Fisheries and Oceans Canada
Ecosystems and Oceans Science

Pêches et Océans Canada
Sciences des écosystèmes et des océans

Canadian Science Advisory Secretariat (CSAS)

Research Document 2016/008

Québec Region

Updated analysis of genetic mixing among Nunavik beluga summer stocks to inform population models and harvest allocation

T. Doniol-Valcroze[1], M.O. Hammill[1], S. Turgeon[1] & L.D. Postma[2]

[1] Maurice-Lamontagne Institute
Fisheries and Oceans Canada
P.O. Box 1000
Mont-Joli, Quebec, G5H 3Z4

[2] Freshwater Institute
Fisheries and Oceans Canada
501 University Crescent
Winnipeg, Manitoba, R3T 2N6

February 2016

Foreword

This series documents the scientific basis for the evaluation of aquatic resources and ecosystems in Canada. As such, it addresses the issues of the day in the time frames required and the documents it contains are not intended as definitive statements on the subjects addressed but rather as progress reports on ongoing investigations.

Research documents are produced in the official language in which they are provided to the Secretariat.

Published by:

Fisheries and Oceans Canada
Canadian Science Advisory Secretariat
200 Kent Street
Ottawa ON K1A 0E6

http://www.dfo-mpo.gc.ca/csas-sccs/
csas-sccs@dfo-mpo.gc.ca

ISSN 1919-5044

Correct citation for this publication:

Doniol-Valcroze, T., Hammill, M.O., Turgeon, S. & Postma, L.D. 2016. Updated analysis of genetic mixing among Nunavik beluga summer stocks to inform population models and harvest allocation. DFO Can. Sci. Advis. Sec. Res. Doc. 2016/008. iv + 13 p.

ABSTRACT

Nunavik hunters harvest beluga from a mixture of stocks, including the Eastern Hudson Bay (EHB) summer aggregation. In 2014, a 3-year management plan proposed by the Nunavik Marine Region Wildlife Board (NMRWB) established a Total Allowable Take for the EHB stock, which relies on genetic analyses of samples obtained from Inuit hunters to determine the proportion of EHB beluga harvested seasonally in different areas of Nunavik.

Using 1,254 harvest samples collected from 1982 to 2013, we updated previous analyses and grouped our results according to the new beluga management boundaries established by the NMRWB. Proportions of EHB beluga in the Hudson Strait harvest remain consistent with previous estimates (11.7% in spring and 23.6% in fall). However, sample sizes for north-eastern Hudson Bay in spring and in Ungava Bay in fall were insufficient for inference.

In 2010, the community of Sanikiluaq (Nunavut) approved a voluntary hunt closure between July 1 and September 30, to assist with EHB beluga recovery. In 2012, the start of the closure date was changed to July 15. The updated proportion of EHB beluga harvested in the Belcher Islands was 2.8% in spring (April 1 – June 30), and 6.5% if spring was extended by two weeks (April 1 – July 14). The proportion was 30.6% in summer (July 1 – September 30) and 0% in fall, which confirms that the voluntary summer hunt closure established by the community of Sanikiluaq is an efficient approach to protect the EHB stock. The samples available from July and August, together with expert knowledge, suggest that extending the spring hunt into July may increase the probability of taking EHB beluga. However, this is based on a limited number of samples and so should be interpreted with caution.

Mise à jour des analyses génétiques du mélange des stocks de belugas du Nunavik afin d’informer les modèles de population et l’allocation de la chasse

RÉSUMÉ

Les Inuits du Nunavik chassent des bélugas qui proviennent de plusieurs stocks, dont l’agrégation estivale de l’est de la baie d’Hudson (EBH). En 2014, un plan de gestion de 3 ans proposé par le Conseil de Gestion des Ressources Fauniques de la Région Marine du Nunavik (CGRFRMN) a établi une prise totale autorisée pour le stock de l’EBH. Ce plan dépend des analyses génétiques d’échantillons recueillis par les chasseurs Inuits afin de déterminer la proportion de bélugas de l’EBH parmi les prises des différentes régions du Nunavik à différentes saisons.

En utilisant 1254 échantillons de bélugas chassés entre 1982 et 2013, nous avons mis à jour les analyses précédentes et regroupé nos résultats selon les limites des nouvelles zones de gestion établies par le CGRFRMN. Les proportions de bélugas de l’EBH parmi les prises du détroit d’Hudson restent comparables aux estimations précédentes (11,7 % au printemps et 23,6 % à l’automne). Par contre, le nombre d’échantillons n’était pas suffisant pour apporter de l’information pour le nord-est de la baie d’Hudson au printemps et pour la baie d’Ungava à l’automne.

En 2010, la communauté de Sanikiluaq (Nunavut) a approuvé une fermeture volontaire de la chasse entre le 1er juillet et le 30 septembre, afin d’aider au rétablissement du stock de l’EBH. En 2012, la date de début de la période de fermeture a été repoussée au 15 juillet. L’estimation mise à jour de la proportion de bélugas de l’EBH prélevés dans les îles Belcher est de 2,8 % au printemps (1er avril – 30 juin), et de 6,5 % si la période printanière est étendue de 2 semaines (1er avril – 14 juillet). La proportion est de 30,6 % en été (1erjuillet – 30 septembre) et de 0 % à l’automne, ce qui confirme que la fermeture volontaire de la chasse pendant la période estivale est une approche efficace pour protéger le stock de l’EBH. Les échantillons disponibles pour les mois de juillet et août, combinés aux connaissances des experts, suggèrent que prolonger la chasse printanière durant le mois de juillet pourrait augmenter la probabilité de prendre des bélugas de l’EBH. Cependant, ces conclusions sont basées sur un nombre limité d’échantillons et doivent donc être interprétées avec précaution.

INTRODUCTION

The beluga (*Delphinapterus leucas*) is a toothed whale with pan-Arctic distribution extending into the Hudson Bay complex in sub-arctic eastern Canada (Richard and Pike 1993). Subsistence hunting of beluga by Nunavik Inuit (in northern Quebec) is directed towards a migratory population that winters in Hudson Strait and the Labrador Sea. Photo-identification, satellite telemetry and genetic studies have shown that beluga exhibit strong seasonal site fidelity to specific congregation areas during summer (Caron & Smith 1990; de March & Postma 2003, Lewis et al. 2009). Despite interbreeding on wintering grounds (Turgeon et al. 2012), cultural conservatism of maternally-transmitted migration routes seems to prevent substantial exchange between these summering aggregations (Colbeck et al. 2012), thus making beluga vulnerable to local extirpation (COSEWIC 2004).This cumulative evidence has led to the current use of discrete summering stocks as management units (e.g., Smith and Hammill 1986, Richard 2010).

Most summer aggregations of beluga across the Canadian Arctic are genetically differentiated by mtDNA analyses (Brennin et al. 1997; Brown Gladden et al. 1999; de March and Postma 2003). In eastern Canada, studies have clearly demonstrated that the eastern Hudson Bay (EHB) stock is differentiated from the adjacent Western Hudson Bay (WHB) stock, although both stocks belong to the same breeding population (Turgeon et al. 2012). The EHB stock was depleted by intensive commercial hunting in the nineteenth century (Reeves & Mitchell 1987). EHB beluga currently number around 3300 animals (Doniol-Valcroze et al. 2014), and were designated by COSEWIC as Threatened in April 1988; their status was re-examined and changed to Endangered in May 2004.

With the signing of the Nunavik Inuit Land Claim Agreement (Anonymous 2008), the Nunavik Marine Region Wildlife Board (NMRWB) became the main instrument of wildlife management for the Nunavik Marine Region (NMR). The objectives of the NMRWB are to establish wildlife management systems that reflect Nunavik Inuit harvesting rights, while being governed by the principles of conservation (NILCA s. 5.1.3 (a) and (c)). Given existing conservation concerns for EHB beluga, the NMRWB proposed a 3-year management plan in 2014 that was approved and implemented by DFO. The plan established a Total Allowable Take (TAT) for the EHB beluga stock.

However, estimating the number of harvested EHB beluga is complex. A common migratory corridor in north-eastern Hudson Bay, Hudson Strait and Ungava Bay, is shared by EHB beluga and beluga from other summer stocks. There is no way for hunters to distinguish among these migratory stocks. Genetic studies indicate that the proportion of each stock in the harvest varies spatially and seasonally (de March & Postma 2003; Turgeon et al. 2012). Therefore, genetic analyses of skin samples provided by hunters have been used to determine the proportions of EHB beluga in seasonal harvests from different areas to inform population models and management schemes.

The 2014 management plan relies substantially on these genetic analyses of harvest samples, specifically the proportion of EHB beluga harvested in different areas of Nunavik. Turgeon et al. (2012) included analysis of data up until 2006 and based their analyses on groupings of sampling data into sub-regions. Given that the NMRWB has proposed new management areas, adjustments to the data grouping are necessary to improve accuracy and better align science advice with the NMRWB's propositions. Additionally, there are recent data available (2007–2013 samples) that could improve the confidence in the proportions currently being used.

Beluga are also observed around the Belcher Islands (within the Nunavut Settlement Area) early in spring and throughout summer and fall, and are harvested by hunters from the community of Sanikiluaq. Their relationship to other summer stocks is unclear but they are not currently considered a distinct management stock and are not surveyed separately during Nunavik beluga censuses (Hammill et al. 2004). Satellite telemetry studies have shown that EHB beluga may be vulnerable to being harvested in the Belcher Islands, especially in summer and fall (Doniol-Valcroze & Hammill 2012), but previous genetic analyses suggest that few EHB beluga are taken during Sanikiluaq spring and fall hunts. There is no formal management plan or legal harvest restriction for Nunavut hunters living in the Belcher Islands. However, the community of Sanikiluaq has enacted beluga hunting rules, involving since 2010 a voluntary annual closure of the summer beluga harvest in the Belcher Islands (between July 1 and September 30) as a conservation measure in support of EHB beluga recovery. In 2012, the start of the voluntary harvest closure start date was changed to July 15.

Within this context, our objectives were to use recently collected harvest samples and the newly-defined management areas and hunting seasons to determine the proportion (and associated uncertainty) of EHB beluga harvested by Nunavik communities and in Sanikiluaq, Nunavut.

MATERIALS AND METHODS

BIOLOGICAL SAMPLING & GENETIC CHARACTERIZATION

Beluga tissue samples (in general, skin) were obtained from Hudson Bay and surrounding areas. A few samples were collected by DFO during deployment of satellite transmitters, but the vast majority of samples were obtained from Nunavik and Nunavut hunters during harvest. In Nunavik, a sampling program was initiated in collaboration with Makivik Corporation in the 1980’s. A similar program is in place in Sanikiluaq as well as western Hudson Bay communities. Hunters participate in the program on a voluntary basis, and receive financial compensation for providing samples.

Samples were collected on-site at the time of the hunt and were provided to DFO along with information such as date and location. Although the availability and reliability of this information has increased through time, it is missing in some cases. Moreover, hunters from some communities in Hudson Bay and Ungava Bay travel to other areas (mostly Hudson Strait) to hunt beluga. It is therefore crucial to assign samples to the correct hunting area. Reports from hunters and Uumajuit wardens were used to locate the exact site where each beluga was killed for both new and previous samples. When hunting location could not be determined with confidence, samples were removed from the analysis.

DNA extraction, molecular determination of sex and sequencing of a portion of the mitochondrial DNA D-loop region were performed using methods described in de March and Postma (2003) and in Postma et al. (2012). DNA sequences were aligned and edited using MEGA ver 5 (Tamura et al. 2011) and haplotypes identified using GenAlEx 6 (Peakall and Smouse 2006).

GENETIC MIXTURE ANALYSIS

Previous studies have shown that the significant mtDNA differentiation among the main summering areas means that they can be used as source samples for a Genetic Mixture Analysis (GMA). Our objective was to update previous estimates of the proportion of EHB beluga in the Nunavik and Sanikiluaq harvests. However, our methodology differs from previous studies in several ways. First, Turgeon et al. (2012) analyzed samples from beluga caught between 1982 and 2006 in all of Hudson Bay and surrounding areas (e.g., Iqaluit, Foxe Basin, northern Hudson Strait). In contrast, our analysis focused only on Nunavik and Sanikiluaq harvests, augmented with samples collected in these areas between 2007 and 2013.

Second, in previous studies, material from belugas harvested in three summering areas, i.e. WHB, EHB and Cumberland Sound, were used as source samples (Turgeon et al. 2010, Turgeon et al. 2012). These analyses suggested that a significant proportion of beluga in the harvest of Sanikiluaq and Nunavik communities exhibited haplotypes that were strongly associated with the Cumberland Sound stock. Based on traditional knowledge and telemetry studies, it is considered extremely unlikely that there is contemporary exchange of individuals between beluga that summer in the Belcher Islands and beluga that summer in Cumberland Sound. Instead, these results most likely reflected a founder effect, where after the last glaciation, animals sharing similar haplotypes dispersed to the Cumberland Sound, and the Belcher Islands areas. Therefore, to minimize confusion, we have performed our analysis using only two source stocks: WHB and EHB.

Third, we have changed the dates and locations for each of the regional harvests to align them with the new management units that are in use since 2014 to manage Nunavik beluga hunt. We grouped harvest locations into two categories: summering areas (WHB, EHB; de March et al. 2002; de March and Postma 2003; COSEWIC 2004) and mixed hunt areas in Nunavik coastal waters along the common seasonal migratory corridor (Fig. 1): northeastern Hudson Bay (NEHB), southern Hudson Strait (HS), Ungava Bay (UNG) and Sanikiluaq (SAN). Here, as in previous studies, source samples included beluga hunted in summering areas in July or August. For NEHB, HS and UNG, we pooled samples into two hunting seasons: a “spring” hunt from February 1 to August 31, and a “fall” hunt from September 1 to January 31. We also investigated proportions in the Ungava Bay harvest in the summer (July-August), because Ungava Bay is considered a summering area for a potentially distinct summer stock.

For Sanikiluaq, we examined two definitions of the spring hunt: one (“Spring”) bounded by the voluntary closure date in place between 2010 and 2012 (i.e., April 1 to June 30) and the other (“Extended Spring”) using the post-2012 closure date (i.e., April 1 to July 14). There were not enough samples to analyze the 2010-2011 and 2012-2013 harvests individually, and therefore all Sanikiluaq samples from 1982 to 2013 were used (in other words, the datasets for the two Sanikiluaq “Spring” and “Extended Spring” periods differed only by the samples taken in the first half of July during the entire study period). Because of low sample size in late-July and August, the Sanikiluaq summer season was investigated based on all July-August samples. Fall (September – November) and winter (December – March) hunting in Sanikiluaq were examined separately because most of the winter samples come from ice entrapment events, at a time when EHB beluga are believed to have left the area.

Based on mtDNA haplotypes, we performed the GMA to estimate the proportion of individuals contributed by the different source stocks in areas and periods with potentially mixed stock composition. As per Turgeon et al. (2012), we used the genetic stock identification method implemented in the software SPAM version 3.7b (Debevec et al. 2000, Alaska Department of Fish and Game 2003). SPAM employs maximum likelihood methods to estimate relative contributions of discrete stocks in a mixture of several stocks, based on a multivariate Dirichlet distribution. The contribution estimates for each stock are computed as those that result in the largest likelihood of obtaining the observed mixture sample. Standard errors around the estimates were computed using a leave-one-out Jackknife. Confidence intervals (95%) were computed assuming that the proportions of each stock in the mixture follow beta distributions.

EFFECT OF CLUSTERING OF SAMPLES WITHIN HUNTING EVENTS

Beluga are known to travel in social groups of related individuals (Colbeck et al. 2012). Therefore, if several beluga from the same group are killed during the same hunting event, they are more likely to share the same haplotypes. This clustering of samples within each hunting event could bias the results if the data in some areas or seasons come from only a few events. One way to account for this additional source of uncertainty would be to perform the Jackknife resampling on hunting events instead of individual samples. However, not all beluga killed in a hunting event are sampled and we usually have no information about the exact number of hunting events on a given day (i.e., whether two beluga killed on the same day were hunted at the same site from the same social group). Therefore, we approximated hunting events by considering that each date was an event. To quantify the uncertainty added by clustering of samples, we computed standard errors using a leave-one-date-out Jackknife (i.e., by removing all samples from a given date at each iteration of the Jackknife, instead of removing one sample at a time).

RESULTS

HAPLOTYPES

Mitochondrial DNA sequences were obtained for 1,637 samples and categorized into haplotypes. No new samples were available for the source area WHB (132 individuals). For the EHB source area, 185 samples were available (vs. 169 in previous analyses). Thanks to increased effort and dedicated sampling programs, a total of 945 samples were available from the Nunavik mixed hunt areas (Table 1, 21 samples from NEHB, 857 samples from HS, 67 samples from UNG), compared to a previous sample size of 413. In addition, 309 samples were available from Sanikiluaq (vs. 152 previously).

GENETIC MIXTURE ANALYSIS

The haplotypes frequencies in the Nunavik harvest are shown in Fig. 2, and the estimated proportions of EHB beluga are given in Table 2. In the spring hunt, the proportions of EHB beluga 11.7% (CV 0.17, N=539) for Hudson Strait, and 8.8% (CV 0.54, N=64) for Ungava Bay. In the fall hunt, these proportions were estimated at 23.6% (CV 0.13, N=318) for Hudson Strait, and 33.2 % (CV 0.38, N=19) for northeast Hudson Bay. The proportion of EHB beluga in the Ungava Bay harvest in the summer months only (July – August) was estimated at 4.3% (CV 0.91, N=46).

Hunts in the northeastern Hudson Bay in spring and Ungava Bay in fall yielded too few samples to provide meaningful estimates of the proportion of EHB animals in the harvest (N=2 and 3 respectively).

In the Sanikiluaq spring harvest (Table 3, Fig. 3), the proportion of EHB beluga was 2.8% (CV 0.64, N=191) for the period April 1 – June 30 and 6.5% (CV 0.36, N=212) for the period April 1 – July 14. The proportion of EHB beluga in the Sanikiluaq summer harvest (July 1 – August 31) was 30.6% (CV 0.35, N=29) and the proportion in the fall hunt was 0.0% (N=33). The proportion of EHB beluga in the winter samples was estimated at 39.8% (CV 0.20, N=56).

When the Jacknife was performed as a leave-one-date-out instead of leave-one-sample-out, the effect of clustering of samples within hunting events (in this case, hunting dates) was to increase the standard errors around the estimates. This increase was due to a lower sample size (less hunting events than samples) as well as the occurrence of low within-event variation vs. high among-event differences (in which case the impact of removing one entire hunting date was higher). For instance, the 56 Sanikiluaq winter samples originated from only 6 hunting events (most of which with low within-event variation in haplotypes), which increased the CV around the estimate from 0.20 to 0.35. Note that the 95% Confidence Intervals given in tables 2 and 3 are calculated using these increased CVs based on the number of hunting events.

DISCUSSION

Using 1,254 harvest samples collected from 1982 to 2013, we have updated previous analyses by Turgeon et al. (2012) to include recent samples and align the definitions of hunting areas and seasons with newly established management schemes established by the NMRWB. Additional samples from the 2007 to 2013 period increased the sample size for Nunavik and Sanikiluaq regions from 413 to 945 and from 152 to 309, respectively. The effect of these larger sample sizes has been to lower the uncertainty around estimates and to increase our confidence in the results.

One major change from previous studies is that we have used two sources instead of three in our genetic mixture analytical framework (i.e., not considering samples from Cumberland Sound as a source stock). We chose this approach because it was considered implausible that Cumberland Sound beluga could be found in the harvest of Nunavik communities, and even more so in the Belcher Islands. This change has had little effect on the estimated proportions of EHB beluga in the harvest, presumably because haplotype frequencies in Cumberland Sound samples resembled those from WHB, and therefore, in the mixed hunt areas, the proportions of samples that were previously assigned to Cumberland Sound were assigned instead to either WHB or unknown sources, not to EHB.

Despite changes made to hunting areas and season dates, as well as the shift from a 3-source to a 2-source analysis, proportions of EHB beluga in the Nunavik harvests remain consistent with previous estimates (with decreased uncertainty). For instance, the proportion of EHB beluga in the Hudson Strait spring harvest was previously estimated at 12.8% (CV 0.38, 95%CI 4.9 – 23.7); now we estimate it at 11.7% (CV 0.17, 95%CI 8.0 – 16.4). The proportion in the Hudson Strait fall harvest, previously estimated at 21.9% (CV 23%, 95%CI 12.8 – 32.5), is now estimated at 23.6% (CV 0.13, 95%CI 17.9 – 29.9). This suggests that proportions of EHB beluga in the Nunavik harvest have remained stable in recent years, and that previous science advice was reasonable despite smaller sample size.

After assigning samples to their exact harvest location (e.g., in Hudson Strait, near Ivujivik), rather than to the community that collected them (e.g., Akulivik), the sample sizes in northeast Hudson Bay in spring and in Ungava Bay in the fall were insufficient for inference (N=2 and 3, respectively). These few samples were all attributed to the WHB source stock, thus no meaningful recommendations can be made for these areas until additional samples are collected. Sample size remains small in northeast Hudson Bay in the fall, and therefore the estimated proportions in that harvest should be used with caution.

The proportion of EHB in the Sanikiluaq spring harvest was previously estimated at 4% (95%CI 0.4 – 11.6). We now estimate it at 2.8% (95%CI 0.3 – 7.7) for the period April 1 – June 30, and at 6.5% (95%CI 2.0 – 13.3) for the extended period April 1 – July 14. The difference between the “Spring” and “Extended Spring” periods is based on only 21 samples collected in the first half of July (2 events in 1994, 1 in 1995, 2 in 2003, 1 in 2004, 3 in 2009 and 1 in 2010), and thus must be interpreted with caution. The proportion was 30.6% (95%CI 5.9 – 64.6) in summer (July 1 – September 30) and 0% in fall, which confirms that the voluntary summer hunt closure established by the community of Sanikiluaq is an efficient approach to protect the EHB stock. The samples available from July and August, together with expert knowledge, suggest that extending the spring hunt into July may increase the probability of taking EHB beluga.

Little consideration has been given to the fall hunt in Sanikiluaq. Satellite telemetry studies have shown that EHB beluga remain around the Belchers in October prior to their migration, and thus should be vulnerable to being harvested by Sanikiluaq hunters. However, as reported previously (Turgeon et al. 2012), our analysis estimated the proportion of EHB beluga in the fall hunt in Sanikiluaq to be 0%. A possible explanation for this paradox is that the location of hunting sites in the fall makes it more likely that WHB beluga are harvested while on their migration route than EHB individuals, but finer details are needed on the exact location at which beluga are harvested.

The Sanikiluaq winter dataset includes 49 samples (out of 56) from ice entrapment events that occurred in the Belcher Islands in 2004, 2011 and 2013, and these samples are responsible for the high winter proportion of EHB beluga (~40%). It is still not clear why EHB beluga would remain in southeastern Hudson Bay in winter, and it is possible that these individuals are not EHB whales and actually belong to a separate, as yet unidentified beluga stock (Postma et al. 2012). The idea that the stock composition of southeast Hudson Bay beluga is more complex than currently defined is also supported by the assignment of a relatively large proportion of the Sanikiluaq harvest samples to an unknown source stock by the GMA analysis.

Several sources of uncertainty arise from the sampling program (e.g., unequal sampling across sex and age classes, uncertainty around sampling dates and locations in older samples). One major source of concern is due to beluga travelling in social groups of related individuals (Colbeck et al. 2012). When several beluga are killed during the same hunting event, they are thus more likely to have similar haplotypes. We addressed the potential effect of the clustering of samples by performing Jackknife resampling on hunting events instead of individual samples. The resulting standard errors around the estimates were substantially larger in most cases, particularly when samples originated from few hunting events. This approach better quantifies the added uncertainty due to cluster sampling, and therefore it would be more conservative to use these “event CVs” in population modelling exercises.

We note a concentration of hunting effort around the communities of Ivujivik and Quaqtaq because hunters from other northeastern Hudson Bay and Ungava Bay communities travel there to harvest beluga. Our sample collection is heavily biased towards these two hunting sites and may not be representative of beluga mixtures in other areas of southern Hudson Strait. However, our updated estimates are fully consistent with provisions of Nunavik’s new management scheme (area boundaries, dates). We recommend that they be used for the EHB beluga population model and management considerations, and that these proportions be updated frequently (e.g., each time a stock assessment is performed).

ACKNOWLEDGEMENTS

We thank the Nunavik hunters and Uumajuit wardens for providing skin samples and reports on catches. We thank the Nunavik Hunting, Fishing and Trapping Association for assistance with the sampling program. We also thank Denise Tenkula for DNA analyses, Peter May for beluga aging data, and the Makivik Corporation and D.W. Doidge from the Nunavik Research Center for coordinating this program. Special thanks to Pierre Duchesne for facilitating the transfer of knowledge regarding the SPAM model and to Jean-François Gosselin for advice on methods and for assistance with figures. This work was supported by Species at Risk funding to the Department of Fisheries and Oceans, the Interdepartmental Recovery Fund (Environment Canada) and the Centre of Expertise for Marine Mammalogy (CEMAM).

REFERENCES CITED

Alaska Department of Fish and Game. 2003. SPAM Version 3.7: Statistics Program for Analyzing Mixtures. Alaska Department of Fish and Game, Commericial Fisheries Division, Gene Conservation Lab.

Anonymous. 2008. Nunavik Inuit Land Claims Agreement. Pages 22-53. Ottawa, Canada.

Brennin, R., Murray, B.W., Friesen, M.K., Maiers, L.D., Clayton, J.W. and White, B.N. 1997. Population genetic structure of beluga whales (*Delphinapterus leucas*): Mitochondrial DNA sequence variation within and among North American populations. Can. J. Zool. 75: 795-802.

Brown Gladden, J.G., Ferguson, M.M., Friesen, M.K. and Clayton, J.W. 1999. Population structure of North American beluga whales (*Delphinapterus leucas*) based on nuclear DNA microsatellite variation and contrasted with the population structure revealed by mtDNA variation. Mol. Ecol. 8: 347-3 63.

Caron, L.M.J. and Smith, T.G. 1990. Philopatry and site tenacity of belugas, *Delphinapterus leucas*, hunted by the inuit at the Nastapoka estuary, eastern Hudson Bay. In Smith, T.G., D.J. St.Aubin, and J.R. Geraci (ed.). Advances in research on the beluga whale,*Delphinapterus leucas*. Can. Bull. Fish. Aquat. Sci. 224: 69-79.

Colbeck, G., Duchesne, P., Postma, L.D., Lesage, V., Hammill, M. & Turgeon, J. 2012. Groups of related belugas (*Delphinapterus leucas*) travel together during their seasonal migrations in and around Hudson Bay. Proceedings of the Royal Society B: Biological Sciences 280 doi: 10.1098/rspb.2012.2552.

COSEWIC. 2004. COSEWIC assessment and update status report on the beluga whale *Delphinapterus leucas* in Canada. Committee on the Status of Endangered Wildlife in Canada. Ottawa. ix + 70 pp.

Debevec, E.M., Gates, R.B., Masuda, M., Pella J., Reynolds, J. and Seeb, L.W. 2000. SPAM (Version 3.2): statistics program for analyzing mixtures. J Hered 91:509–510

de March, B.G.E. and Postma, L.D. 2003. Molecular genetic stock discrimination of belugas (*Delphinapterus leucas*) hunted in eastern Hudson Bay, Northern Quebec, Hudson Strait, and Sanikiluaq (Belcher Islands), Canada, and comparisons to adjacent populations. Arctic 56:111-124.

Doniol-Valcroze, T., Gosselin, J.-F. and Hammill, M.O. 2014. Impacts of a flexible Total Allowable Take system on beluga conservation in the Nunavik Marine Region. DFO Can. Sci. Advis. Sec. Res. Doc. 2014/004. v + 17 p.

Doniol-Valcroze, T. and Hammill, M. O. 2012. Harvest advice for beluga in the Belcher, King George, and Sleeper Islands in relation to the eastern Hudson Bay stock. DFO Can. Sci. Advis. Sec. Res. Doc. 2011/125. iv + 8 p.

Hammill, M.O., Lesage, V. Gosselin , J.-F. Bourdages, H. de March, B. G.E. and Kingsley, M.C.S. 2004. Changes in abundance of northern Quebec (Nunavik) beluga. Arctic 57:183-195.

Lewis, A.E., Hammill, M., Power, M., Doidge, D.W. & Lesage, V. 2009. Movement and Aggregation of Eastern Hudson Bay Beluga Whales (*Delphinapterus leucas*): A Comparison of Patterns Found through Satellite Telemetry and Nunavik Traditional Ecological Knowledge. Arctic 62: 13-24.

Peakall, R. and Smouse, P.E. 2006. GENALEX 6: genetic analysis in excel. Population genetic software for teaching and research. Mol. Ecol. Notes 6:288-295.

Postma, L.D., Petersen, S.D., Turgeon, J., Hammill, M.O., Lesage, V., and Doniol-Valcroze, T. 2012. Beluga whales in James Bay: a separate entity from eastern Hudson Bay belugas? DFO Can. Sci. Advis. Sec. Res. Doc. 2012/074. iii + 23 p.

Reeves, R.R. and Mitchell, E.D. 1987. History of white whale (*Delphinapterus leucas*) exploitation in eastern Hudson Bay and James Bay. Can. Spec. Publ. Fish. Aquat. Sci. 95. 45p.

Richard, P.R., 2010. Stock definition of belugas and narwhals in Nunavut. DFO Can. Sci. Advis. Sec. Res. Doc. 2010/022. iv + 14.

Richard, P.R. and Pike, D.G. 1993. Small whale co-management in the eastern Canadian Arctic: a case history and analysis. Arctic 46:138–143.

Smith, T.G. and Hammill, M.O. 1986. Population estimates of white whale, *Delphinapterus leucas*, in James Bay, Eastern Hudson Bay and Ungava Bay. Can. J. Fish. Aquat. Sci. 43: 1982-1987.

Stewart, R.E.A., Campana, S.E., Jones, C.M. and Stewart, B.E. 2006. Bomb radiocarbon dating calibrates beluga (*Delphinapterus leucas*) age estimates. Can. J. Zool. 84:1840–1852.

Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M. and Kumar, S. 2011. MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. Mol. Biol. Evol. 28: 2731-2739.

Turgeon, J. Duchesne, P. Postma, L. D. and Hammill, M. O. 2010. Spatiotemporal distribution of beluga stocks (Delphinapterus leucas) in and around Hudson Bay: Genetic mixture analysis based on mtDNA haplotypes. DFO Can. Sci. Advis. Sec. Res. Doc. 2009/011. iv + 14 p.

Turgeon, J., Duchesne, P., Colbeck, G.J.C., Postma, L. and M.O. Hammill. 2012. Spatiotemporal segregation among summer stocks of beluga (*Delphinapterus leucas*) despite nuclear gene flow: implication for an endangered population in eastern Hudson Bay (Canada). Conserv. Gen. 13:419-433.

TABLES AND FIGURES

Table 1. Number of samples available for each management area and each hunting season, for the 1982-2013 period.

Area	**Spring**				**Fall**			**Winter**			
	May	**June**	**July**	**Aug**	**Sept**	**Oct**	**Nov**	**Dec**	**Jan**	**Feb**	**March**
Hudson Strait	3	423	107	6	28	189	100	1	0	0	0
Ungava Bay	0	18	40	6	0	2	0	1	0	0	0
NE Hudson Bay	2	0	0	0	1	18	0	0	0	0	0

Sanikiluaq	**Spring**		**Summer**		**Fall**			**Winter**			
	May	**June**	**July**	**Aug**	**Sept**	**Oct**	**Nov**	**Dec**	**Jan**	**Feb**	**March**
	56	**135**	**26**	**3**	**17**	**14**	**2**	**37**	**0**	**12**	**7**

Sanikiluaq extended spring[*]	**Spring**			**Summer**		**Fall**			**Winter**			
	May	**June**	**July 1-14**	**July 15-31**	**Aug**	**Sept**	**Oct**	**Nov**	**Dec**	**Jan**	**Feb**	**March**
	56	135	21[**]	3[**]	3	17	14	2	37	0	12	7

** The July 15 closure date has been in use since 2012. However, the analysis used all samples collected between April 1 and July 14 over the period 1982-2013.*

*** The exact day of the month was uncertain for 2 of the 26 July samples from Sanikiluaq, and therefore these samples could not be assigned to the first or second half of the month.*

Table 2. Proportions of beluga (%) from each source stock in the harvest of Nunavik mixed hunt areas, based on genetic mixture analysis of mtDNA haplotype distribution. Software used: SPAM (Debevec et al. 2000). N samples: number of individual samples; N events: number of different hunting dates; WHB: Western Hudson Bay; EHB: Eastern Hudson Bay; 95%CI: 95% confidence interval based on variance among hunting events; CV: coefficients of variation based on individual samples / hunting events. ND: not determined (small sample size).

	N samples	N events	%WHB	95% CI	(CV samples /events)	%EHB	95% CI	(CV samples /events)	Unknown
Spring (Feb 1 – Aug 31)									
Hudson Strait	539	252	**82.2**	76.9-86.6	(0.02/0.03)	**11.7**	8.0-16.4	(0.17/0.19)	6.1%
NE Hudson Bay	2	1	**ND**	-	-	**ND**	-	-	ND
Ungava Bay	64	42	**83.4**	72.5-92.0	(0.06/0.06)	**8.8**	1.9-20.3	(0.54/0.55)	7.8%
Fall (Sept 1 – Jan 31)									
Hudson Strait	318	131	**73.3**	65.8-80.2	(0.04/0.05)	**23.6**	17.0-30.9	(0.13/0.15)	3.2%
NE Hudson Bay	19	7	**56.3**	28.3-82.2	(0.23/0.25)	**33.2**	14.9-54.7	(0.38/0.31)	10.5%
Ungava Bay	3	3	**ND**	-	-	**ND**	-	-	ND

Table 3. Proportions of beluga (%) from each source stock in the Sanikiluaq harvest, based on genetic mixture analysis of mtDNA haplotype distribution. Software used: SPAM (Debevec et al. 2000). N samples: number of individual samples; N events: number of different hunting dates; WHB: Western Hudson Bay; EHB: Eastern Hudson Bay; CV: coefficients of variation based on individual samples / hunting events. Cis and CVs are missing when proportion is zero.

Season	N samples	N events	%WHB	95% CI	(CV samples /events)	%EHB	95% CI	(CV samples /events)	Unknown
Spring (April 1 – June 30)	191	81	**78.9**	70.7-86.1	(0.03/0.05)	**2.8**	0.3-7.7	(0.64/0.70)	18.3%
Extended spring* (April 1 – July 14)	212	92	**76.5**	68.6-83.6	(0.03/0.05)	**6.5**	2.0-13.3	(0.36/0.45)	17.0%
Summer (July 1 – August 31)	29	16	**55.7**	23.8-85.1	(0.19/0.29)	**30.6**	5.9-64.6	(0.35/0.51)	13.8%
Fall (September 1 – November 30)	33	24	**97.0**	89.2-99.9	(0.01/0.03)	**0.0**	-	-	3.0%
Winter (December 1 – March 31)	56	6	**28.1**	7.8-55.1	(0.28/0.44)	**39.8**	14.8-68.2	(0.20/0.35)	32.1%

** The July 15 closure date has been in use since 2012. However, the analysis uses all samples collected between April 1 and July 14 over the period 1982-2013.*

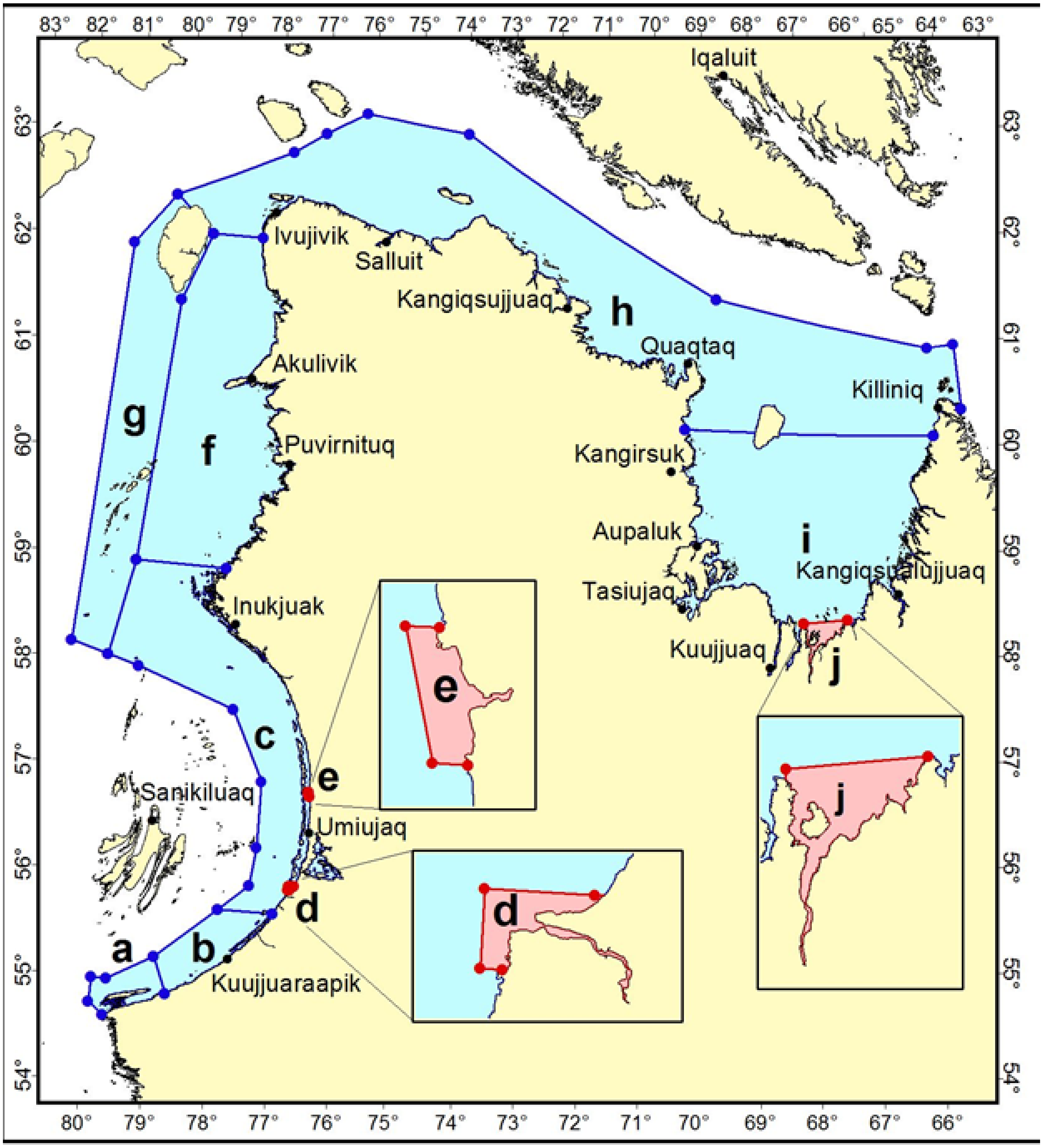

Figure 1. Map of Nunavik communities and management areas for Nunavik beluga (source: Nunavik Marine Region Wildlife Board). In our analysis, the Hudson Strait mixed hunt corresponds to area "h", Ungava Bay to area "i",northeast Hudson Bay to area "f", and the eastern Hudson Bay arc to areas "b", "c", "d" and "e".

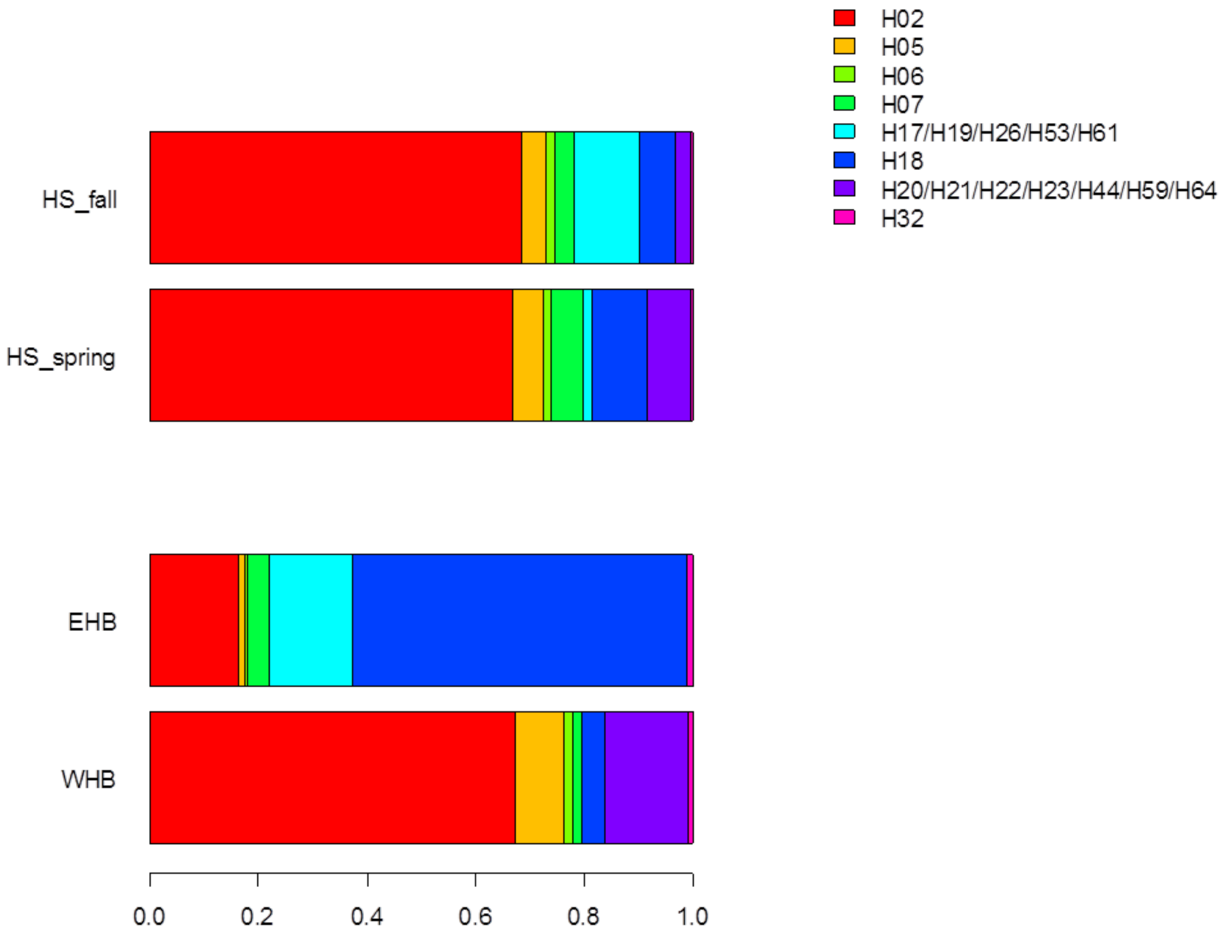

Figure 2. Frequency plot of haplotypes in source areas (bottom, EHB and WHB), and in mixed hunt areas (top). HS_spring and HS_fall: Hudson Strait harvests in spring and fall, respectively. Colour legend shows haplotypes or groups of haplotypes.

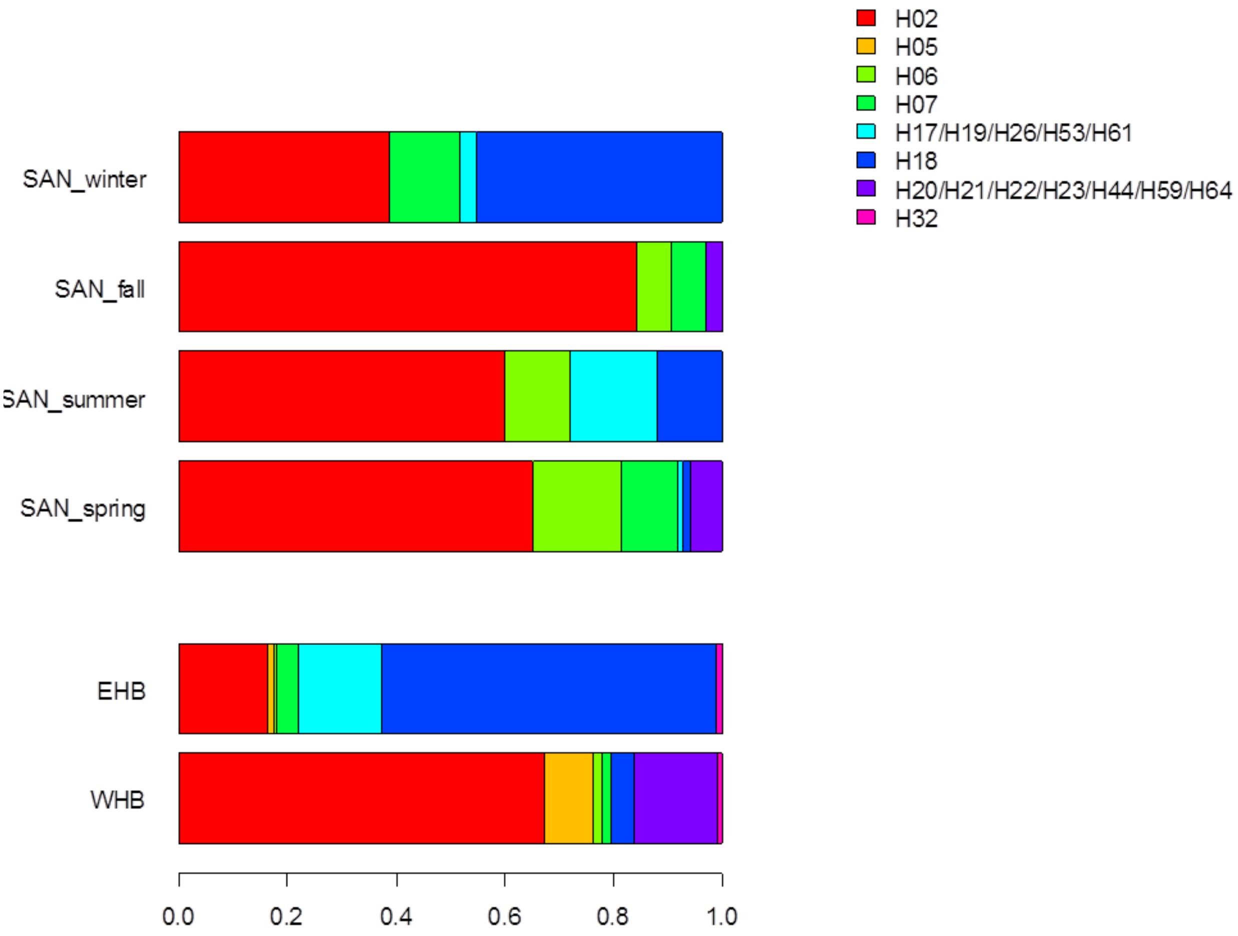

Figure 3. Frequency plot of haplotypes in source areas (bottom, EHB and WHB), and in the Sanikiluaq harvest at different seasons (top). Spring cut-off date is July 14 inclusively. Colour legend shows haplotypes or groups of haplotypes.