Status Review of the Sakhalin Bay-Amur River Beluga Whale (*Delphinapterus leucas*) under the Marine Mammal Protection Act

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U.S. Department of Commerce
National Oceanic and Atmospheric Administration
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NOAA Technical Memorandum NMFS-OPR-51
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List of Acronyms

BRT	biological review team
DNA	deoxyribonucleic acid
DPS	distinct population segment
EEZ	Exclusive Economic Zone
ESA	Endangered Species Act
GAMMS	Guidelines for Assessing Marine Mammal Stocks
IUCN	International Union for Conservation of Nature
IWC	International Whaling Commission
IWC SC	International Whaling Commission's Scientific Committee
K	carrying capacity
MMPA	Marine Mammal Protection Act
MNPL	maximum net productivity level
mtDNA	mitochondrial DNA
NMFS	National Marine Fisheries Service
NOAA	National Oceanic and Atmospheric Administration
OSP	optimum sustainable population
PBR	potential biological removal
PCFG	Pacific Coast feeding group
SAR	stock assessment report
SEDM	structured expert decision making
Team	status review team

Status Review of the Sakhalin Bay-Amur River Beluga Whales

1. Introduction

Section 3(1)(A) of the Marine Mammal Protection Act (MMPA) (16 U.S.C. 1362(1)(A)) defines the term "depletion" or "depleted" to include any case in which "the Secretary, after consultation with the Marine Mammal Commission and the Committee of Scientific Advisors on Marine Mammals…determines that a species or a population stock is below its optimum sustainable population." Section 3(9) of the MMPA (16 U.S.C. 1362(9)) defines "optimum sustainable population [OSP]…with respect to any population stock, [as] the number of animals which will result in the maximum productivity of the population or the species, keeping in mind the carrying capacity [(K)] of the habitat and the health of the ecosystem of which they form a constituent element." The National Oceanic and Atmospheric Administration's (NOAA) National Marine Fisheries Service's (NMFS) regulations at 50 CFR 216.3 clarify the definition of OSP as a population size that falls within a range from the population level of a given species or stock that is the largest supportable within the ecosystem (i.e., carrying capacity, or K) to its maximum net productivity level (MNPL). MNPL is the population abundance that results in the greatest net annual increment in population numbers resulting from additions to the population from reproduction, less losses due to natural mortality. Historically, MNPL has been expressed as a range of values (between 50 and 70 percent of K) determined on a theoretical basis by estimating what stock size, in relation to the historical stock size, will produce the maximum net increase in population (42 FR 12010, March 1, 1977). In practice, NMFS has determined that stocks with populations under the mid-point of this range (i.e., 60 percent of K) are depleted (42 FR 64548, December 27, 1977; 45 FR 72178, October 31, 1980).

The MMPA allows interested parties to petition NMFS to initiate a status review to determine whether a species or stock of marine mammals should be designated as depleted. Section 115(a)(3) of the MMPA (16 U.S.C. 1383b(a)(3)) requires NMFS to publish a notice in the *Federal Register* that such a petition has been received and is available for public review. Within 60 days of receiving a petition, NMFS must publish a finding in the *Federal Register* as to whether the petition presents substantial information indicating that the petitioned action may be warranted.

If NMFS makes a positive 60-day finding, NMFS must promptly initiate a review of the status of the petitioned population stock of marine mammals. No later than 210 days after receipt of the petition, NMFS must publish a proposed rule as to the status of the species or stock, along with the reasons underlying the proposed status determination. Following a 60-day minimum comment period on the proposed rule, NMFS must publish a final rule within 90 days of the close of the comment period on the proposed rule.

2. Petition to designate the Sakhalin Bay-Amur River stock of beluga whales as depleted under the MMPA

2.1 Summary of petition

On April 23, 2014, NMFS received a petition from the Animal Welfare Institute, Whale and Dolphin Conservation, Cetacean Society International, and Earth Island Institute (petitioners) to "designate the Sakhalin Bay-Amur River stock of beluga whales as depleted under the MMPA." The petition presents information asserting that NMFS has authority to designate stocks outside of U.S. jurisdictional waters as depleted. The petition asserts the Sakhalin Bay-Amur River population of beluga whales comprises a stock under the MMPA and that this stock is below its OSP and qualifies for a depleted designation. The petitioners also argue that the stock continues to decline and faces a number of threats. The petition alleges that the causes of this stock's decline include: large-scale commercial hunting from 1915-1963 and renewed commercial hunting in 1999; unsustainable removal for captive display; incidental mortality from fishing operations; accidental drowning during live-capture operations for captive public display; vessel strikes; and other anthropogenic threats including oil and gas development, expansion of fisheries, pollution and climate change.

The petitioners suggest that genetic and satellite tag tracking data indicate the existence of at least two beluga whale populations in the Sea of Okhotsk: one in the northeastern region and the other in the western region. The petition goes on to present information suggesting that the beluga whales in the western region of the Sea of Okhotsk comprise, and should be managed as, more than one stock. The petitioners state that for the beluga whales in the western region of the Sea of Okhotsk, evidence of distinct matrilineal lines, separate summer birthing and feeding distributions, and high site fidelity, indicate that the region supports more than one stock of beluga whales, including a distinct Sakhalin Bay-Amur River stock. The petitioners state that the International Union for Conservation of Nature (IUCN) has recognized the existence of a distinct Sakhalin Bay-Amur River stock (see Reeves et al. 2011). Additionally, the petition asserts that the International Whaling Commission's Scientific Committee (IWC SC) recognized the Sakhalin-Amur beluga whales as a separate stock in 1999.[1]

The petition presents information from 2009 and 2010 aerial surveys indicating that the best current abundance estimate of the Sakhalin Bay-Amur River beluga whales is 3,961 whales (see Reeves et al. 2011). The petitioners assert that this estimate is well below 60 percent of the lowest available estimate of historical abundance (7,000-10,000; Berzin and Vladimirov 1990), and that the Sakhalin Bay-Amur River population of beluga whales therefore qualifies as depleted. The petition also notes that, after reviewing the available information on the status of beluga whales globally, the IWC SC described the Sakhalin-Amur- stock of beluga whales as having a "likely depleted status relative to historical abundance" (see IWC Report of the Sub-Committee on Small Cetaceans 2000).[2]

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[1] It should be noted that the IUCN and IWC's use of the term "stock" differs from the definition of a stock as defined by the MMPA and used by NOAA.

[2] It should be noted that the IWC's determination of "depletion" differs from the MMPA's depletion definition.

2.2 Agency finding

NMFS reviewed the information presented in the petition, readily available in the agency's files, and submitted through the public comment process, and determined that the petition presented substantial information indicating that the petitioned action may be warranted. Pursuant to section 115(a)(3)(B) of the MMPA, NMFS published its finding in the *Federal Register* on August 1, 2014 and informed the public that the agency would promptly initiate a status review (79 FR 44733). NMFS then established a status review team (Team) to conduct the review.

3. Distribution, abundance, and threats to beluga whales in the Sakhalin Bay-Amur River

3.1 Distribution and migration

Beluga whales (*Delphinapterus leucas*) are small, toothed whales distributed throughout the Arctic, and inhabit subarctic regions of Russia, Greenland, and North America (Figure 1). They are found in the Arctic Ocean and its adjoining seas, including the Sea of Okhotsk, the Bering Sea, the Gulf of Alaska, the Beaufort Sea, Baffin Bay, Hudson Bay, and the Gulf of St. Lawrence. Beluga whales may also be found in large river deltas and upstream at certain times of the year.

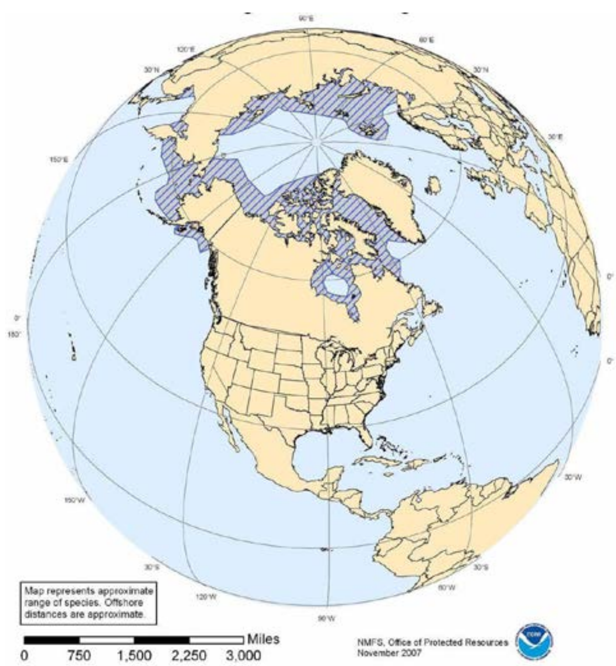

Figure 1. Map of beluga whale global distribution.

Beluga whale distributions show marked seasonal changes. Generally, there is a winter distribution in which the whales are found in deeper waters often associated with pack ice. In the spring and summer, there is a calving/feeding distribution in which the whales are found in warmer coastal estuaries, bays, and rivers where they may molt (Finley 1982) and give birth to and care for their calves (Sergeant and Brodie 1969). Migration between wintering and summering grounds may cover thousands of kilometers or may occur within a large bay or estuary (Reeves 1990).

Stock boundaries sometimes overlap spatially, and in such cases, the geographical delineation of beluga whale (also called white whale) stocks must have a temporal component. Migrating whales from different stocks may approach and move past a given site in "waves," while a summer "resident" stock moves into that same area for an extended period. For example, the Eastern Chukchi Sea stock is temporally delineated as the group of whales that arrives in Kotzebue Sound or Kasegaluk Lagoon as the ice begins to break up and remains there for at least several weeks. Earlier in the year, whales from the Beaufort Sea stock move through this area in the spring lead system. Thus, the annual catch at Alaskan villages such as Point Hope, Kivalina and Barrow can consist of whales from both of these stocks, depending on the time of year the whales are taken.

Beluga whales are found throughout much of the Sea of Okhotsk, including Shelikov Bay in the northeast and throughout the western Sea of Okhotsk including the Amur River estuary, the nearshore areas of Sakhalin Bay, in the large bays to the west, Nikolaya Bay, Ulbansky Bay, Tugursky Bay and Udskaya Bay, and among the Shantar Islands (Fig. 3). Use of the bays and estuaries in the western Sea of Okhotsk is limited primarily to summer months; the whales move into the ice-covered offshore areas of the western Sea of Okhotsk in the winter (Melnikov 1999). In the Sakhalin Bay and Amur Estuary region, whales' arrival and departure appear to be linked to fish runs (Solovyev et al. 2015). In this document, we refer to the beluga whales found in the Amur River estuary and the nearshore areas of Sakhalin Bay (Figure 2) during summer as the Sakhalin Bay-Amur River beluga whales**.** Beluga whales are not found to the south of the Amur River estuary area, though whales in the region have been seen arriving from the direction of Tatar Strait to the south (Solovyev et al. 2015).

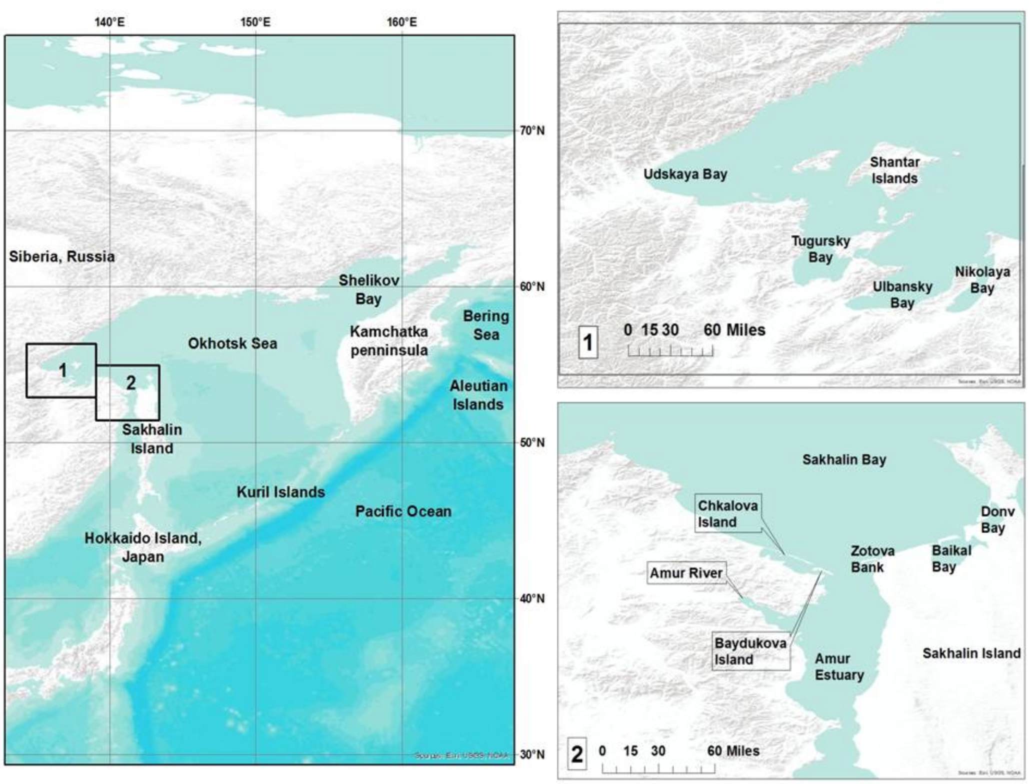

Figure 2. Map of Sea of Okhotsk

3.2 Abundance estimates of beluga whales in the Sakhalin Bay-Amur River beluga whale population

The best available estimate of abundance beluga whales in the Sakhalin Bay-Amur River area is 3,961 (Reeves et al. 2011). This estimate was based on surveys conducted in 2009 and 2010 (Shpak et al. 2011) and was further reviewed by an IUCN scientific panel of beluga whale experts (Reeves et al. 2011). The minimum population estimate for the Sakhalin-Amur population was determined to be 2,891 (Reeves et al. 2011). Comparable direct estimates of abundance from other areas are not available, hence direct estimates of trends are not feasible.

3.3 Current threats to Sea of Okhotsk beluga whales

Information on potential sources of serious injury and mortality is limited for the Sea of Okhotsk beluga whales. The IUCN panel (Reeves et al. 2011) identified subsistence harvest, death during live-capture for public display, entanglement in fishing gear, vessel strike, climate change, and pollution as human activities that may result in serious injury or mortality to Sea of Okhotsk beluga whales. The greatest amount of available information is from the annual take from the commercial hunt. As noted in the petition and the IUCN review, monitoring of other types of mortality in the Sea of Okhotsk is low, if existent at all, and information on possible threats and sources of mortality in Sea of Okhotsk beluga whales is highlighted by a lack of substantiated data, and is largely anecdotal. The IUCN panel emphasized the lack of data regarding other sources of mortality, and noted that "any animals taken by humans, including those killed or injured in fishing gear, struck by vessels, or accidentally drowned during live-capture operations, should be considered when evaluating the sustainability of any level of intentional removals" (Reeves et al. 2011).

Although the full extent of other sources of mortality cannot be determined, there is reason to believe that a suite of activities that threaten beluga whales in this area do occur (Reeves et al. 2011), and they cannot be fully discounted or assumed to be zero.

4. Response to petition - Do the Sakhalin Bay-Amur River beluga whales constitute a stock under the Marine Mammal Protection Act?

4.1 Review of MMPA definition of stock and summary of beluga whale stock delineation under the MMPA, IWC and IUCN

Section 115 of the MMPA grants NMFS the authority to designate as depleted a species or stock of marine mammals. Because the petitioners did not petition NMFS to designate an entire species as depleted, the first question that the Team considered is whether the Sakhalin Bay-Amur River population of beluga whales constitutes a stock, as defined under the MMPA.

4.1.1 The Marine Mammal Protection Act and definition of "stock"

The MMPA defines "population stock" as "a group of marine mammals of the same species or smaller taxa in a common spatial arrangement, that interbreed when mature" (MMPA section 3(11)).

Section 117 of the MMPA requires NMFS and the U.S. Fish and Wildlife Service to prepare stock assessment reports (SARs) for all marine mammal stocks occurring in waters under U.S. jurisdiction.

The SARs contain information on the identity and geographic range of the stock, population statistics related to abundance, trend, annual productivity, notable habitat concerns, and human-caused mortality and serious injury by source.

NMFS convened a workshop in June 1994 to develop guidelines for preparing SARs. The Guidelines for Assessing Marine Mammal Stocks (Wade and Angliss 1997; subsequently revised in NMFS 2005) (hereafter referred to as GAMMS) were devised by NMFS to ensure that SARs are developed in a repeatable, transparent manner consistent with the intent of the MMPA. These guidelines are followed for all marine mammal stock assessment reports, and have provided guidance for revisions to stock structure (e.g., identifying prospective stocks). The current guidelines, GAMMS II (NMFS 2005), have the following section on stock definition:

> "Many types of information can be used to identify stocks of a species: e.g., distribution and movements, population trends, morphological differences, differences in life history, genetic differences, contaminants and natural isotope loads, parasite differences, and oceanographic habitat differences. Different population responses (e.g., different trends in abundance) between geographic regions is also an indicator of stock structure, as populations with different trends are not strongly linked demographically. When different types of evidence are available to identify stock structure, the report must discuss inferences made from the different types of evidence and how these inferences were integrated to identify the stock.
>
> "Evidence of morphological or genetic differences in animals from different geographic regions indicates that these populations are reproductively isolated. Reproductive isolation is proof of demographic isolation, and, thus, separate management is appropriate when such differences are found. Demographic isolation[3] means that the population dynamics of the affected group is more a consequence of births and deaths within the group (internal dynamics) rather than immigration or emigration (external dynamics). Thus, the exchange of individuals between population stocks is not great enough to prevent the depletion of one of the populations as a result of increased mortality or lower birth rates.
>
> "Failure to detect differences, however, does not mean that populations are not demographically or reproductively isolated. Dispersal rates, though sufficiently high to homogenize morphological or genetic differences detectable between putative populations, may still be insufficient to deliver enough recruits from an unexploited population (source) to an adjacent exploited population (sink) so that the latter remains a functioning element of its ecosystem.

[3] A further revision, GAMMS III, is not yet final, but proposed changing "demographically isolated" to "demographically independent," since this was the intent of GAMMS II and is how the Agency has been interpreting the MMPA definition. NMFS considers in addition, the term "demographic independence" a better description than the term "demographic isolation". As such, this document will use the term "demographic independence".

"Insufficient dispersal between populations where one bears the brunt of exploitation coupled with their inappropriate pooling for management could easily result in failure to meet MMPA objectives. For example, it is common to have human-caused mortality restricted to a portion of a species' range. Such concentrated mortality (if of a large magnitude) could lead to population fragmentation, a reduction in range, or even the loss of undetected populations, and would only be mitigated by high immigration rates from adjacent areas.

"Therefore, careful consideration needs to be given to how stocks are identified. In particular, where mortality is greater than a Potential Biological Removal (PBR) level calculated from the abundance just within the oceanographic region where the human-caused mortality occurs, serious consideration should be given to identifying an appropriate management unit in this region. In the absence of adequate information on stock structure and fisheries mortality, a species' range within an ocean should be divided into stocks that represent defensible management units. Examples of such management units include distinct oceanographic regions, semi-isolated habitat areas, and areas of higher density of the species that are separated by relatively lower density areas. Such areas have often been found to represent true biological stocks where sufficient information is available. In cases where there are large geographic areas from which data on stock structure of marine mammals are lacking, stock structure from other parts of the species' range may be used to draw inferences as to the likely geographic size of stocks. There is no intent to identify stocks that are clearly too small to represent demographically isolated biological populations, but it is noted that for some species genetic and other biological information has confirmed the likely existence of stocks of relatively small spatial scale, such as within Puget Sound, WA, the Gulf of Maine, or Cook Inlet, AK."

In practice, NMFS has interpreted the language "interbreed when mature" in the MMPA definition of stock to mean cases in which either:

1. Mating occurs primarily among members of the same demographically independent group, or
2. The group migrates seasonally to a breeding ground where its members breed with members of the same group as well as with members of other demographically distinct groups which have migrated to the same breeding ground from a different feeding ground.

Taylor (1997) explored the definition of population in light of the management objectives of the MMPA, and developed a model to examine dispersal rates and provided several examples (Figure 3) where localized removals lead to local extirpation, which arguably violates the ecosystem goals of the MMPA. If human caused mortality for the entire population were to act disproportionately on certain groups, those groups could be extirpated, depending on whether the amount of immigration from other groups was below a certain dispersal rate threshold (which varied with simulation conditions). For all models tested, when dispersal fell below a few percent of the population per year, recruitment into the population with human caused mortality was insufficient to compensate for removal, and population levels declined below those sought by management objectives. Therefore, Taylor (1997) concluded that populations should be managed separately if dispersal between them is less than several percent per year. Further clarification of the different interpretations of the term "stocks" under the MMPA, the

Magnuson-Stevens Fisheries Conservation and Management Act and the Endangered Species Act (ESA) (where legal protection is given to Distinct Population Segments (DPS) have been provided in Eagle et al. (2008).

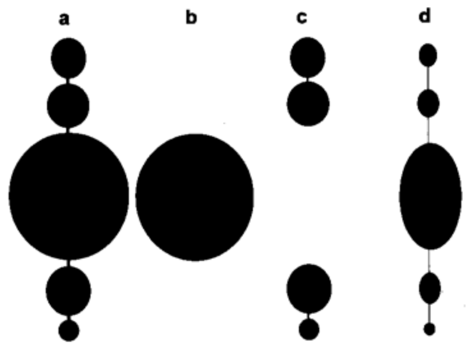

Figure 3. Original figure 1 from Taylor (1997). Distribution of five pristine populations (a), versus potential distributions after 50% of the total abundance is removed (b-d). Width represents abundance; length represents distance.

4.1.2 Identifying marine mammal stocks pursuant to the MMPA

Most U.S. marine mammal stocks remain as originally delimited following the 1994 amendments to the MMPA; however, several new stocks have been proposed and accepted since that time. These stock designations provide context to how the GAMMS definition of “stock” has been implemented. The cases most relevant to the Sakhalin Bay-Amur River beluga whale stock question posed here are those involving interpretation of genetic data. Selected cases follow.

Example: Harbor seals and harbor porpoises

Several stocks of harbor seals (*Phoca vitulina*) (O'Corry-Crowe et al. 2003) and harbor porpoises (*Phocoena phocoena*) (Chivers et al. 2002, 2007; Rosel et al. 1999) were delineated primarily on the basis of mitochondrial DNA (mtDNA) control region sequence data. In these cases, statistically significant differences in haplotype frequencies were used to delineate stocks. Samples were usually from a period of less than a decade. The argument for demographic independence was that the mtDNA results indicated female philopatry to a locale, which would mean that recovery of a local population would depend on the number of females in that area regardless of male dispersal.

Example: North Atlantic humpback whale stock structure

Humpback whale (*Megaptera novaeangliae*) stock structure in the North Atlantic was revised in 2000 to reflect strong fidelity to summer feeding grounds. The original Western North Atlantic stock, first delineated in 1995, was revised to recognize a more geographically limited Gulf of Maine stock. While whales using the Gulf of Maine feeding area, as well as those using other feeding areas in the North Atlantic, belong to a much larger group that breeds in the western Caribbean Sea (Palsbøll et al. 1997, 2001), calves learn their migratory route and feeding ground from their mothers and photographic-identification has shown high fidelity to feeding grounds. There are frequency differences in mtDNA between the animals using the feeding grounds in the North Atlantic but no nuclear DNA differences between most of the North Atlantic feeding grounds (those whose members breed in the western

Caribbean). Thus, the mtDNA reflects the demographic independence of the feeding ground populations.

Example: North Pacific gray whale stock structure

Another potentially relevant case relates to gray whale stock structure, which includes a case where uncertainty about the magnitude of internal versus external recruitment was addressed using Structured Expert Decision Making (SEDM). A task force was convened to consider all the lines of evidence relating to three potential gray whale (*Eschrichtius robustus*) stocks in the North Pacific: whales that feed off Sakhalin Island (known as western North Pacific gray whales), whales that feed from central California to Southeast Alaska (commonly known as the Pacific Coast Feeding Group, or PCFG), and the remaining gray whales that feed elsewhere in Alaska and northeastern Russia (commonly known as eastern North Pacific gray whales). Western North Pacific gray whales differ from eastern North Pacific gray whales both in mtDNA and nuclear DNA (LeDuc et al. 2002) and the task force concluded that these animals should constitute separate stocks under the MMPA (Weller et al. 2013). The task force was not able to determine whether the PCFG met the definition of stock under the MMPA. The PCFG differs from the eastern North Pacific stock in frequencies of mtDNA but not in nuclear markers. These frequency differences are relatively small and simulations suggested that the magnitude of these differences was compatible with internal and external recruitment at similar levels (Lang et al. 2011). The task force report states: “Presently, both the photo-identification and genetics data indicate that the levels of internal versus external recruitment are comparable, but these are not quantified well enough to determine if the population dynamics of the PCFG are more a consequence of births and deaths within the group (internal dynamics) rather than related to immigration and/or emigration (external dynamics).” Because of the uncertainties in interpreting the genetic and photo-identification data, the task force employed SEDM to express the differences in interpretation held by different members. The team was evenly divided on whether the PCFG merited being a stock because data indicated that it is a borderline case with respect to whether recruitment is more from internal or external recruitment (Weller et al. 2013).

Example: Beluga whale stock delineation in Alaska

Five beluga stocks are delineated in Alaskan waters based on genetic evidence, discontinuous summer distributions, and distinct population trends exhibited in different regions (Allen and Angliss 2015). The original inference that these qualify as stocks was based on Traditional Ecological Knowledge from Alaska Natives and on scientific analyses of summer distributions and spring and fall migrations (Seaman et al. 1985; Frost and Lowry 1990; Withrow et al. 1994). This inference has since been strengthened by genetic comparisons (O’Corry-Crowe et al. 1997). The five stocks are Cook Inlet, Bristol Bay, Eastern Bering Sea, Eastern Chukchi Sea, and Beaufort Sea (Figure 4). The beluga whales of the Cook Inlet stock remain within Cook Inlet throughout the year (Hobbs et al. 2005). A small population of around 20 beluga whales of unknown origin resides in Yakutat Bay (O’Corry-Crowe 2007) and is included in the Cook Inlet stock. While the Cook Inlet Stock is separated from the other four stocks by the physical barrier of the Alaska Peninsula, the four western stocks were thought to all winter in the Bering Sea.

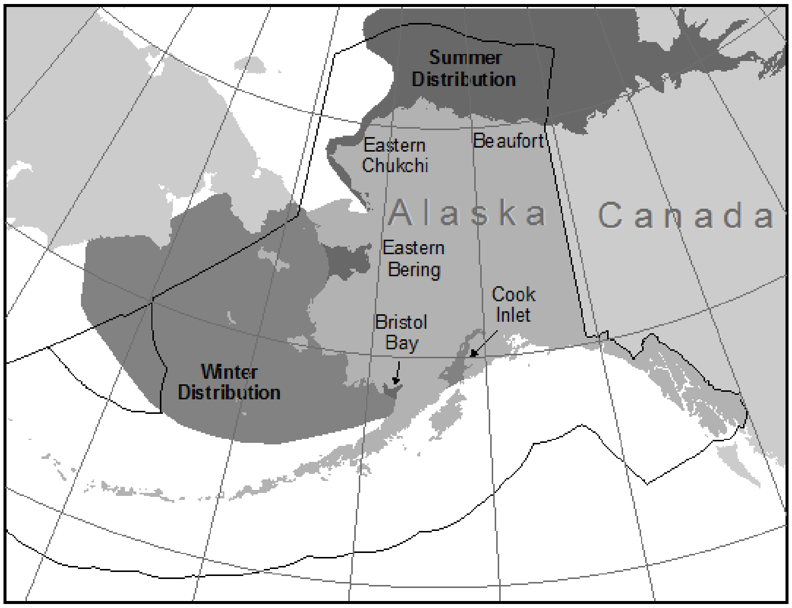

Figure 4. Approximate distribution of beluga whales in Alaska waters. The dark shading displays the summer distribution of the five stocks. Winter distributions are depicted with lighter shading. Source: Angliss and Allen (2015).

O'Corry-Crowe et al. (1997) used mtDNA to delineate five stocks within Alaska waters using samples collected primarily by hunters. The stocks were differentiated by frequency differences of mitochondrial haplotypes with a few haplotypes found across the range but some haplotypes found only in a single stock. Some of those "unique" haplotypes were found in relatively high frequencies within a stock. These frequency differences resulted in very high probabilities that the stocks were genetically distinct. The frequency differences in Alaska were similar to the findings of frequency differences among the bays within the Sea of Okhotsk (Shpak et al. 2011). O'Corry-Crowe et al. (1997) also examined differences by age and sex categories and found that while the differences between older males were significant, they were not as great as immature males or females, suggesting that there may be a low level of male-mediated gene flow among the populations that winter in the Bering Sea.

4.1.3 International Whaling Commission beluga whale stock delineation

In 1999, the IWC discussed what constituted a stock or management unit of beluga whales (white whales). The IWC's Sub-Committee on Small Cetaceans agreed that management units should be established with the goal of maintaining beluga whales throughout the full extent of their historical range (IWC Report of the Sub-Committee on Small Cetaceans, 2000). The Sub-Committee agreed to apply a precautionary approach and started from the assumption that estuarine groups are separate stocks unless they are shown to be otherwise. On that basis, the Sub-Committee recognized the Sakhalin-Amur beluga whales as a stock (IWC Report of the Sub-Committee on Small Cetaceans 2000).

4.1.4 International Union for Conservation of Nature (IUCN) beluga whale stock delineation

The IUCN convened a panel in 2011 to review the results of research on belugas in the Sakhalin Bay–Amur River region of eastern Russia and to consider whether the commercial removal of beluga whales from the Sakhalin Bay-Amur River area was sustainable (Reeves et al. 2011). The panel considered evidence relating to whether these animals were demographically independent from other Sea of Okhotsk beluga whales, and found three lines of evidence pertinent to evaluating the appropriate unit to conserve to meet the stated goal of the Beluga Project[4], "to estimate the sustainable annual quota from Sakhalinsky Bay." The lines of evidence include: (1) strong site fidelity to summering areas, which is a learned behavior that may lead to patterns in maternally-inherited mtDNA (e.g., unique haplotypes or differences in haplotype frequencies); (2) direct genetic data; and (3) satellite tagging data. Based on evaluation of these lines of evidence, the IUCN panel concluded that there are several credible options for stock boundary delineation for a Sakhalin-Amur stock, including (a) Sakhalinsky Bay, the Amur region, and the southeastern Shantar region (the largest option); (b) between Chkalov Island and Zotov Bank (the smallest option), reflecting the area used by tagged whales during the live-capture season; or (c) Sakhalinsky Bay (including Zotov Bank and Baikal Bay) and the Amur estuary and river. The panel considered option (c) to be the preferred hypothesis.

4.2. Response to petition - review of stock structure

At the broadest geographic scale in the Sea of Okhotsk, there is strong evidence for genetic differentiation, at both mtDNA and nuclear DNA, between beluga whales that summer in the northeastern Sea of Okhotsk off the west Kamchatka coast (east of 145° E longitude) and those that summer in the western Sea of Okhotsk from Sakhalin Bay to Udskaya Bay, west of 145° E longitude (Meschersky et al. 2013). Since this petition involves individuals in the western aggregations, the Team agreed that the northeastern aggregations need no further consideration in this status review as they are clearly distinct from the beluga whales in the western Sea of Okhotsk.

The Team identified two stock structure questions relevant to addressing the petition: 1) Are beluga whales that summer in the Sakhalin Bay-Amur River region demographically independent from beluga whales summering in the rest of the western Sea of Okhotsk? And, if so, 2) what are the geographic boundaries of the stock? Two lines of evidence were considered to answer these questions: 1) genetic comparisons among the summering aggregations in the western Okhotsk; and 2) movement data collected using satellite transmitters.

4.2.1 Rationale for demographic independence of Sakhalin Bay-Amur River beluga whales

Genetic Data

A variety of genetic studies have been performed on beluga whales from the western Sea of Okhotsk (Meschersky et al. 2008, 2013; Meschersky and Yazykova 2012). The first step in considering the strength of these genetic data is to consider whether the samples adequately represent a random selection of the population(s) in question to determine whether the sampling could result in a false positive (finding difference between the aggregations when there was none). In these studies, 107 individuals have been sampled from the Sakhalin Bay-Amur River area over seven sampling years with relatively even sampling per year and an overall relatively even split between males (57) and females (50). However, Meschersky et al. (2013) suggested that there was a duplicate sample so we considered

[4] The "Beluga Project" refers to the review undertaken by the IUCN Panel (Reeves et al. 2011).

the correct number to be 106. This sampling is fairly robust and likely sufficiently representative of the haplotypic frequency distribution of the full population. Sampling from the four other bays in the western Sea of Okhotsk (Nikolaya, Ulbansky, Tugursky, and Udskaya) has been less thorough, most of it having been conducted in a single year and the samples from all four bays are skewed towards males (Meschersky et al. 2013). The IUCN panel expressed concerns over this sampling (see above). The sample size from Nikolaya Bay is particularly small, making it difficult to draw conclusions about the relationship of whales in this bay to the other bays based on genetic data.

The genetic comparisons between samples from the beluga whales of the Sakhalin Bay-Amur River and the beluga whales of the other bays consistently found significant differentiation in mtDNA haplotype frequencies among bays (Meshersky et al. 2013). As in the Alaska example, in some cases haplotypes were found that were unique to a bay, indicating that most recruitment is internal. For example, although the most common haplotype is the same in both Sakhalin (found in 37 of 106 animals sampled) and Udskaya Bays (19 of 46 animals sampled), the second and third most common haplotypes in Sakhalin Bay (27 and 17 of 106 animals sampled) were not found in Udskaya Bay (0 and 0 of 46 animals sampled), nor anywhere else that was sampled, and the second and third most common haplotypes that are present in Udskaya Bay (16 and 6 of 46) were each found in only a single individual in Sakhalin Bay (1 and 1 of 106) (Meschersky et al. 2013). Significant differentiation was also found between Sakhalin and Ulbansky Bays and Sakhalin and Tugursky Bays, but not between Sakhalin Bay and the adjacent Nikolaya Bay, though the small sample size may have played a role in the latter comparison (Meschersky 2012). Although the sampling in Udskaya, Tugursky, and Ulbansky Bays is not optimal, frequency differences are so strong as to be unlikely to have come from a biased sample of a large, panmictic western Sea of Okhotsk aggregation. The bias towards males in the other bays also lessens the chance that a disproportionate number of samples came from mothers and offspring (which would have the same mtDNA haplotype). The presence of some common haplotypes across bays suggests there may be some external recruitment or, alternatively, founding events have been recent enough that there has not been sufficient time for lineage sorting amongst the bays, resulting in some common haplotypes over large geographic ranges.

Analysis of nuclear microsatellite markers found no evidence for genetic differentiation among the bays of the western Sea of Okhotsk with the exception of a comparison of Sakhalin Bay to the distant Ulbansky Bay (Meschersky 2012; Meschersky et al. 2013). This negative finding for differentiation in nuclear DNA does not rule out that beluga whales in these different summer feeding areas could constitute stocks under the MMPA (see harbor seal, harbor porpoise, and humpback examples above). The mtDNA differences alone are sufficient evidence for demographic independence.

Telemetry Data

Though sparse, telemetry data from satellite tags support the conclusions drawn from the genetic data. From 2007-2010, 22 beluga whales were tagged at Sakhalin Bay. Tags transmitted for 2.5-9.5 months, with an average of six months. Most whales stayed close to the tagging site in summer (Shpak et al. 2010), though several tagged whales were sighted in Nikolaya Bay in summer (Shpak et al. 2011). Ten whales tagged in 2010 moved in the fall to Nikolaya Bay and the eastern Shantar region and four went as far as Ulbansky Bay, spending up to three months in these areas. In winter, tagged whales moved north and west into offshore waters (Shpak et al. 2012). Though not very many whales have been tagged, the data available to date suggest whales present in the summer in Sakhalin Bay also use Nikolaya Bay, but there is little evidence for movement between Sakhalin Bay and the other bays further to the west during spring and summer.

Geographical and Ecological Separation

Beluga whales in other better-studied areas form strong social groups that follow learned, predictable annual movements between breeding and feeding areas. Summer aggregations often focus on seasonally available fish runs, like salmon runs (Melnikov 1999). Site fidelity to summer feeding areas is not uncommon in cetaceans and can often result in genetic differentiation in mtDNA (see humpback whale example above; Palsbøll et al. 1997, 2001). In some cases, site fidelity is strong enough and occurs over a long enough time period that mtDNA lineage sorting can occur, resulting in mtDNA haplotypes unique to a given feeding area. Additional examples of the long-term nature and isolation of these aggregations are cases of several rivers in eastern Hudson Bay and Ungava Bay, Canada where beluga whales were locally hunted to low levels and have not rebounded or been recolonized from other populations (Reeves and Mitchell 1987a,b; Kingsley 2000; Hammill et al. 2004). A population in Alaska found in the Kuskokwim River delta that was also hunted to very low levels in the 1950s has not recovered (pers. com. John Burns).

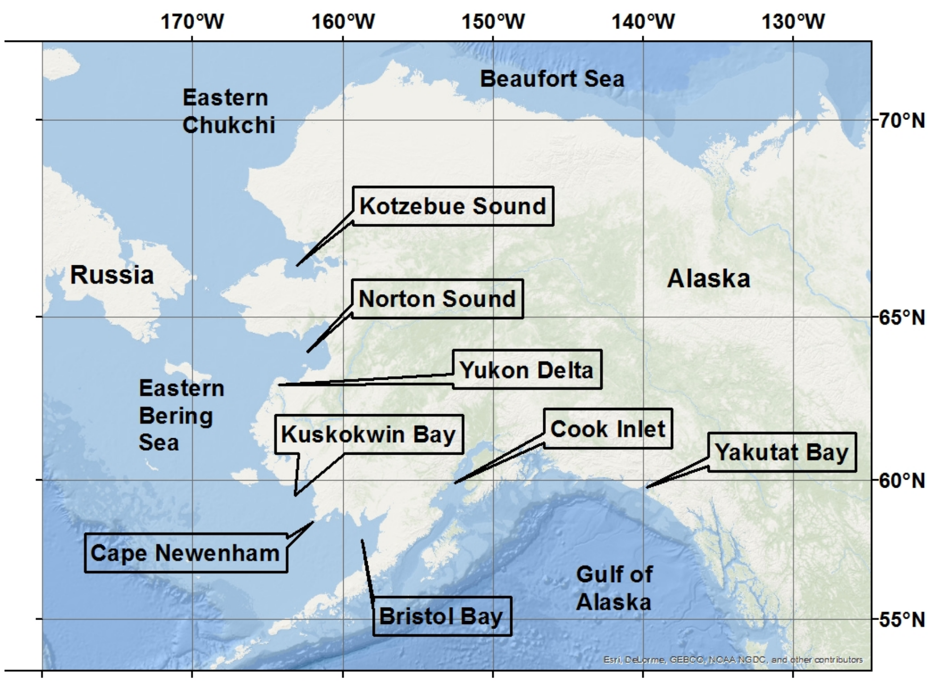

Figure 5. Map of Alaska beluga whale areas

Sakhalin Bay-Amur River beluga whales exhibit behaviors and frequency differences in mtDNA haplotypes (see above) consistent with the general beluga whale life history strategy seen in Alaska, and therefore would be similar to aggregations defined as stocks within Alaska. The two Alaska beluga stocks with movements and seasonal cycles most similar to the Sakhalin Bay-Amur River beluga whales are the Eastern Bering Sea stock and the Bristol Bay stock (Figure 5). The Eastern Bering Sea beluga whales spend summers feeding on salmon runs in the Yukon River delta, in Norton Sound and south along the coast as far as Scammon Bay, and are occasionally found many miles upstream from the mouth of the river. In the winter these belugas move offshore into the Bering Sea and south along the coast to Kuskokwim Bay and east of Cape Newenham (Lowry et al. 1999; Angliss and Allen 2015; ABWC unpublished data[5]). The Bristol Bay beluga stock spends its summers feeding on salmon runs in Nushagak Bay, Kvichak Bay and the tributaries to the estuaries. In the winter the Bristol Bay beluga whales move into deeper, partially ice-covered waters south and east of Cape Constantine (Frost and Lowry 1990; Angliss and Allen 2015; NMFS, ADFG unpublished data[6])

Together genetic and movement data indicate that beluga whales in the western Sea of Okhotsk exhibit life history characteristics and levels of differentiation very similar to beluga whales in Alaska that have been designated as stocks. Genetic mtDNA differentiation among the bays and evidence for limited movement into Nikolaya and Ulbansky Bays strongly suggest the Sakhalin Bay-Amur River aggregation of beluga whales represent a stock as defined under the MMPA, and limits the discussion of boundaries to whether the belugas in Nikolaya Bay or Ulbansky Bay should be included.

4.2.2 Rationale against demographic independence of Sakhalin Bay-Amur-River beluga whales

The primary rationale against separating the Sakhalin Bay-Amur-River beluga whales from beluga whales in bays further west is that the genetic sampling in the other bays is concentrated in one or two years and is skewed towards males, allowing potential for a false positive finding. In addition, there are no long-term data to allow interpretation of the temporal stability of the mtDNA haplotype frequency differences. Finally, the lack of nuclear DNA (microsatellite) differentiation among most summer feeding areas in the western Sea of Okhotsk (the exception being between Sakhalin Bay-Amur River and Ulbansky Bay) is consistent with interbreeding between animals that aggregate in Sakhalin Bay and the other bays. Because these animals spend some parts of the year together (i.e., winter), it is plausible that recruitment into a summer aggregation could be both internal and external. However, the nuclear data available to date are too weak, given the level of and design of the sampling, to assess how much internal versus external recruitment there is.

The satellite tag data indicated that some whales captured and tagged in Sakhalin Bay in mid-summer entered Nikolaya Bay in the fall. Four whales tagged in Sakhalin Bay in summer visited Ulbansky Bay in the fall (Shpak et al. 2011), suggesting some Sakhalin whales may move to bays to the west before moving off shore in the winter. However, since these movements took place in the fall and breeding occurs in the spring, these movements likely represent seasonal migratory pathways rather than mixing of breeding stocks. In addition, those satellite-tagged individuals that transmitted into the winter

[5] Maps and description available at http://www.north-slope.org/departments/wildlife-management/co-management-organizations/alaska-beluga-whale-committee/abwc-research-projects/eastern-bering-sea-stock-projects
[6] Maps and description available at http://www.north-slope.org/departments/wildlife-management/co-management-organizations/alaska-beluga-whale-committee/abwc-research-projects/bristol-bay-stock-projects

months were tracked to the central and northern Sea of Okhotsk. Thus, contact and interbreeding among belugas from different summering areas may occur offshore in the spring before they return to the summer grounds.

Finally, because the area concerned is relatively small and has no significant barriers to movement, it is reasonable to assume that a local extirpation would eventually be recolonized by beluga whales from one of the other bays. However, there are no direct data to support this, and examples of removals in Alaska suggest recolonization would be unlikely in a single generation.

4.3 Conclusion about demographic independence

4.3.1 Structured Expert Decision Making

When data are either not available or not clearly conclusive, a method called Structured Expert Decision Making (SEDM) is sometimes employed as a means to elicit expert opinion while also characterizing uncertainty within the expert opinion. In some NMFS Endangered Species Act status reviews, Biological Review Teams (BRTs) have adopted formal methods, such as SEDM, to express plausibility for use in guiding its analysis of Distinct Population Segments (DPS) and in assessing the risks to the population(s). This method has also been referred to as the "FEMAT" method because it is a variation of a method used by scientific teams evaluating options under the Northwest Forest Plan (Forest Ecosystem Management Assessment Team). Under SEDM, each expert is asked to distribute plausibility points among the choices/scenarios for a given statement reflecting his or her opinion of how likely that choice or option correctly reflected the population status. If the expert is certain of a particular option, or feels it is the only plausible scenario, he or she could assign all points to that option. An expert with less certainty about which option best reflected reality, or best reflected the population's status, could split the points among two or more options. This method has been used in all status review updates for anadromous Pacific salmonids since 1999 (Good et al. 2005), as well as in reviews of Southern Resident killer whales (*Orcinus orca*), West Coast rockfishes, Pacific herring (*Clupea pallasii*), Pacific groundfish, North American green sturgeon (*Acipenser medirostris*), black abalone (*Haliotis cracherodii*), Hawaii false killer whales (*Pseudorca crassidens*), and humpback whales (*Megaptera novaeangliae*).

In the humpback whale status review (Bettridge et al. 2015), BRT members distributed 100 likelihood points among the defined scenarios or options, reflecting their expert opinion of the relative likelihood that the status of a specific DPS fell into each of three risk categories. Then the team discussed how they had allocated points and subsequently had a chance to revise their scores.

In the Hawaii false killer whale status review (Oleson et al. 2010), BRT members distributed ten points between the arguments for and against each question where there was uncertainty. Team members agreed to view resulting scores with names associated to facilitate discussion and assure that semantic uncertainty was not responsible for any disparate votes. The BRT discussed the scores and, in some cases, members adjusted scores when prior articulation of the arguments had been unclear.

SEDM was also used by a task force considering whether the Pacific Coast Feeding Aggregation of gray whales constituted a stock under the MMPA (Weller et al. 2013). For some questions, the experts distributed 100 points among five options (strongly agree, strongly disagree, neutral, somewhat disagree and strongly disagree) for each question. After completing this SEDM exercise, the task force concluded that the format of questions running from strongly agree to strongly disagree was not optimal because it had to be clarified in the text whether "disagreement" was because the data were uncertain or whether the case was borderline.

4.3.2 Beluga Whale Status Review Team SEDM

Because of the limited evidence available regarding the stock structure of the Sakhalin Bay-Amur River beluga whales relative to other western Sea of Okhotsk beluga whales, the Team used SEDM procedures to evaluate the available genetic and telemetry data for beluga whales in the western Sea of Okhotsk as they relate to delineating stocks. Learning from the gray whale lesson, this beluga status review team decided on a different formulation of questions for the stock delineation exercise. For each question, each of the ten Team members assigned 100 plausibility points across multiple statements that spanned what was felt to be plausible for the question. The Team agreed that members should allocate points evenly across all possible statements for a given question if they felt the available data were insufficient to address the statement. Scores were then averaged to produce a single score for each statement.

It took several rounds of discussion to get the wording of the questions and associated statements to the point where all experts understood and agreed on the meaning/intent of each statement. The Team considered eight questions: three that pertained to how similar Sea of Okhotsk beluga whales were to Alaska beluga whales (to give insight to how evidence used to delineate stocks within Alaska could be used by analogy in the Sea of Okhotsk), four that pertained to different lines of evidence about the demographic independence of Sakhalin Bay-Amur River beluga whales with respect to beluga whales elsewhere in the western Sea of Okhotsk, and a final statement that pertained to the plausibility of demographic independence of Sakhalin Bay/Amur-River beluga whales when all lines of evidence were taken together.

Responses to questions concerning similarities between Alaska and Okhotsk beluga whales

<u>Question 1</u>. Allot plausibility points to the following statements considering DNA evidence:

Option	**AVG**
The pattern of differentiation in mtDNA observed among beluga whales in areas within the western Sea of Okhotsk is similar to the pattern observed in beluga whale aggregations defined as the Bristol Bay and Norton Sound stocks within Alaska	82.5
The pattern of differentiation in mtDNA observed in beluga whales among areas within the western Sea of Okhotsk is not similar to the pattern observed in beluga whale aggregations defined as the Bristol Bay and Norton Sound stocks within Alaska	17.5

Interpretation: There was a high level of agreement that the pattern of mtDNA differentiation observed among beluga whales in the western Sea of Okhotsk is similar to that seen in beluga whale stocks delineated in Alaska (82.5% agreement with no expert strongly supporting the alternative). The Team agreed the term "pattern" did *not* refer to the magnitude of genetic differentiation, which depends on effective population size, but rather meant finding strong statistical frequency differences between the strata. Bristol Bay and Norton Sound were chosen to be most similar to the western Sea of Okhotsk with respect to geography and behavior.

Question 2. Allot plausibility points to the following statements considering evidence about movement patterns including summer site fidelity:

Option	AVG
Movement patterns observed in the western Sea of Okhotsk are similar to movement patterns observed in beluga whale aggregations defined as stocks within Alaska	80.0
Movement patterns observed in the western Sea of Okhotsk are not similar to patterns observed in beluga whale aggregations defined as stocks within Alaska	20.0

Interpretation: There was a high level of agreement that telemetry-based movement patterns observed in western Sea of Okhotsk beluga whales are similar to movement patterns observed in beluga whale aggregations defined as stocks within Alaska (80.0% agreement with no expert strongly supporting the alternative).

Question 3. Allot plausibility points to the following statements considering the cumulative evidence from questions 1 and 2 about the similarity of western Sea of Okhotsk beluga whales to stocks of beluga whales in Alaska:

Option	AVG
The overall mtDNA and movements data observed in western Sea of Okhotsk beluga whales are similar to mtDNA and movements data observed in beluga whale aggregations defined as stocks within Alaska such that they can be considered analogous	83.1
The overall mtDNA and movements data observed in western Sea of Okhotsk beluga whales are not similar to mtDNA and movements data observed in beluga whale aggregations defined as stocks within Alaska such that they cannot be considered analogous	16.9

Interpretation: There was a high level of agreement that both mtDNA data and studies of movements of beluga whales in the western Sea of Okhotsk are similar to the finding of similar studies of mtDNA and movements conducted on beluga whale aggregations defined as stocks within Alaska such that they can be considered analogous (83.1% agreement with no expert strongly supporting the alternative).

Responses to questions regarding the support of separate lines of evidence for alternative areas that delimit the stock to which Sakhalin Bay-Amur River beluga whales belong

Question 4. Allot plausibility points to the following statements considering mtDNA evidence:

Option	AVG
Beluga whales in Sakhalin Bay-Amur River are demographically independent from other western Sea of Okhotsk beluga whales	54.4
Beluga whales in Sakhalin Bay-Amur River and Nikolaya Bay together are demographically independent from other western Sea of Okhotsk beluga whales	39.4
Beluga whales in Sakhalin Bay-Amur River, Nikolaya Bay, and Ulbansky Bay together are demographically independent from other western Sea of Okhotsk beluga whales	4.4
There are no demographically independent groups within the western Sea of Okhotsk (i.e., the western Sea of Okhotsk is one demographically independent population)	1.9

Interpretation: There was strong agreement that the mtDNA evidence suggests there are multiple demographically independent populations of beluga whales in the western Sea of Okhotsk and that Sakhalin Bay-Amur River beluga whales are demographically independent from beluga whales in Ulbansky Bay and the bays to the west. Members were less certain whether Sakhalin Bay-Amur River beluga whales belong to a stock that summers only in the Sakhalin Bay-Amur River region or in a larger area that includes Nikolaya Bay.

Question 5. Allot plausibility points to the following statements considering evidence about nuclear DNA:

Option	AVG
There is complete random mating within beluga whales in the western Sea of Okhotsk	25.4
There could be some non-random mating within the western Sea of Okhotsk that is either too recent or at too low a level to be detected given current sample sizes and marker numbers	52.9
Sakhalin Bay-Amur River beluga whales mate primarily with each other	21.8

Interpretation: Conclusions concerning demographic independence among locations with the western Sea of Okhotsk that could be drawn from nuclear DNA evidence were less certain overall, with the greatest support (53%) for the potential for some non-random mating within the western Sea of

Okhotsk. The remaining points were split roughly equally between the other two statements. Overall, the Team expressed uncertainty with this statement due to concerns about the adequacy of the sampling and markers used in the nuclear DNA studies completed at the time.

Question 6. Allot plausibility points to the following statements considering all genetic evidence:

Option	AVG
Sakhalin Bay-Amur River is a demographically independent population	46.9
Sakhalin Bay-Amur River and Nikolaya Bay together are a demographically independent population	44.4
Sakhalin Bay-Amur River, Nikolaya Bay, and Ulbansky Bay together are a demographically independent population	6.9
There are no demographically independent groups within the western Sea of Okhotsk (i.e., the western Sea of Okhotsk is one demographically independent population)	1.9

Interpretation: There was strong agreement that the genetic evidence does not support that the Sakhalin Bay-Amur River beluga whales are members of the same stock as those found in Ulbansky Bay. There was very little support for there being no demographically independent populations within the western Sea of Okhotsk. There was nearly equal support for Sakhalin Bay-Amur River either being demographically independent alone or being part of a slightly larger demographically independent population that includes Nikolaya Bay.

Question 7. Allot plausibility points to the following statements considering only telemetry evidence:

Option	AVG
Sakhalin Bay-Amur River is demographically independent from other western Sea of Okhotsk beluga whales	23.8
Sakhalin Bay-Amur River and Nikolaya Bay together are demographically independent from other western Sea of Okhotsk beluga whales	32.5
Sakhalin Bay-Amur River, Nikolaya Bay, and Ulbansky Bay together are demographically independent from other western Sea of Okhotsk beluga whales	23.1
There are no demographically independent populations within the western Sea of Okhotsk (the western Sea of Okhotsk is one demographically independent population)	18.1

Interpretation: The relatively even allotment of points across options indicated that experts felt the telemetry data were relatively weak in addressing stock delineation questions. During discussion of this question, there was some disagreement resulting from different members' interpretations of telemetry data. Some felt that since the telemetry data revealed that animals tagged within the Sakhalin Bay-Amur River generally stayed close to that area there was sufficient information to draw conclusions about demographic independence. Others felt that in general the telemetry data were weak because there is no way to distinguish between internal and external recruitment based on movements of animals already recruited to a feeding group.

Stock delineation question based on all lines of evidence

Question 8. Allot plausibility points to the following statements considering all evidence:

Option	**AVG**
Sakhalin Bay-Amur River is a demographically independent population	44.4
Sakhalin Bay-Amur River and Nikolaya Bay together are a demographically independent population	42.5
Sakhalin Bay-Amur River, Nikolaya Bay and Ulbansky Bay together are a demographically independent population	11.9
There are no demographically independent groups within the western Sea of Okhotsk (the western Sea of Okhotsk is one demographically independent population)	1.3

Interpretation: There was strong agreement that the genetic evidence does not support that the Sakhalin Bay-Amur River beluga whales are members of the same stock as those found in Ulbansky Bay. There was very little support for there being no demographically independent groups within the western Sea of Okhotsk. Although there is more support for Sakhalin Bay-Amur River beluga whales belonging to a stock that summers only in that region, there is nearly equal support for Sakhalin Bay-Amur River belugas being part of a slightly larger demographically independent population that also includes Nikolaya Bay.

4.3.3 Structured Expert Decision Making Summary

The experts were largely in agreement that Sakhalin Bay-Amur River beluga whales were either their own stock or belonged to a stock that also included whales that summer in Nikolaya Bay. These results were largely based on mtDNA evidence as the allocation of points was very similar between the mtDNA evidence alone and all evidence taken together. The experts also strongly supported that both movements and mtDNA patterns were analogous between stocks of beluga whales in Alaska and belugas within the western Sea of Okhotsk.

5. Response to petition - Estimation of depletion level for Sakhalin Bay-Amur River belugas

As described above, the Team concluded that Sakhalin Bay-Amur River beluga whales do represent a demographically independent population and have characteristics similar to beluga whale stocks in Alaska. Therefore, the second question to be analyzed by the Team was whether the stock is depleted.

5.1 Back calculation of carrying capacity

Management objectives under the MMPA are intended to maintain marine mammal populations within their OSP ranges or, if the population is below the lower bound of OSP, to recover to OSP in a reasonable length of time. NOAA has defined OSP as a population size that falls within a range from the population level of a given species or stock that is the largest supportable within the ecosystem (i.e., carrying capacity, or K) to its MNPL. Historically, MNPL has been expressed as a range of values between 50 and 70 percent of K. To determine a population's depletion level, or abundance relative to K, we need to have an idea of historical K. K, the equilibrium population level before impact by man (direct or indirect), can be difficult to measure. One technique employed by NMFS has been the back-calculation method, which assumes that the historical population was at equilibrium, and that the environment has not changed greatly. The approach of back-calculation is to look at the current population and then calculate historical carrying capacity based on how much the population has been reduced by human actions.

NMFS applied this approach in the management of the subsistence hunt of the Cook Inlet beluga whale stock (73 FR 60976, October 15, 2008). The Cook Inlet beluga whale depletion level was estimated using a back calculation of carrying capacity. In 1998, Cook Inlet beluga whales were determined to be depleted when the population had fallen from an estimated 653 animals in 1994 to 347 animals in 1998. In 1999, a moratorium on the hunt was implemented until a co-management plan could be developed. The harvest plan developed under the co-management agreement only allowed a subsistence hunt if it would allow the stock to recover to OSP in 100 years with 95% confidence. Carrying capacity (K) for the Cook Inlet Beluga whale stock was determined to be 1,300 whales in 1979 (Calkins 1984) and the lower limit of OSP was set at 60% of K, or 780 belugas.

5.2 Application of back-calculation to Sakhalin Bay–Amur River beluga whales

The available data for the Sakhalin Bay-Amur River stock of beluga whales are a time series since 1915 (Shpak et al. 2011) of hunt and live-capture for display data and an estimate of abundance in 2009-2010 (Reeves et al. 2011). These data, plus an estimate of the stock's productivity, allow back-calculation of the historical stock size (i.e., K) that probably existed prior to the beginning of the catch history. It was not feasible to develop an estimate of any additional anthropogenic mortality on this stock.

A population model was used to perform these calculations. In short, for each year, the model calculates the expected number of animals added to the stock by natural population growth and it subtracts the number removed by the hunts, and then the model grows or shrinks the population for the next year according to the difference between the growth and the removals. A computer spreadsheet search routine finds the value of K that is large enough to have accommodated the removals and low enough to have resulted in a population in 2009-2010 that matches the observed abundance in those years.

The population equation is $N_{t+1} = N_t(1+r(1- (N_t/K)^z)-H_t$ where:

N_t is the population size in year t,

r is the annual rate of increase (productivity) when the population is small,

K is the carrying capacity,

z controls the rate at which productivity declines as N_t approaches K, and

H_t is the removals in year t.

The values of r and z have not been measured for Sakhalin Bay-Amur River beluga whales so values (r=0.04 and z=2.39) are used in the "base case." The value for r= 0.04 is a default value for cetaceans used in PBR calculations (NMFS 2005), and z=2.39 is in the middle of the range considered reasonable for cetaceans (Breiwick and York 2009). Alternate plausible values for r and z were also evaluated to test the model's sensitivity to changes in these parameters.

Once the back-calculation estimated the value of K that resulted in the estimated population size in 2009-2010, the population model was projected forward to 2015 to estimate the current population size. The current depletion level was then calculated by dividing the 2015 stock size (estimated by the model) by the estimated carrying capacity (K).

5.2.1 Data Input: Catch History

Commercial hunts of the Sakhalin Bay-Amur River beluga whale population began in 1915 (Shpak et al. 2011) and subsistence hunts have occurred prior to, during, and since this date (Appendix). The largest commercial hunts occurred in 1927-1934 with a peak recorded catch of 2,817 in 1933, and then declined substantially. Shpak et al. (2011) indicate that the focus of the commercial catch moved to other areas of the Sea of Okhotsk after the 1930s, suggesting that the Sakhalin Bay-Amur River population was sufficiently depleted that catch rates had declined. There are a number of years with known but poorly documented hunts, and years for which more than one estimate is provided. A complete catch history is required to estimate carrying capacity by the back-calculation method, so two options were considered: a "high take" and a "low take" scenario. The high take scenario gives a conservative estimate of depletion, because higher take results in a higher estimated historic K and a more depleted current population relative to K (i.e., lower percentage of K). The low take scenario uses what is thought to be the lowest take possible and provide a minimum estimate for K, resulting in a less depleted current population relative to K (i.e., higher percentage of K). The low take scenario thus provides an upper bound for the population's status relative to K. Both options used the catch data from Shpak et al. (2011).

The low take scenario used the take estimates when they were available, and when more than one estimate of take was available, used the lowest value. Years with no indication that takes occurred were left blank and treated as zero. The low take option is included to evaluate whether this unlikely scenario would still result in a depleted population.

The high take scenario used the take estimates where they were available, and when more than one estimate of take was available, used the highest value. For years when hunts are thought to have occurred but no record is available, missing values were estimated or interpolated from adjacent years with similar hunts. The high take scenario is considered the better of the two because it accounts for times when takes are known to have occurred but are not documented. Additionally, we did not account for beluga whales that are struck and lost because these data are not available, so the high take option may even be an underestimate.

Large-scale beluga whale harvests in the Sakhalin Bay-Amur River began in 1915. Prior to that the subsistence hunt in the Sakhalin Bay-Amur River was estimated at between five and 30 animals per year in the 1800s (Shpak et al. 2011); these values were used for the low take and high take scenario, respectively. The subsistence hunt is thought to have existed for many years prior to 1915 (Shpak et al. 2011), so the population was already reduced somewhat below its pristine carrying capacity by 1915. This is accounted for in the back-calculation by running the model for 100 years (1815-1915) with a take of five or 30 animals per year. This reduces the population estimate by less than 0.5% prior to onset of the directed commercial hunt.

While commercial catch data are available for the period 1915-1919, the Team found no such data for the period 1919-1924. Missing data could indicate that no commercial catch occurred due to military activity (low take scenario), or commercial catches may have continued but were unreported (high take scenario, estimated as the average of catch in 1918 and 1925). Furthermore, no catch was reported in 1931 and 1932; therefore the low take scenario for these years is zero and the high take scenario is the average of reported takes in 1930 and 1933. Starting in 1938 to 1986, there are no records of commercial takes in the Sakhalin Bay-Amur River until 1986, when captures for live display began. During the period 1938 to 1955, no commercial takes are reported but Shpak et al. (2011) indicates that unofficial sources reported that some commercial takes occurred during this period. From 1956 through 1959, takes for the entire Okhotsk Sea are estimated to be 800 annually but these are thought to have come largely from the large bays to the west of Sakhalin Bay-Amur River. Thus, for 1938-1959 we use zero for the low take and set the high take scenario at 100 per year to account for possible takes from the Sakhalin Bay-Amur River. After 1960, the commercial take of belugas throughout the Okhotsk Sea had ended (Shpak et al. 2011), so both the low and high options are zero during 1960-1985. In 1986, live capture removals began (Fisher and Reeves 2005). However, there are no take records for the period 1986-1999, so the Team used the average of takes reported during 2000-2012 for the high take scenario and zero for the low take scenario. This average is also used for the high take scenario in 2013 and 2014, and zero for the low take scenario because records are not yet available.

5.2.2 Data Input: 2009-2010 Abundance Estimate

The most recent estimate of abundance, 3,961, is based on aerial surveys done in 2009 and 2010 (Reeves et al. 2011). The Team used abundance estimates from only the Sakhalin Bay–Amur River area because there was no current abundance estimate of the Nikolaya Bay region, but few animals are thought to be in Nikolaya Bay in the survey period compared to the Sakhalin Bay-Amur River, so the estimate accounts for nearly all of the population (Shpak et al. 2011). The estimate includes a correction factor, which accounts for beluga whales that were submerged during overflight and not available to be counted.

5.2.3 Results: Estimated Carrying Capacity and Depletion Level

The calculated K, projected 2015 abundance, and depletion level (% of K) results are shown in Table 1. The table shows calculations using the high and the low catch scenarios, and it also shows the degree of sensitivity of the high catch option to a range of plausible values of r and z. The value of z = 1 results in a population model with the MNPL at 50% of K, z = 2.39 results in a model with MNPL at 60% of K, and z = 5.04 results in a model with MNPL at 70% of K.

Trial	Catch	r	z	K	Projected 2015 abundance	% of K	Sensitivity (% Change in K from Base Case)
1 (Base)	High	0.04	2.39	17,700	4,520	25.5%	0%
2	High	0.03	2.39	18,000	4,068	22.6%	2%
3	High	0.02	2.39	20,800	4,056	19.5%	18%
4	High	0.04	5.04	16,600	4,571	27.4%	-6%
5	High	0.04	1	19,500	4,349	22.3%	10%
6	Low	0.04	2.39	13,200	4,626	35.0%	-25%

Table 1. Estimated carrying capacity (K) and depletion levels for various model parameter sets.

We considered the value of K resulting when r = 0.04 (the default for MMPA potential biological removal level calculations for cetaceans; NMFS 2005), z = 2.39, and the high take scenario (which assumes some medium level of catch for years with missing data in which take is thought to have occurred) to be the "base case."[7] Additional columns indicate the projected 2015 abundance, and the percent of K (depletion level) that the 2015 abundance represents. The final column shows the percentage change in K relative to the base case. Changes in r and z (trials 2-5) resulted in only small changes in K.

According to the base case scenario, the population in 1960 reached a minimum of 1,343 (Figure 6) following high historical harvests and an average take level during 1938 to 1959 of 130 animals per year. The back-calculation indicates that the greatest decline occurred during the 1930s due to high take levels and that the population may be slowly increasing at recent take levels (between 28 and 53 animals per year, of which between five and 30 are taken as subsistence). However, there is no direct evidence that such an increase is occurring. The current depletion level, 25.5% of K, is far below the stock's OSP, which NMFS has in practice considered to be reached at a depletion level of 60% K. The

[7] The take levels for the period 1938-1959 were set at 100 to account for possible takes; a sensitivity analysis (results not shown in the table) in which the take levels were increased by 100 and decreased by 100 resulted in K increasing and decreasing by less than 1,200 animals respectively.

team was concerned that for several years the commercial removals were known to have occurred but could only be estimated, in particular the 100 takes per year between 1938 and 1959, and considered an extreme example in which only the documented takes were considered. Even this optimistic scenario with both low commercial and subsistence catches (trial 6) results in a population at 35.0% of K, below OSP. Thus the team concluded that while takes were not the fully documented that it was unnecessary to attempt to further resolve take numbers within the range because both scenarios fell below OSP.

We described the abundance estimate of 3,961 as a conservative estimate because Nikolaya Bay was not included. If we add 500 to the abundance estimate to account for Nikolaya Bay and run the model using the base case parameters, the result is an increase of less than 100 animals in the estimate of K, but the estimate of depletion would be 28.9% of K. Thus, having an abundance estimate for Nikolaya Bay would not change the estimate of K significantly; it would result in a slightly higher population relative to K, but the population would still be below OSP.

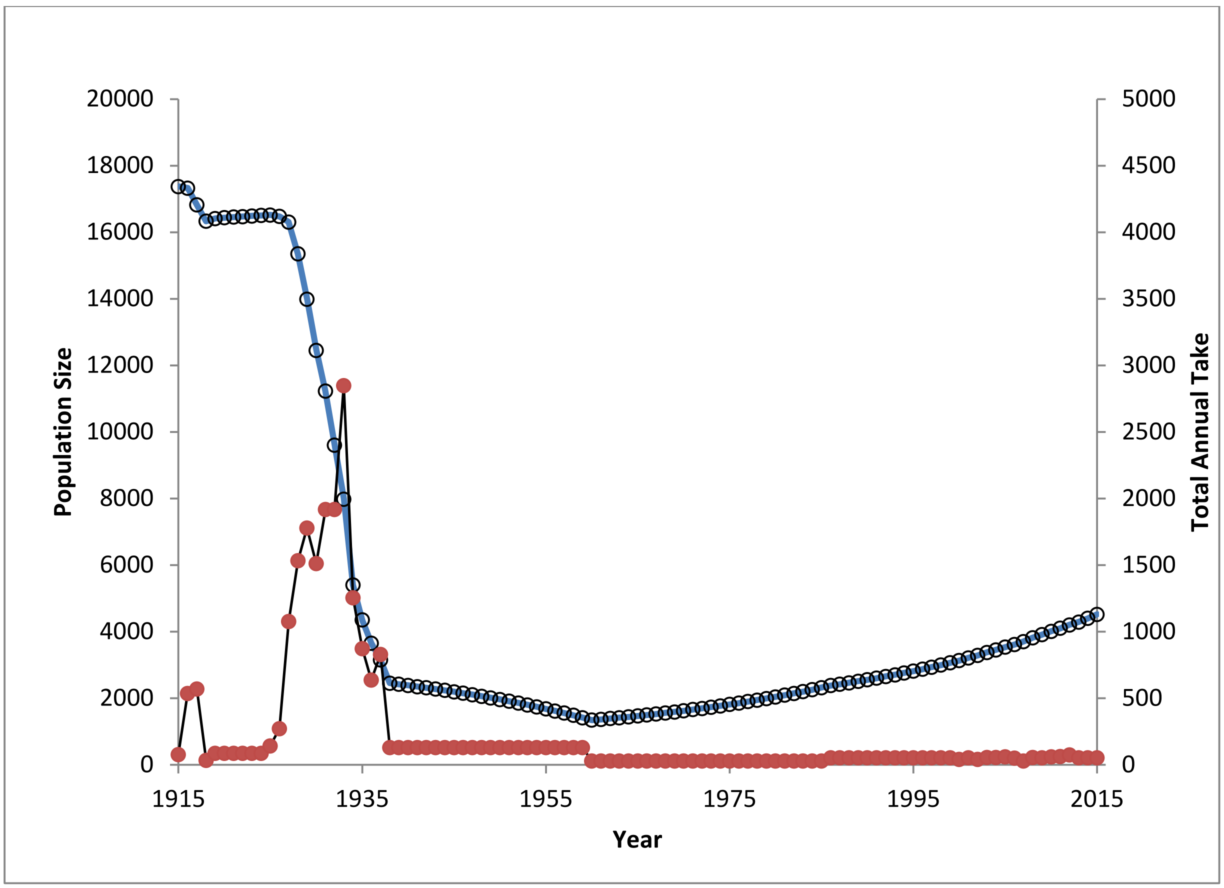

Figure 6. Annual estimated abundance (blue line/open circles) and annual takes (black line/red circles) from the base case population model. Takes peaked in 1933 when the population had already declined by > 50%. The population abundance reached a minimum in 1960, then slowly began to increase.

6. Summary

NMFS received a petition from the Animal Welfare Institute, Whale and Dolphin Conservation, Cetacean Society International, and Earth Island Institute to designate the Sakhalin Bay-Amur River beluga whales as depleted under the MMPA. The petition asserts this group of whales constitutes a stock and that this stock is below its OSP and qualifies for a depleted designation. NMFS found the petitioned action may be warranted. NMFS established a status review team (referred to as the Team), to review the status of the beluga whales in the Sakhalin Bay-Amur River portion of the Okhotsk Sea using the best, currently available information. The Team's review involved two steps. First, to determine whether the Sakhalin Bay-Amur River beluga whales constitute a stock under the MMPA, and then, second, if these whales meet the definition of stock, determine the depletion level for the stock. In regard to the first step, the Team agreed that there was strong evidence for genetic differentiation within the Sea of Okhotsk in both mtDNA and nuclear DNA, between beluga whales that summer in the western Sea of Okhotsk from Sakhalin Bay to Udskaya Bay (west of 145^{o} E longitude) and those that summer in the northeastern Sea of Okhotsk off the west Kamchatka coast (east of 145^{o} E longitude). Because of the limited evidence regarding the stock structure of the Sakhalin Bay-Amur River relative to other western Sea of Okhotsk beluga whales, the Team used SEDM procedures to evaluate the available genetic and telemetry data for beluga whales in the western Sea of Okhotsk as they relate to delineating stocks. Using SEDM procedures, eight questions concerning the interpretation of the genetic (mtDNA and nuclear DNA) and telemetry data as well as the similarities with how beluga whale stocks in Alaska have been delineated were addressed. The Team concluded that the movement and mtDNA patterns of the beluga whales in the western Sea of Okhotsk were analogous to beluga whales in Bristol Bay and Norton Sound Alaska, which are defined as demographically independent stocks under the MMPA. The Team concluded that Sakhalin Bay-Amur River whales were either their own stock or they belonged to a stock that also summers in Nikolaya Bay. More genetic and tagging data would be needed to conclude more precisely how belugas in Nikolaya Bay relate to belugas in the Sakhalin Bay – Amur River area.

Since the Team concluded the Sakhalin Bay-Amur River whales constitute a stock, the Team next addressed the question of whether the stock was depleted using time series of abundance and catch (commercial and subsistence) data in a back-calculation population model. The Team used the abundance estimates in 2009-10 from the Sakhalin-Amur River region, and developed an estimate of the time series of catch since 1915, including minimum and maximum scenarios for years in which catch was uncertain. The back-calculation investigated the sensitivities of the effects of an assumed range of plausible parameter values and the high and low catch estimate scenarios. In conclusion, the current depletion level under the high take scenario was 25.5% K and under the low take scenario was 41.7% K, both below OSP, which is reached at a depletion level of 60% K, where K is considered the abundance in approximately 1914.

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Appendix

Table of takes used in the back calculation of carrying capacity values. Values in bold are inferred, blanks indicate no data. The low option uses only reported data, the high take includes estimated takes in some year. Years for which the low option is blank have no available reports of takes. For years with more than one reported value (see Shpak et al. 2011), the lowest value was used in the low option and the highest value was used in the high option.

	Commercial hunt		Subsistence hunt		Total removals	
Year	Low	High	Low	High	Low	High
1915	16	48	5	30	21	78
1916	507	507	5	30	512	537
1917	539	539	5	30	544	569
1918	3	3	5	30	8	33
1919		**58**	5	30	5	88
1920		**58**	5	30	5	88
1921		**58**	5	30	5	88
1922		**58**	5	30	5	88
1923		**58**	5	30	5	88
1924		**58**	5	30	5	88
1925	112	112	5	30	117	142
1926	241	241	5	30	246	271
1927	497	1047	5	30	502	1077
1928	1504	1504	5	30	1509	1534
1929	1749	1749	5	30	1754	1779
1930	1481	1481	5	30	1486	1511
1931		**1888**	5	30	5	1918
1932		**1888**	5	30	5	1918
1933	2817	2817	5	30	2822	2847
1934	1225	1225	5	30	1230	1255
1935	842	842	5	30	847	872
1936	606	606	5	30	611	636
1937	512	800	5	30	517	830

	Commercial hunt		Subsistence hunt		Total removals	
Year	Low	High	Low	High	Low	High
1938		**100**	5	30	5	130
1939		**100**	5	30	5	130
1940		**100**	5	30	5	130
1941		**100**	5	30	5	130
1942		**100**	5	30	5	130
1943		**100**	5	30	5	130
1944		**100**	5	30	5	130
1945		**100**	5	30	5	130
1946		**100**	5	30	5	130
1947		**100**	5	30	5	130
1948		**100**	5	30	5	130
1949		**100**	5	30	5	130
1950		**100**	5	30	5	130
1951		**100**	5	30	5	130
1952		**100**	5	30	5	130
1953		**100**	5	30	5	130
1954		**100**	5	30	5	130
1955		**100**	5	30	5	130
1956		**100**	5	30	5	130
1957		**100**	5	30	5	130
1958		**100**	5	30	5	130
1959		**100**	5	30	5	130
1960		0	5	30	5	30
1961		0	5	30	5	30
1962		0	5	30	5	30
1963		0	5	30	5	30
1964		0	5	30	5	30
1965		0	5	30	5	30

	Commercial hunt		Subsistence hunt		Total removals	
Year	Low	High	Low	High	Low	High
1966		0	5	30	5	30
1967		0	5	30	5	30
1968		0	5	30	5	30
1969		0	5	30	5	30
1970		0	5	30	5	30
1971		0	5	30	5	30
1972		0	5	30	5	30
1973		0	5	30	5	30
1974		0	5	30	5	30
1975		0	5	30	5	30
1976		0	5	30	5	30
1977		0	5	30	5	30
1978		0	5	30	5	30
1979		0	5	30	5	30
1980		0	5	30	5	30
1981		0	5	30	5	30
1982		0	5	30	5	30
1983		0	5	30	5	30
1984		0	5	30	5	30
1985		0	5	30	5	30
1986	**0**	**23**	5	30	28	53
1987	**0**	**23**	5	30	28	53
1988	**0**	**23**	5	30	28	53
1989	**0**	**23**	5	30	28	53
1990	**0**	**23**	5	30	28	53
1991	**0**	**23**	5	30	28	53
1992	**0**	**23**	5	30	28	53
1993	**0**	**23**	5	30	28	53

Year	Commercial hunt Low	Commercial hunt High	Subsistence hunt Low	Subsistence hunt High	Total removals Low	Total removals High
1994	**0**	**23**	5	30	28	53
1995	**0**	**23**	5	30	28	53
1996	**0**	**23**	5	30	28	53
1997	**0**	**23**	5	30	28	53
1998	**0**	**23**	5	30	28	53
1999	**0**	**23**	5	30	28	53
2000	10	10	5	30	15	40
2001	22	22	5	30	27	52
2002	10	10	5	30	15	40
2003	26	26	5	30	31	56
2004	25	25	5	30	30	55
2005	31	31	5	30	36	61
2006	20	20	5	30	25	50
2007	0	0	5	30	5	30
2008	25	25	5	30	30	55
2009	24	24	5	30	29	54
2010	30	30	5	30	35	60
2011	33	33	5	30	38	63
2012	44	44	5	30	49	74
2013	**0**	**23**	5	30	28	53
2014	**0**	**23**	5	30	28	53