that this was uncertain. Additional scientific research (satellite tagging, genetic studies), combined with ATK, supports recognition of James Bay Belugas as a separate DU. These animals constitute a large (2011 estimate of *ca.* 15,000 whales, Gosselin *et al.* 2013), non-migratory population that remains in the James Bay area year-round instead of migrating to Hudson Strait like Belugas from the WHB and EHB DUs. Information on this DU is available from aerial surveys (Jonkel 1969; Smith and Hammill 1986; Kingsley 2000; Gosselin *et al.* 2002, 2009, 2013; Gosselin 2005), satellite-tagging (Bailleul *et al.* 2012; Postma *et al.* 2012), genetic studies (Turgeon *et al.* 2009; Postma *et al.* 2012), and ATK (Jonkel 1969; McDonald *et al.* 1997; Lewis *et al.* 2009; Breton-Honeyman *et al.* 2013). Cardinal (2013) called it the "Hudson Bay-James Bay" DU, whereas DFO refers to the "James Bay" summer stock (Richard 2010). Whales tagged in eastern James Bay (Bailleul *et al.* 2012) remained in James Bay year-round, and "James Bay" may be a more accurate designation for this DU. Samples for genetic analysis have been obtained from Cape Jones Island, Long Island, and other areas of James Bay (Postma *et al.* 2012).

Lines of Evidence

1. Phylogenetics

Samples from this DU consist of haplotypes related to both the Atlantic (eastern) and Pacific (western) refugia (clades) (Postma *et al.* 2012). In general, the higher frequency haplotypes in this DU are part of the Pacific or western clade.

2. Genetic Diversity, and Structure

Several authors have suggested that the population affinity of animals harvested by the community of Sanikiluaq is uncertain (*e.g*., de March and Maiers 2001) or that the hunts target animals from more than one stock (Brown Gladden *et al.* 1997). Recent analysis (GMA, Turgeon *et al.* 2012) identified an unknown stock mixture that was hypothesized to be the JB DU. This work was followed up using genetics and telemetry, which further support the differentiation of JB (Postma *et al.* 2012; Bailleul *et al.* 2012) (Figure 2).

Nuclear markers, as is typical for Belugas, show shared ancestry with other DUs although frequency analysis show significant differentiation between James Bay and other DUs (EHB and WHB) and also the Sanikiluaq harvest (Postma *et al.* 2012). This suggests the Sanikiluaq harvest may be primarily a mixed harvest of EHB and WHB animals. Individual-based Bayesian analysis provides weak evidence that JB experiences less gene flow in that JB animals tend to have higher ancestry assigned to one genetic cluster (Figure 5 in Postma *et al.* 2012).

There is some evidence for another DU in southeastern Hudson Bay and/or James Bay. This evidence is from samples of ice-entrapped Belugas collected near the Belcher Islands. The haplotype mixture of these entrapments (n=28 in 2004; n=9 in 2011; n=12 in 2013) differs from EHB, WHB, and JB haplotype mixtures (L. Postma pers. comm.) (see Figure 3). Turgeon *et al.* (2012) commented that the haplotypes observed in Sanikiluaq harvests are unique but did not hypothesize why. ATK holders in Sanikiluaq differentiate between local whales and those that migrate out of the bay or accidentally become trapped in ice. Further analysis with increased sampling is required to resolve whether a distinct DU exists around the Belcher Islands.

3. Morphology

There are no scientific studies of the body size (length-at-age, asymptotic length, etc.) of James Bay Beluga whales. Comparative information available via ATK is conflicting. Some ATK holders described James Bay Belugas as larger than those from EHB (Doidge *et al.* 2002; Gislason 2007); others indicated that JB Belugas are shorter and fatter than other Belugas (Breton-Honeyman *et al.* 2013).

4. Movement, Behaviour, and Life History Strategies

Both ATK and scientific research confirm the sedentary (*i.e.*, non-migratory) nature of this DU. Jonkel (1969) first reported over-wintering of Belugas in James Bay, after observing whales in open leads around the major islands while conducting Polar Bear research in 1969. Inuit have long known about the existence of overwintering whales in James Bay. Schwartz (1976) reported Inuit observations that Belugas retreated to areas of open water west of Charlton Island during the winter, where they occasionally become trapped in ice. Many different ATK studies describe the presence of an overwintering population in Hudson Bay and James Bay (Kemp 1982; McDonald *et al.* 1997; Doidge *et al.* 2002; Lewis *et al.* 2009; Breton-Honeyman *et al.* 2013).

Scientific (*i.e*., satellite-tagging) research and ATK provide somewhat different information on wintering locations. All whales tagged in James Bay remained there throughout the winter, in the vicinity of Cape Hope Island, although distribution in the offshore area was greater than in summer and fall (Bailleul *et al.* 2012). None of these tagged whales travelled north into Hudson Bay. In contrast, Inuit report that these whales summer around James Bay and winter near the Belcher Islands in open water (Breton-Honeyman *et al.* 2013). During winter, Belugas are seen at the floe edge southwest and west of the Belcher Islands and in eastern James Bay, southeastern Hudson Bay (Chisasibi), and southwestern Hudson Bay (Winisk) (McDonald *et al.* 1997). The area around Long Island is also noted by ATK holders as a wintering location for these Belugas, as is an area of strong current between the Belcher Islands and James Bay (McDonald *et al.* 1997; Lewis *et al.* 2009; Breton-Honeyman *et al*. 2013). Knowledge holders note that this wintering population is different from migrating whales or those that become entrapped in the ice accidentally (McDonald *et al.* 1997).

Belugas appear in April at ice cracks north of the Belcher Islands (McDonald *et al.* 1997). Sanikiluaq and Kuujjuarapik residents also see whales as soon as cracks start to appear in the ice, which can be as early as mid-May at Kuujjuarapik (Breton-Honeyman *et al.* 2013). The population affinity of these animals is unknown. None of the whales satellite-tagged in James Bay moved north to the Belcher Islands area, but all tags had also failed by mid-March (Bailleul *et al.* 2012). The JB Beluga population is large (*ca.* 15,000 whales, Gosselin *et al.* 2013), so the 12 animals whose tags transmitted beyond the summer months are not necessarily representative of its overall winter distribution. They were all tagged at the same location and had the same haplotype but were tagged in three successive years. Postma *et al*. (2012) used these data to conclude that the proportion of migrating beluga, if any, is likely lower than 2%.

Belugas belonging to the JB DU aggregate in the summer in James Bay (satellite-tagging and aerial survey observations) and possibly in southwestern Hudson Bay (ATK observations). In October, Belugas are reported to still be feeding in southern James Bay, near Moose Factory and in Hannah Bay (McDonald *et al.* 1997). Belugas are also present along the Ontario coast of Hudson Bay, near the Severn and Winisk rivers, in May through September (Richard 2010) but their population affinity is uncertain.

5. Distribution

As described above, this DU is limited to the James Bay area year-round, and possibly the southeast Hudson Bay coast north to the Belcher Islands. It is separated from other DUs for most of the year, although there may be some overlap with whales from the WHB and EHB DUs, particularly around the Belcher Islands. Of the beluga tagged in WHB and EHB only one has ventured into northern JB (Richard and Orr 2003; Smith *et al.* 2007) suggesting the overlap may be minimal.

Discreteness and Significance

The JB DU occupies James Bay during both summer and winter and is largely discrete from the other Hudson Bay DUs. Morphological differences reported by ATK are equivocal. ATK suggests that some mixing of stocks occurs in Hudson Bay at certain times during the year, centring on the Belcher Islands (Gislason 2007; DFO 2011; Brown and Fast 2012; Breton-Honeyman *et al.* 2013). Genetic analyses indicate the potential for a separate or mixed population in this area (Turgeon *et al.* 2009; Postma *et al.* 2012). Samples from the Belcher Islands have a mixture of haplotypes that are typical of eastern Hudson Bay and haplotypes typical of Southeast Baffin or Western Arctic, plus an unusual quantity of rare and unique haplotypes (Turgeon *et al.* 2009). Nuclear markers indicate significant differentiation between James Bay and other DUs (EHB and WHB) (Postma *et al.* 2012). Additional research is required to determine if there is additional structure of the Beluga harvested around the Belcher Islands. Organochlorine contaminant concentrations also suggest differences in Sanikiluaq Beluga samples compared to others from Hudson Bay (Innes *et al.* 2002a; Stern *et al.* 2005).

Belugas in the JB DU are exceptional, perhaps unique, among the Belugas of Hudson Bay (*i.e*., WHB and EHB DUs) in that they choose to remain in the region year-round. While some individuals of the other DUs winter in Hudson Bay, few may do so by choice. Loss of the JB DU would result in a significant gap in the species' range (the loss of Belugas from James Bay) and result in the loss of a special (non-migratory) adaptation within the greater Hudson Bay region.

Proposed DU Structure for Belugas in Canada

Based on this review, eight Designatable Units (DUs) of Belugas are supported in Canadian waters (Table 7). All seven that were recognized and assessed in 2004 (COSEWIC 2004) qualify under the current Guidelines, although the former WHB boundary has been modified to recognize the one newly proposed DU (James Bay, DU8: JB). This new DU consists of animals that were formerly assigned to the Western Hudson Bay DU (DU5), which may be more accurately named the "Western-Northern-Southern Hudson Bay" DU (following DFO's name for the summer stock, Richard 2010). Additional satellite-tracking and genetic studies, some of which are ongoing, may support further divisions of the current DUs leading, for example, to a new DU centred on the Belcher Islands and a possible split of DU2 (EHA-BB) into multiple DUs. Further research is also needed to refine the boundary between EHA-BB and CS with respect to potential overlap in Davis Strait, and the boundary between EHA-BB and WHB in northern Foxe Basin.

All of the DUs proposed in this report are founded to a considerable degree on summer distribution and differences in mitochondrial haplotype frequencies are probably reflective of strong female fidelity to estuaries. Overlap of the winter distribution and during migration for some of the proposed DUs may have contributed to some gene flow and low observed levels of differentiation at nuclear markers, although a Canada wide analysis of these data are needed. Interbreeding by animals from different DUs may occur in wintering areas (Turgeon *et al.* 2012), but the strong adherence to traditional migration routes, a maternally transmitted feature of Beluga behaviour, may prevent substantial genetic exchange between DUs that are seasonally sympatric (Innes *et al.* 2002a; Colbeck *et al.* 2013). The large population size, long life-spans, and overlapping generations helps to maintain genetic diversity and the current set of markers and samples may not be sufficient to detect barriers to nuclear gene flow even if they exist.

Genetic studies were used in many cases to demonstrate discreteness and to infer significance in some cases. The strongest evidence comes from mitochondrial DNA markers, which are maternally inherited and thus represent female lineages that return to specific summer locations. Nuclear markers (bi-parentally inherited) show evidence of male-mediated gene flow among locations as may be expected if winter breeding ranges overlap. DFO has been the primary accumulator of samples and each genetics publication tends to use all previous samples plus recent samples at the time, creating highly concordant results over time.

Information on morphology (size, growth rates, etc.) was presented where available, but this was not used as a major factor to determine discreteness. DU designations were proposed when several lines of evidence provided support for both discreteness and significance. The full weight of evidence was stronger for some DUs than for others, and the level of confidence in this proposed overall DU structure is high based on the data currently available.

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Authorities Contacted

Ole Nielsen, Fisheries and Oceans Canada, Winnipeg, MB

Lianne Postma, Fisheries and Oceans Canada, Winnipeg, MB

Kristin Westdal, Oceans North Canada, Winnipeg, MB

Biographical Summary of Report Writers

Dr. Jeff W. Higdon is a consulting biologist based in Winnipeg, MB. His PhD is from the University of Manitoba, where he carried out research on the biogeography and conservation of world pinnipeds. He has conducted extensive field research on Arctic marine mammals, including Belugas in both Nunavut and Manitoba, and has experience in collecting and interpreting Aboriginal Traditional Knowledge. Current research activities include developing Arctic monitoring programs, conducting risk assessments, reviewing industrial development projects, and preparing wildlife species status updates.

Dr. Stephen D. Petersen is the Head of Conservation and Research for Assiniboine Park Zoo in Winnipeg, MB. He has a MSc from Acadia University and a PhD from Trent University where he studied landscape and population genetics of Arctic mammals, in particular Polar Bears, Ringed Seals, and Peary Caribou. Before joining the Zoo he conducted marine mammal genetics research with the Arctic Aquatic Research Division of Fisheries and Oceans in Winnipeg. He continues to actively study Arctic marine and terrestrial mammals.

D. Bruce Stewart (MSc), Head of Arctic Biological Consultants, has studied aquatic ecosystems throughout northern Canada since 1976, traveling very extensively to conduct field studies and work with communities. For Belugas, he has helped identify critical habitat and compiled Aboriginal Traditional Knowledge and catch histories. Bruce has also provided expert advice on aquatic resources, species at risk, parks initiatives, and resource developments to government, industry, Inuit, and First Nations. He has completed many comprehensive reviews related to marine and freshwater environments, including *An overview of the Hudson Bay Marine ecosystem* and the current COSEWIC status updates for the Atlantic Walrus, Narwhal and Bearded Seal.

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Table 4. Degree of overlap in summer range (S), spring and fall migration routes (M), and winter range (W) for Beluga DUs[1]. Cell values: N= little or no overlap, ? = uncertainty in degree of overlap (see footnotes), and O =overlap.

Table 5. Comparison of contaminant profiles among different Beluga DUs, with colour coding for comparisons that are similar, uncertain, and different. Comparisons are difficult due to variable data quality, patchy sampling, differences in animal age, sampling years, monitoring intensity, etc. Contaminant studies generally provide information that demonstrates differences in dietary exposure to contaminants but are of limited value for determining discreteness. As a result, contaminant data were not particularly informative and were not considered as primary data sources for the delineation of DUs. Blank cells indicate no data, and “--” indicates cells under the diagonal. All data are from sources cited in main report text.

Table 6. Comparison of genetic differences (*e.g.*, mitochondrial and nuclear markers) among different Beluga DUs using frequency based methods (no Bayesian Analyses). “Moderate” to “highly” significantly different pairwise comparisons are highlighted in yellow, “low” but significantly differentiated pairs are highlighted in green, and undifferentiated pairs are highlighted in blue. Comparisons are difficult due to variable data groupings, patchy sampling, and inconsistent methods.

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Figure 2. MtDNA haplotype frequencies grouped by DU within Canada. Colour sections of each pie represent the most common haplotypes in the entire dataset. Sample sizes for each DU ranged from 67 (JB) to 460 (N-WHB). Mixed samples (northern Quebec, Sanikiluaq) and entrapment samples (Sanikiluaq) are not included. Data from L. Postma, unpublished.

Figure 3. Beluga mtDNA haplotype frequencies at 14 locations in Canada. Areas of the pies are proportional to sample size (L. Postma, unpublished data).

Table 1. Currently recognized Beluga DUs, from COSEWIC (2004), with their assessment histories.

Population	2004 Status	Assessment History	Comments
Eastern Beaufort Sea	Not at Risk	Designated Not at Risk in 1985	
Eastern High Arctic - Baffin Bay	Special Concern	Designated Special Concern in 1992	
Cumberland Sound	Threatened	Southeast Baffin Island-Cumberland Sound population was designated Endangered in 1990	Structure of the population redefined in 2004 and named “Cumberland Sound population”, and Southeast Baffin Island animals included as part of Western Hudson Bay population.
Ungava Bay	Endangered	Designated Endangered in 1988	
Western Hudson Bay	Special Concern	Designated Not at Risk in 1993	Population redefined in 2004 to include those Southeast Baffin Island animals outside Cumberland Sound, previously considered part of “Southeast Baffin Island-Cumberland Sound population”.
Eastern Hudson Bay	Endangered	Designated Threatened in 1988	
St. Lawrence Estuary	Endangered	Designated Endangered in 1983 and 1997, re-examined and designated Threatened in May 2004, re-examined and designated Endangered in 2014	Formerly St. Lawrence River population

Table 2. Comparison of population groupings last assessed by COSEWIC (2004), summer stocks identified by DFO for management purposes in the Nunavut Settlement Area (DFO 2010; Richard 2010), and potential DUs identified through Aboriginal Traditional Knowledge (ATK) (Cardinal 2013). Grey shading indicates disagreement with the COSEWIC (2004) DUs.

Populations (COSEWIC 2004)	**Summer stocks (DFO 2010; Richard 2010)**	**ATK DUs (Cardinal 2013)**
Eastern Beaufort Sea	Eastern Beaufort Sea	Eastern Beaufort Sea
Eastern High Arctic - Baffin Bay	Eastern High Arctic - Baffin Bay	Eastern High Arctic - Baffin Bay
Cumberland Sound	Cumberland Sound	Cumberland Sound
Ungava Bay	n/a[1]	Ungava Bay
Western Hudson Bay	Western-Northern-Southern Hudson Bay	Western Hudson Bay
	James Bay	Hudson Bay - James Bay
Eastern Hudson Bay	Eastern Hudson Bay	Eastern Hudson Bay
St. Lawrence Estuary	n/a[1]	St. Lawrence Estuary

[1] Not included in DFO assessment

Table 3. Comparison of morphological differences (*e.g.*, length-at-age, weight-at-length, asymptotic lengths) among different Beluga DUs. Comparisons are difficult due to variable data quality, patchy sampling, inconsistent methods, and uncertainly in age estimates due to having different researchers read GLGs. In addition, morphological differences have limited usefulness as an indicator of discreteness or significance due to effects of environmental seasonality. Growth is plastic, and likely related to environmental factors, and care must therefore be exercised when using morphological features. Furthermore, for some comparisons, information is equivocal. All data are from sources cited in main report text. Colour codings indicate comparisons that are similar, uncertain, and different. Blank cells indicate no data available for comparison, and "--" indicates cells below the diagonal.

DU	**EHA-BB**	**CS**	**UB**	**WHB**	**EHB**	**JB**	**STL**
EBS	EBS whales longer/larger	EBS whales longer/larger		EBS whales longer/larger	EBS whales longer/larger		
EHA- BB	--	Similar (but some data conflicting)	UB whales smaller (length)	EHA-BB larger/longer	EHA-BB larger/longer		
CS	--	--	UB whales smaller (length)	CS larger/longer	CS larger/longer		
UB	--	--	--	Similar in length	Similar in length		
WHB	--	--	--	--	Similar (some data conflicting)		Similar in length and weight
EHB	--	--	--	--	--	Limited data, ATK is conflicting	Similar in length and weight
JB	--	--	--	--	--	--	

Table 4. Degree of overlap in summer range (S), spring and fall migration routes (M), and winter range (W) for Beluga DUs[1]. Cell values: N= little or no overlap, ?= uncertainty in degree of overlap (see footnotes), and O =overlap.

DU/Season		**EHA-BB**			**CS**			**UB**			**WHB**			**EHB**			**JB**			**STL**		
		S	**M**	**W**	**S**	**M**	**W**	**S**	**M**	**W**	**S**	**M**	**W**	**S**	**M**	**W**	**S**	**M**	**W**	**S**	**M**	**W**
EBS	**S**	?[2]			N			N			N			N			N			N		
	M		N			N			N			N			N			N			N	
	W			N			N			N			N			N			N			N
EHA-BB	**S**				N			N			N			N			N			N		
	M					N			N			N			N			N			N	
	W						N			N			N			N			N			N
CS	**S**							N			N			N			N			N		
	M								N			N			N			N			N	
	W									N[3]			N[3]			N[3]			N			N
UB	**S**										N			N			N			N		
	M											?[4]			?[4]			N			N	
	W												O[5]			O[5]			N			N
WHB	**S**													N			?[6]			N		
	M														O			?[6]			N	
	W															O			N			N
EHB	**S**																?[6]			N[6]		
	M																	N			N	
	W																		N			N
JB	**S**																			N		
	M																				N	
	W																					N

[1] DUs: EBS = Eastern Beaufort Sea; EHA-BB = Eastern High Arctic – Baffin Bay; CS = Cumberland Sound; UB = Ungava Bay; WHB = Western Hudson Bay; EHB = Eastern Hudson Bay; STL = St. Lawrence Estuary; JB = James Bay.

[2] EBS and EHA-BB summer ranges presumed to be separated by multi-year ice in the central Arctic, which could change in the future.

[3] CS DU winters at the mouth of Cumberland Sound, which is hundreds of km north of the core wintering area(s) of the adjacent DUs.

[4] Migration route of UB DU not known (DU may be extirpated), overlap with other DUs possible in Hudson Strait.

[5] Winter overlap of UB and WHB and EHB DUs probable, but no information for UB (possibly extirpated).

[6] Movements of JB DU not well known, could overlap with WHB in summer (in southern Hudson Bay) or migration (some animals move eastward across Hudson Bay); EHB in summer.

Table 5. Comparison of contaminant profiles among different Beluga DUs, with colour coding for comparisons that are similar, uncertain, and different. Comparisons are difficult due to variable data quality, patchy sampling, differences in animal age, sampling years, monitoring intensity, etc. Contaminant studies generally provide information that demonstrates differences in dietary exposure to contaminants but are of limited value for determining discreteness. As a result, contaminant data were not particularly informative and were not considered as primary data sources for the delineation of DUs. Blank cells indicate no data, and “--” indicates cells under the diagonal. All data are from sources cited in the main report text.

Parameter	DU	EHA-BB	CS	UB	WHB	EHB	JB	STL
PCB	**EBS**	Similar			Similar			Different[4]
Hg[1]		Similar	Similar		Similar	Similar		
OC[2]		Similar[3]			Different	Different		
PCB	**EHA- BB**	--			Similar			Different[4]
Hg		--	Similar		Similar	Similar		
OC		--	Different		Different	Different		
PCB	**CS**	--	--					
Hg		--	--		Similar	Similar		
OC		--	--		Different	Different		
PCB	**UB**	--	--	--				
Hg		--	--	--				
OC		--	--	--				
PCB	**WHB**	--	--	--	--			Different[4]
Hg		--	--	--	--	Similar		
OC		--	--	--	--	Different	Uncertain[5]	
PCB	**EHB**	--	--	--	--	--		
Hg		--	--	--	--	--		
OC		--	--	--	--	--	Uncertain[5]	
PCB	**JB**	--	--	--	--	--	--	
Hg		--	--	--	--	--	--	
OC		--	--	--	--	--	--	

[1] Total mercury (Hg) was historically higher in EBS compared to eastern Canadian Arctic DUs, regional differences have diminished over time and are no longer statistically significant (Lockhart *et al.* 2005).

[2] OC = organochlorine contaminant concentrations.

[3] OC profiles suggest sub structuring in EHA-BB DU.

[4] PCB and sPCAs levels are higher in STL DU (also different congeners).

[5] OC suggests Sanikiluaq harvests different

Table 6. Comparison of genetic differences (*e.g.*, mitochondrial and nuclear markers) among different Beluga DUs using frequency based methods (no Bayesian Analyses). “Moderate” to “highly” significantly different pairwise comparisons are highlighted in yellow, “low” but significantly differentiated pairs are highlighted in green, and undifferentiated pairs are highlighted in blue. Comparisons are difficult due to variable data groupings, patchy sampling, and inconsistent methods.

DU	**EHA-BB**	**CS**	**UB**	**WHB**	**EHB**	**JB**	**STL**
EBS	mtDNA[3] and nDNA[4]	mtDNA[3] and nDNA[4]	No data available for comparison	mtDNA[3] and nDNA[4]	mtDNA[2] and nDNA[4]	not compared to date	mtDNA[3] and nDNA[4]
EHA- BB	--	mtDNA[3] and nDNA[4]	No data available for comparison	mtDNA[3] and nDNA[4]	mtDNA[3] and nDNA[4]	not compared to date	mtDNA[3] and nDNA[4]
CS	--	--	No data available for comparison	mtDNA[3] and nDNA[2]	mtDNA[2,3] and nDNA[2]	not compared to date	mtDNA[3] and nDNA[4]
UB	--	--	--	No data available for comparison	No data available for comparison	No data available for comparison	No data available for comparison
WHB	--	--	--	--	mtDNA[2] and nDNA[1,2]	mtDNA[1] and nDNA[1]	mtDNA[3] and nDNA[4]
EHB	--	--	--	--	--	mtDNA[1] and nDNA[1]	mtDNA[3] and nDNA[4]
JB	--	--	--	--	--	--	Not compared to date

1. Postma *et al*. 2012. 2. Turgeon *et al*. 2012. 3. Brown Gladden *et al*. 1997. 4. Brown Gladden *et al*. 1999

Table 7. Evidence supporting the discreteness and significance (following COSEWIC 2009) of designatable units (DU) for Beluga (*Delphinapterus leucas*). Geographical coverage limitations prevent complete cross-comparisons of data among the DUs, so the discreteness and significance comparisons for a particular DU may be in relation to one or more DUs. Y=available data supported discreteness or significance; += available data contributed some support; N = available data did not support; - = no data were available. Phylogenetic divergence is an exception, where the Ys only differ from the Ns, and vice versa.

Name of Designatable Unit (DU)	Discreteness					Significance		
	Genetic Distinctiveness	Morphological differences	Movement, behaviour, and life history traits	Summer distribution		Phylogenetic divergence (N from Y)	Local adaptation to ecological setting	Irreplaceable/ extensive gap
DU1: Eastern Beaufort Sea (EBS)	Y	+	Y	Y		N	-	Y
DU2: Eastern High Arctic – Baffin Bay (EHA-BB)	Y	+	+	Y		N	-	Y
DU3: Cumberland Sound (CS)	Y	+	Y	Y		N	+	Y
DU4: Ungava Bay (UB)	-	-	-	-		-	-	Y
DU5: Western Hudson Bay (WHB)	Y	+	+	Y		N	-	Y
DU6: Eastern Hudson Bay (EHB)	Y	+	Y	Y		Y	+	Y
DU7: St. Lawrence Estuary (STL)	Y	N	Y	Y		Y	+	Y
DU8: James Bay (JB)	Y	-	Y	Y		N	+	Y

Table 8. Summary of significant pairwise differences between proposed DUs (from Tables 3-6):

1. Genetics - only moderate to highly sig diff (Table 6)
2. Contaminants (Table 5)
3. Spatial separation (Table 4)
4. Length at age (Table 3)

	EHA-BB	**CS**	UB	WHB	EHB	JB	STL
EBS	1. mtDNA/nDNA 2. 3. All seasons(?) 4. size	1. mtDNA/nDNA 2. 3. All seasons 4. size	1. 2. 3. All seasons 4.	1. mtDNA/nDNA 2. OC 3. All seasons 4. size	1. mtDNA/nDNA 2. OC 3. All seasons 4. size	1. 2. 3. All seasons 4.	1. mtDNA/nDNA 2. PCB 3. All seasons 4.
EHA-BB		1. 2. OC 3. All seasons 4.	1. 2. 3. All seasons 4. size	1. 2. OC 3. All seasons 4. size	1. 2. OC 3. All seasons 4. size	1. 2. 3. All seasons 4.	1. mtDNA/nDNA 2. PCB 3. All seasons 4.
CS			1. 2. 3. All seasons 4. size	1. mtDNA 2. OC 3. All seasons 4. size	1. mtDNA 2. OC 3. All seasons 4. size	1. 2. 3. All seasons 4.	1. mtDNA/nDNA 2. 3. All seasons 4.
UB				1. 2. 3. Summer 4.	1. 2. 3. Summer 4.	1. 2. 3. All seasons 4.	1. 2. 3. All seasons 4.
WHB					1. mtDNA 2. 3. Summer 4.	1. mtDNA 2. 3. Winter 4.	1. mtDNA/nDNA 2. PCB 3. 4.
EHB						1. mtDNA 2. 3. Winter/migration 4.	1. mtDNA/nDNA 2. PCB 3. All seasons 4.
JB							1. 2. 3. All seasons 4.

Figure 1. Distribution of Belugas in Canada and proposed DUs: (DU1) Eastern Beaufort Sea; (DU2) Eastern High Arctic-Baffin Bay; (DU3) Cumberland Sound; (DU4) Ungava Bay; (DU5) Western Hudson Bay; (DU6) Eastern Hudson Bay; (DU7) St. Lawrence Estuary; and (DU8) James Bay (modified from map in COSEWIC 2004). This adds DU8, James Bay, to the DUs used in the 2004 assessment.

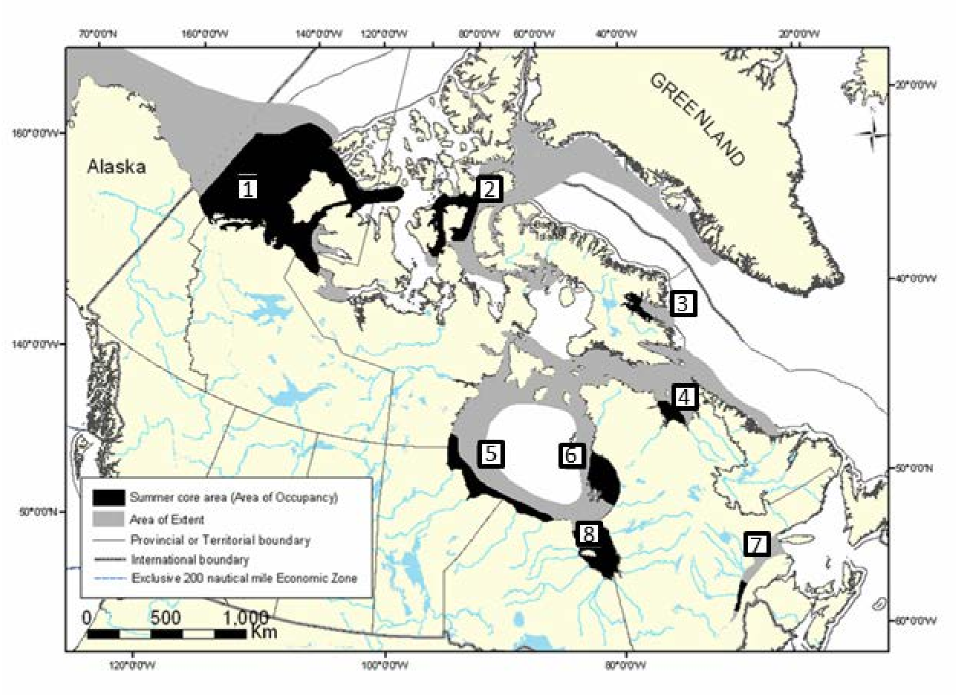

Figure 2. MtDNA haplotype frequencies grouped by DU (excluding Ungava Bay) within Canada. Colour sections of each pie represent the most common haplotypes in the entire dataset. Sample sizes for each DU ranged from 67 (JB) to 460 (N-WHB). Mixed samples (northern Quebec, Sanikiluaq) and entrapment samples (Sanikiluaq) are not included. Data from L. Postma, unpublished.

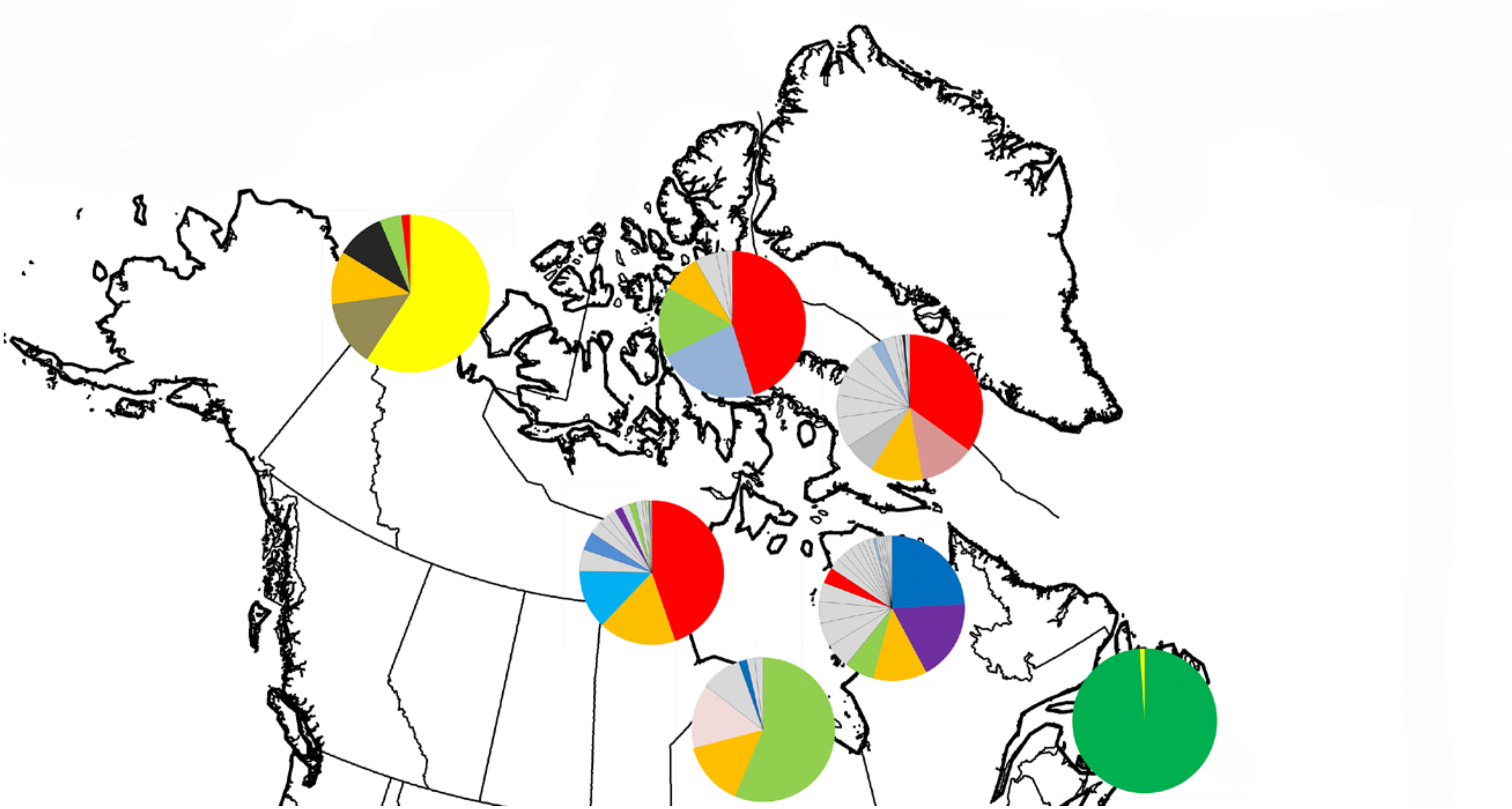

Figure 3. Beluga mtDNA haplotype frequencies at 14 sites in Canada. Areas of the pies are proportional to sample size (L. Postma, unpublished data).