

UNIVERSITÉ DU QUÉBEC À RIMOUSKI

**CARACTÉRISATION DES POPULATIONS DE BÉLUGAS DE L'EST
DE L'ARCTIQUE CANADIEN À L'AIDE DES ISOTOPES STABLES
ET DES ÉLÉMENTS TRACES**

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PAR

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AVANT-PROPOS

Ce mémoire est présenté sous la forme d'un article à être soumis à une revue scientifique.

Contribution des auteurs

Bien que Véronique Lesage, Émilien Pelletier, Lianne Postma, Robert E.A. Stewart, Gary Stern et Mike O. Hammill soient co-auteurs de l'article, le manuscrit doit être considéré comme le mémoire de l'étudiante.

V. Lesage et E. Pelletier ont guidé l'étudiante lors de la planification du travail de laboratoire et lors de l'analyse des données et de la rédaction du mémoire et ont fournis l'idée originale. L. Postma a fourni une grande partie des échantillons ainsi que les résultats génétiques nous ayant permis de valider nos analyses discriminantes. G. Stern et R.E.A. Stewart ont coordonné l'échantillonnage sur le terrain pour les animaux du Nunavut. M. O. Hammill a coordonné l'échantillonnage au Nunavik, en lien étroit avec les dirigeants de Makivik, a apporté un support financier à È. Rioux et a contribué à travers des efforts soutenus depuis plusieurs années, à obtenir la collaboration des Inuit pour faire du programme d'échantillonnage un succès. È. Rioux a fait les analyses en laboratoire, a fait les analyses statistiques et a rédigé le mémoire.

RÉSUMÉ

Selon des études se basant sur la distribution estivale des bélugas et l'analyse de leur ADN mitochondrial, il existerait au moins deux populations de bélugas dans la baie d'Hudson, soit celles de l'est et de l'ouest. Des bélugas sont aussi observés aux îles Belcher, dans le bassin Foxe, le long de la côte de l'Ontario et dans la baie James, mais leur appartenance est incertaine. Les voies migratoires des bélugas de la population de l'est de la baie d'Hudson, qui sont considérés en voie de disparition au Canada, et celles de la population beaucoup plus saine de l'ouest de la baie d'Hudson se chevauchent, rendant ainsi difficile la protection de la population de l'est de la baie d'Hudson lors de la chasse automnale et printanière dans le détroit d'Hudson. Des échantillons de peau de béluga ont été récoltés dans neuf régions de la baie d'Hudson et du détroit d'Hudson au cours des années 1989 à 2009 pour déterminer les rapports d'isotopes stables du carbone ($\delta^{13}\text{C}$) et d'azote ($\delta^{15}\text{N}$) ($N = 1070$ ind.) et les concentrations de 27 éléments traces ($N = 308$ ind.). L'objectif de l'étude était de déterminer si les traceurs chimiques de la diète pouvaient aider à discriminer les populations et de ce fait, estimer la proportion de bélugas de l'est de la baie d'Hudson dans la chasse d'automne du détroit d'Hudson. Les valeurs de $\delta^{13}\text{C}$ et $\delta^{15}\text{N}$ étaient semblables entre les périodes (1989-1999, 2000-2009), mais variaient significativement entre les sexes, les régions et les saisons. Les concentrations en éléments traces variaient également entre les régions et les saisons, mais étaient similaires entre les sexes. En utilisant les signatures isotopiques des populations d'été comme sources dans une analyse discriminante, nous avons déterminé que les bélugas mâles et femelles de la population de l'est de la baie d'Hudson représentaient respectivement 41% et 60% de la récolte d'automne du détroit d'Hudson sud ainsi que 9% et 0% de celle du détroit d'Hudson nord. Une validation de ces résultats à l'aide des assignations effectuées par la génétique indique que 66% des individus ont été assignés à la même population par les méthodes isotopique et génétique, mais que la méthode génétique sous-estimait fort probablement la proportion de bélugas appartenant à la population de l'est de la baie d'Hudson. L'analyse intégrant les isotopes stables et les éléments traces est prometteuse, mais la taille d'échantillon pour définir certaines des populations d'été, dont celle de l'est de la baie d'Hudson, est actuellement insuffisante pour bien les qualifier, menant à des résultats douteux. D'autre part, l'examen des résultats de cette analyse a révélé une certaine homogénéité des classes d'âge et des sexes lors d'un même événement de chasse, suggérant une possible persistance de la ségrégation estivale des mâles adultes et des femelles accompagnées de juvéniles durant la période de migration automnale. Cette étude a démontré l'utilité des marqueurs biochimiques et de cette nouvelle approche comme des compléments valables à la génétique dans la discrimination et la protection des populations de mammifères marins.

Mots clés : Béluga, Arctique Canadien, Isotope Stable, Élément Trace, Population, Structure, Analyse discriminante

ABSTRACT

In Hudson Bay, at least two beluga stocks are recognized based on summer aggregations and mtDNA analyses, i.e., the eastern and western Hudson Bay populations. Beluga occur elsewhere (e.g., Belcher Islands, James Bay, northern Ontario, Foxe Basin), but stock identity is unclear. The *Endangered* eastern Hudson Bay beluga and those from the healthier western Hudson Bay stock migrate through Hudson Strait where they are harvested during their fall and spring migrations, making difficult the protection of the eastern Hudson Bay stock. Beluga skin samples were collected from nine regions of Hudson Bay and Hudson Strait during 1989–2009, and were analysed for carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotope ratios ($N = 1070$ ind.) and concentrations of 27 trace elements ($N = 308$ ind.). Our goal was to determine whether feeding ecology could help discriminate among stocks and estimate the proportion of eastern Hudson Bay beluga in Hudson Strait fall harvests. $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values were similar between periods (1989–1999, 2000–2009), but varied significantly among sex, regions and seasons. Similarly, trace element concentrations varied according to geographical area and season, but were similar between males and females. Membership of beluga in the Hudson Strait fall harvest was assessed using stable isotope signatures and trace element concentrations of summering stocks in the various regions as sources in a discriminant functions analysis. Based on stable isotope signatures alone, male and female eastern Hudson Bay beluga represented 41% and 60% of the southern Hudson Strait fall harvest, respectively, while they represented 9% and 0% of the northern Hudson Strait fall harvest. Using probabilistic genetic assignments as eastern Hudson Bay vs non-eastern Hudson Bay as a way to determine the degree of agreement among methods, it was determined that 66% of the individuals were similarly assigned by the isotopic and genetic methods. However, the genetic approach most likely underestimated the proportion of eastern Hudson Bay beluga in the harvest. The analysis using both stable isotopes and trace elements is promising, but sample size for defining summering stocks, including eastern Hudson Bay beluga, is currently too small to qualify these stocks. Nevertheless, examination of these results revealed certain homogeneity in age and sex classes within a harvest event, suggesting a possible persistence during the fall migration of the summer segregation between adult males and females with juveniles. These results illustrate the usefulness of chemical markers as a valuable complementary tool to genetic in the discrimination and protection of marine mammal stocks.

Keywords : Beluga, Canadian eastern Arctic, Stable Isotope, Trace Element, Population, Structure, Discriminant Analysis

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CHAPITRE 1- INTRODUCTION GÉNÉRALE

1.1 L'ÉCOLOGIE ALIMENTAIRE DES MAMMIFÈRES MARINS

L'écologie est une science qui étudie les interactions entre les organismes vivants et leur environnement (Bowen and Sniff 1999). Cette discipline s'intéresse au comportement des individus au sein d'une population, à la reproduction, à la recherche de nourriture, à la protection contre les prédateurs ainsi qu'à la distribution des individus, des espèces et des populations. L'alimentation est un facteur déterminant pour la survie des espèces et est habituellement étroitement liée à la répartition saisonnière et à l'abondance des individus (Bowen and Sniff 1999). La quantité et le type de nourriture consommé par les mammifères marins ne sont pas très bien connus chez plusieurs espèces, particulièrement les cétacés et les espèces plus hauturières. En plus, la diète varie souvent avec l'âge (Kurle and Worthy 2001, Lawson and Hobson 2000), le sexe (Sinisalo et al. 2008, Tucker et al. 2007), la région (Angerbjorn et al. 1994), la période de l'année (Lawson and Hobson 2000) ainsi que l'abondance et la disponibilité des proies (de Stephanis et al 2008, Lee et al. 2005).

1.2 L'UTILISATION DES MARQUEURS CHIMIQUES

De nombreuses approches permettent d'étudier la diète des mammifères marins. Toutefois, la majorité de ces méthodes se basent sur des observations indirectes puisqu'il n'est pas facile d'observer directement l'alimentation des mammifères marins et souvent difficiles d'approche. En effet, ces animaux sont présents dans des régions difficile d'accès et passent la majeure partie de leur temps sous l'eau (Bowen and Sniff 1999). L'analyse de contenus stomacaux et des fèces permettent d'obtenir de l'information sur la diète récente de l'organisme (Dehn et al. 2007, Hammill et al. 2005, Holst et al. 2001). Elles reposent sur l'identification des structures dures telles que le squelette et les otolites des poissons

ainsi que les becs des céphalopodes (Bowen 2000). Toutefois, l'identification des proies consommées et leur proportion dans la diète, se base seulement sur les structures dures qui sont retrouvées dans le système digestif puisque les structures molles sont plus rapidement digérées et difficilement disponibles. Les structures qui se digèrent plus lentement amènent un biais puisqu'elles seront surestimées par rapport à celles qui se digèrent plus facilement (Bowen 2000). En plus, certaines parties des otolites peuvent être brisées et peuvent empêchées l'identification de l'organisme. Il faut aussi porter attention aux contenus analysés selon qu'ils proviennent d'un animal échoué ou mort puisque la composition de la diète pourrait représenter celle d'un animal moribond ou blessé et non d'un animal en santé (Barros and Clarke 2002). Enfin, compte tenu de la digestion relativement rapide chez les mammifères marins, les contenus digestifs sont souvent biaisés vers une alimentation à proximité du lieu d'échantillonnage.

Depuis quelques décennies, de nouvelles approches ont été développées afin d'améliorer les connaissances actuelles sur l'alimentation des mammifères marins. Ce sont, entre autres, l'analyse des acides gras et des rapports de certains isotopes stables. Ces techniques mesurent la quantité de certains éléments dans l'organisme et donnent de l'information sur la nourriture assimilée pendant une période de temps beaucoup plus longue qu'avec les méthodes traditionnelles (Kelly 2000, Lesage et al. 2001, Tieszen et al. 1983). Les acides gras représentent un large groupe de molécules lipidiques retrouvés en très grandes quantités dans tous les organismes. L'analyse de ces acides gras dans l'animal permet d'estimer la diète du prédateur et d'étudier les interactions trophiques et la structure des écosystèmes (Budge et al. 2006, Iverson et al. 2004). En effet, les acides gras sont entreposés en grandes quantités dans les tissus de l'animal dans leur forme originale (Tollit et al. 2010). Les acides gras sont donc transférés de la proie vers le prédateur avec peu ou pas de modifications. L'analyse des acides gras permet d'avoir une idée de la composition de la diète à différentes échelles spatiales et temporelles (Iverson et al. 1997, Smith et al. 1996, Smith et al. 1997). La présence de certains acides gras plus rarissimes dans les tissus du prédateur permet d'avoir des informations sur la consommation de proies ou de taxa

précis (Tollit et al. 2010). Finalement, l'utilisation des acides gras permet aussi d'estimer la diète au niveau quantitatif avec des modèles statistiques comme le QFASA (Budge et al. 2006, Iverson et al. 2004). Le QFASA se base sur le principe que les proies ont des signatures en acide gras caractéristiques et que ces signatures sont intégrées dans le prédateur de façon prévisible. L'estimation de la diète peut donc se faire puisque le modèle statistique compare les signatures en acides gras de toutes les proies potentielles avec celles du prédateur (Iverson et al. 2004). Cependant, cette procédure nécessite la connaissance du métabolisme de déposition des acides gras en plus de celle de la composition en acide gras de toutes les proies potentiellement importantes du prédateur qui doivent couvrir l'étendue spatiale et temporelle du prédateur.

1.2.1 L'analyse des isotopes stables

Les signatures isotopiques du carbone ($\delta^{13}\text{C}$) et de l'azote ($\delta^{15}\text{N}$) peuvent fournir de l'information sur la diète de l'animal (Dennard et al. 2009, Hammill et al. 2005, Lesage et al. 2001), sur la position trophique du prédateur (Lesage et al. 2001, Post 2002, Ruiz-Cooley et al. 2004), sur l'utilisation de l'habitat (Post 2002) ainsi que sur les patrons de migration (Schell et al. 1989, Schell et al. 1998). Les rapports des isotopes stables reflètent la nourriture consommée et assimilée sur une période de temps assez longue (semaines, mois, années) en comparaison à l'analyse des contenus stomacaux qui reflète la nourriture consommée sur une plus courte période de temps (jours) (Kelly 2000, Tieszen et al. 1983). Chaque tissu intègre la signature isotopique sur des périodes de temps différentes selon le taux de renouvellement des protéines du tissu (Hobson and Clark 1992, Rubenstein and Hobson 2004, Tieszen et al. 1983). La peau et les muscles intègrent l'information sur une période de 2 à 3 mois suivant l'échantillonnage tandis que le foie intègre l'information sur une période de quelques jours (Hicks et al. 1985, St. Aubin et al. 1990, Tieszen et al. 1983).

Plus précisément, le rapport des isotopes de l'azote permet de déterminer la position trophique du prédateur puisqu'un enrichissement prédictible en ^{15}N est observé à chaque niveau trophique (DeNiro and Epstein 1981, Post 2002). Les tissus du prédateur sont généralement enrichis de 3 à 5‰ par rapport à ceux de ses proies. Cette différence de rapport des isotopes de l'azote entre le prédateur et ses proies s'explique par le fait qu'il y a une proportion plus importante de ^{14}N que de ^{15}N dans les déchets azotés des consommateurs. Cependant, cet enrichissement varie selon les taxa, la diète et les tissus utilisés (Caut et al. 2009). Le rapport isotopique du carbone est généralement utilisé afin de déterminer la source de carbone et l'habitat utilisé (Post 2002). En effet, l'enrichissement trophique est généralement plus faible dans le cas du carbone, soit de l'ordre de 1‰, faisant ainsi un traceur plus adéquat des sources de carbone. Cette différence de rapport des isotopes du carbone entre les sources s'explique par le fait qu'il existe une différence dans la fixation des isotopes du carbone par les plantes terrestres en C_3 , C_4 , et la végétation marine en C_3 . Le $\delta^{13}\text{C}$ permet de déterminer si l'animal s'alimente plus au niveau benthique que pélagique, près des côtes ou plus au large, ou s'il dépend de ressources aquatique d'eau douce ou d'eau salée. En effet, le rapport isotopique du carbone est plus faible dans la chaîne alimentaire benthique que pélagique puisqu'il y a un enrichissement en ^{13}C des producteurs primaires en présence de faibles quantités de nutriments (France 1995). Le rapport isotopique du carbone est également plus faible dans la chaîne alimentaire côtière qu'hauturière puisque les conditions de l'eau, par exemple une quantité moindre de CO_2 retrouvée plus près des côtes, le taux de croissance des producteurs primaires ainsi que les valeurs de $\delta^{13}\text{C}$ dans les sources de carbone inorganique dissous diffèrent (Post 2002). La différence entre le rapport isotopique du carbone entre l'eau douce et l'eau salée s'explique par les différences sources de carbone fixées dans les chaînes alimentaires. Effectivement, la chaîne marine, appauvrit en ^{13}C , fixe le carbone provenant des bicarbonates tandis que la chaîne aquatique fixe le carbone du CO_2 (Bearhop et al. 1999, Peterson and Fry 1987).

1.2.2 L'analyse des éléments traces

Les éléments traces présents dans l'environnement marin proviennent de sources naturelles et/ou anthropiques. Certains éléments traces, tels que le mercure et le cadmium, s'accumulent en très grandes quantités à chaque niveau de la chaîne alimentaire, des proies aux prédateurs (Stavros et al. 2007). La diète est un facteur important pouvant expliquer l'accumulation de ces éléments traces (Monaci et al. 1998, Stavros et al. 2007). En effet, un mammifère marin piscivore accumulera principalement du mercure tandis qu'un mammifère marin teutophage accumulera essentiellement du cadmium (Bustamante et al. 1998). La région où l'animal s'est alimenté peut aussi être un facteur important dans l'accumulation de ces éléments traces (Monaci et al. 1998, Seixas et al. 2007). Cependant, ce ne sont pas tous les éléments traces qui s'accumulent chez les mammifères marins. Ces animaux sont capables d'en réguler plus d'un. Les éléments traces sont dynamiques, activement régulés, dépendant du transport des molécules et une compétition existe pour les sites de liaison (McGeer et al. 2003). Les différentes concentrations en éléments traces retrouvées chez les mammifères marins sont dues à plusieurs facteurs tels que le taux d'accumulation spécifique pour chaque espèce, tissu (Lavery et al. 2008) et élément trace. Le taux d'accumulation de certains métaux peut être relié à l'âge, au sexe (Brookens et al. 2007, Stavros et al. 2008) et peut aussi dépendre de la région où se trouve l'animal (Born et al. 2003, Dietz et al. 2000).

Les éléments traces essentiels et non-essentiels sont de plus en plus utilisés avec les isotopes stables afin de mieux comprendre l'utilisation de l'habitat, les relations trophiques des mammifères marins et la distinction des populations (Born et al. 2003, Brookens et al. 2007, Sanpera et al. 1996). Les éléments traces essentiels agissent comme cofacteurs dans les activités enzymatiques de nombreuses voies biochimiques (Bryan et al. 2007) tandis que les éléments non-essentiels étaient connus, jusqu'à présent, pour n'avoir aucune fonction biochimique autre qu'interférer avec les éléments essentiels (Anderson et al. 2010). De nos jours, les connaissances évoluent et certains éléments traces non-essentiels

ont des rôles dans plusieurs fonctions biochimiques (Finney and O'Halloran 2003, Kraemer et al. 2005).

1.3 DISCRIMINATION DES POPULATIONS

Une population (stock en anglais) peut être définie comme un groupe d'individus pouvant être géré et exploité indépendamment des autres groupes (Outridge and Stewart 1999). La distinction des populations est importante afin d'assurer la pérennité de l'espèce et de prévenir son déclin (Wang 2002). De meilleures connaissances sur l'utilisation de l'habitat et sur l'écologie alimentaire des mammifères marins pourraient aider à identifier les populations. En effet, l'analyse des rapports des isotopes stables et des concentrations de certains éléments traces ont parfois été mis à contribution pour différencier les populations (de March and Postma 2003, Herman et al. 2005, Kunito et al. 2002, Outridge et al. 2003). Ces nouvelles approches sont basées sur la théorie qu'un groupe d'animaux exploitant les mêmes ressources et habitant les mêmes régions auront dans leurs tissus des éléments isotopiques et élémentaires similaires permettant ainsi leur différenciation des autres groupes (Born et al. 2003, Outridge et al. 2003). Cependant, il est nécessaire de connaître les valeurs des isotopes stables à la base de la chaîne alimentaire tels que les signatures isotopiques du phytoplancton et de la matière organique particulaire ou des consommateurs de premier ordre puisque celles-ci varient grandement tant au niveau spatial que temporel (DeNiro and Epstein 1978, 1981, Iken et al. 2005, Post 2002). Les études génétiques mesurent les interactions entre les individus sur plusieurs générations tandis que les analyses des rapports d'isotopes stables ou les concentrations de certains éléments traces mesurent les interactions entre un individu et son environnement sur une période beaucoup plus courte et n'excédant pas celle de sa vie. La génétique permet donc d'établir les populations selon des processus survenant sur de très longues durées en comparaison aux analyses isotopiques ou d'éléments traces qui elles, établissent les populations à l'échelle d'une seule génération (Outridge et al. 2003).

1.4 BIOLOGIE ET ÉCOLOGIE DU BÉLUGA

1.4.1 Le béluga

Le béluga (*Delphinapterus leucas*) est un cétacé à dents, complètement blanc à l'âge adulte, faisant partie de la famille des Monodontidae. Il tire son nom du mot russe *belukha* qui signifie blanc, d'où l'appellation ancienne de marsouin blanc et de baleine blanche (O'Corry-Crowe 2002). Cette petite baleine est admirablement bien adaptée à l'environnement arctique et subarctique en raison de l'absence de nageoire dorsale et de la présence d'une peau très épaisse lui permettant de briser les glaces d'une épaisseur d'environ 10 cm (Stewart and Stewart 1989). Le béluga possède une couche de graisse très épaisse lui permettant de résister aux températures froides de l'Arctique (O'Corry-Crowe 2002).

1.4.2 Habitat du béluga

Les bélugas peuvent entreprendre des migrations saisonnières, mais leur amplitude varie grandement selon les populations. L'été, de fortes concentrations de bélugas fréquentent les estuaires, les embouchures de rivières, les baies et les îlets (COSEWIC 2004, Finley et al. 1982). Ils y reviennent à chaque année pour des raisons qui ne sont pas encore très claires à ce jour. Ils pourraient s'y rendre pour la mue saisonnière (St.Aubin et al. 1990), pour la mise bas, pour faciliter les soins aux nouveaux nés étant donné la présence des eaux plus chaudes (Finley et al. 1982, O'Corry-Crowe 2002), pour s'y alimenter ou pour réduire les risques de prédation. À l'automne, plusieurs populations de bélugas de l'Arctique utilisent les eaux profondes pour se rendre vers les sites d'hivernage (COSEWIC 2004). Ils passent l'hiver dans des régions où la banquise n'est pas trop épaisse, près de la limite des glaces et dans les polynies où l'accouplement a probablement lieu (O'Corry-Crowe 2002, Stewart and Stewart 1989).

1.4.3 Distribution des bélugas au Canada

Le béluga a une distribution circumpolaire. Au Canada, il est retrouvé de la mer de Beaufort jusqu'à l'extrême est de l'Arctique et dans la mer du Labrador. On retrouve aussi des bélugas plus au sud, dans la baie James et dans l'estuaire du Saint-Laurent. Cinq populations de bélugas sont reconnues dans l'est de l'Arctique canadien, soit celles de l'Extrême Arctique, de la baie de Cumberland, du sud-est de l'île Baffin, de l'est de la baie d'Hudson et de l'ouest de la baie d'Hudson (Brown Gladden et al. 1999, COSEWIC 2004, de March and Postma 2003). Les limites géographiques de la distribution saisonnière de ces populations sont mal connues et il est possible que d'autres populations de bélugas existent (de March et al. 2002, Hammill et al. 2004). En effet, des bélugas sont observés saisonnièrement dans les régions de la baie James, des îles Belcher, dans le bassin de Foxe et dans le sud et le nord-ouest de la baie d'Hudson, mais leur appartenance demeure à ce jour incertaine. De plus, le béluga est une espèce qui peut migrer sur de longues distances et il peut y avoir un chevauchement des différentes populations au cours du déplacement de ces animaux à différentes époques de l'année. C'est le cas notamment des populations de l'est et de l'ouest de la baie d'Hudson et de la baie d'Ungava qui migrent saisonnièrement toutes les trois à travers le détroit d'Hudson (COSEWIC 2004, de March and Postma 2003).

La distinction des populations de bélugas dans l'est de l'Arctique canadien est primordiale à la gestion de cette espèce chassée à des fins de subsistance par les communautés Inuit puisque certaines de ces populations sont en péril. L'identité des populations est basée sur des études génétiques de l'ADN mitochondrial et des microsatellites (de March and Maier 2001, de March and Postma 2003, de March et al. 2002) et sur la distribution estivale des bélugas (Caron and Smith 1990).

1.4.4 Taille des populations et statut

Le comité sur le statut des espèces en péril au Canada a désigné les populations de l'est de la baie d'Hudson et de la baie d'Ungava comme en voie de disparition (COSEWIC 2004), alors que les autres populations ont été jugées préoccupantes ou menacées. La population de l'est de la baie d'Hudson compterait environ 3000 individus (abondance corrigée pour les individus en plongée) selon l'inventaire aérien de 2008 tandis que celle de la baie d'Ungava en compterait probablement moins de 50 individus (MPO 2009). La population de la baie de Cumberland compte environ 2000 bélugas (abondance corrigée pour les individus en plongée) en 2002 et a été désignée menacée (MPO 2005). La population de l'ouest de la baie d'Hudson a été désignée comme préoccupante et comptait environ 57 300 bélugas en 2004 (abondance corrigée pour les individus en plongée) (Richard 2005). Un nombre important de bélugas était présent dans la région de la baie James lors de l'inventaire aérien de 2008, mais leur appartenance à une population est incertaine. L'abondance, non corrigée pour les individus en plongée, est estimée à 9300 bélugas dans la baie James (MPO 2009). Des analyses de contaminants organochlorés, de l'ADNmt et de 15 microsatellites ont montré que les bélugas observés dans la partie sud-est de l'île Baffin forment probablement une population distincte des autres (de March et al. 2004, Turgeon et al. 2008). Cependant, il est difficile d'estimer l'abondance et de déterminer le statut de cette population.

1.5 L'EXPLOITATION ET L'IMPORTANCE POUR LES COMMUNAUTÉS NORDIQUES

Les Européens ont été les premiers à développer la chasse commerciale des bélugas à la fin des années 1600. De 1750 à 1905, une chasse non régulière a été faite dans la région sud de la baie d'Hudson avant que la compagnie de la baie d'Hudson entre en jeu en 1909 (Finley et al. 1982). Cette chasse commerciale, qui a été très intense, a mis certaines populations de bélugas en péril et encore aujourd'hui leur rétablissement n'est pas assuré (Finley et al. 1982, Hammill et al. 2009, Lesage et al. 2009). Des mesures ont été établies à

la suite de la diminution des populations de bélugas. Le Canada a interdit la chasse commerciale en 1972 et seule la chasse de subsistance est encore permise (entre 400 et 700 bélugas par année entre 1988 et 1996). Depuis 1986, un plan de gestion a été mis en marche afin d'assurer une gestion durable (Stewart and Lockhart 2005). Ce plan établit des quotas à chaque communauté et interdit ou permet la chasse dans certains secteurs et à certaines périodes de l'année (Finley et al. 1982, Lesage et al. 2009, Stewart and Lockhart 2005). Par exemple, la chasse est interdite dans l'estuaire du Saint-Laurent et dans certains secteurs de la baie d'Ungava et dans l'arc de l'est de la baie d'Hudson (COSEWIC 2004). Toutefois, même avec ces mesures de gestion, certaines populations ont de la difficulté à se rétablir (Hammill et al. 2004).

La chasse traditionnelle des bélugas est très importante pour la culture et l'économie des Inuits habitant l'Arctique canadien. La graisse du béluga est utilisée dans la fabrication de l'huile à lampe tandis que la peau est utilisée dans la fabrication de tentes et de bottes. La peau du béluga est aussi une importante source de nutriments pour les Inuits qui la mangent (Finley et al. 1982, Stewart and Lockhart 2005).

Il est donc important d'augmenter nos connaissances sur l'écologie alimentaire et sur l'identité des populations de béluga afin que ces communautés puissent continuer à le chasser tout en protégeant la ressource.

1.6 OBJECTIFS DE L'ÉTUDE

L'objectif global de cette étude est d'évaluer l'utilité des rapports des isotopes stables du carbone et de l'azote et de la concentration en éléments traces pour l'identification des populations de bélugas de l'est de l'Arctique canadien. Les objectifs plus spécifiques de ce projet sont de :

- 1- Caractériser la variation saisonnière, interannuelle et décennale de l'écologie alimentaire dans ces diverses régions.
- 2- D'établir la contribution de la population de l'est de la baie d'Hudson, qui est en voie de disparition, dans la chasse d'automne du détroit d'Hudson.
- 3- Coupler l'information des isotopes stables et des éléments traces à la génétique afin de valider ou de bonifier les limites déjà établies des différentes populations à partir de la génétique et de la distribution géographique estivale.

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**CHAPITRE 2 - DEFINING STOCK STRUCTURE OF THE HARVEST AND
WINTERING ASSEMBLAGES OF CANADIAN EASTERN ARCTIC BELUGA
(*DELPHINAPTERUS LEUCAS*) FROM STABLE ISOTOPE RATIOS AND
TRACE ELEMENT CONCENTRATIONS**

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Defining stock structure of the harvest and wintering assemblages of Canadian eastern Arctic beluga (*Delphinapterus leucas*) from stable isotope ratios and trace element concentrations

2.1 ABSTRACT

In Hudson Bay, at least two beluga stocks are recognized based on summer aggregations and mtDNA analyses, i.e., the eastern and western Hudson Bay populations. Beluga occur elsewhere (e.g., Belcher Islands, James Bay, northern Ontario, Foxe Basin), but stock identity is unclear. The *Endangered* eastern Hudson Bay beluga and those from the healthier western Hudson Bay stock migrate through Hudson Strait where they are harvested during their fall and spring migrations, making difficult the protection of the eastern Hudson Bay stock. Beluga skin samples were collected from nine regions of Hudson Bay and Hudson Strait during 1989–2009, and were analysed for carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotope ratios ($N = 1070$ ind.) and concentrations of 27 trace elements ($N = 308$ ind.). Our goal was to determine whether feeding ecology could help discriminate among stocks and estimate the proportion of eastern Hudson Bay beluga in Hudson Strait fall harvests. $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values were similar between periods (1989–1999, 2000–2009), but varied significantly among sex, regions and seasons. Similarly, trace element concentrations varied according to geographical area and season, but were similar between males and females. Membership of beluga in the Hudson Strait fall harvest was assessed using stable isotope signatures and trace element concentrations of summering stocks in the various regions as sources in a discriminant functions analysis. Based on stable isotope signatures alone, male and female eastern Hudson Bay beluga represented 41% and 60% of the southern Hudson Strait fall harvest, respectively, while they represented 9% and 0% of the northern Hudson Strait fall harvest. Using probabilistic genetic assignments as eastern Hudson Bay vs non-eastern Hudson Bay as a way to determine the degree of agreement among methods, it was determined that 66% of the individuals were similarly assigned by the isotopic and genetic methods. However, the genetic approach most likely underestimated the proportion of eastern Hudson Bay beluga in the harvest. The analysis using both stable isotopes and trace elements is promising, but sample size for defining summering stocks, including eastern Hudson Bay beluga, is currently too small to qualify these stocks. Nevertheless, examination of these results revealed certain homogeneity in age and sex classes within a harvest event, suggesting a possible persistence during the fall migration of the summer segregation between adult males and females with juveniles.

These results illustrate the usefulness of chemical markers as a valuable complementary tool to genetic in the discrimination and protection of marine mammal stocks.

2.2 INTRODUCTION

An understanding of discontinuities in species distribution is important for effective management and conservation. Temporally or spatially-structured populations with unique population dynamics may occur as a result of habitat patchiness, demographic and life history variability, genetic sub-structuring and adaptability (Cope and Punt 2009, Secor 1999, Waples 1991). Resource units, often referred to as stocks, may exist within populations and can usually be managed independently (Cope and Punt 2009, Ihssen et al. 1981, Stewart 2008). However, stocks must be defined over scales relevant to ecological sustainability and population resilience when they are defined in the perspective of human removals (i.e., harvest stocks) (Cope and Punt 2009, Salt and Walker 2006).

Several methods have been proposed to define stocks based on ecological scales (Begg et al. 1999a, Begg et al. 1999b, Ihssen et al. 1981, Rugh et al. 2003), but genetic approaches having been highly popular over the last few decades (Palsbøll et al. 2007). Recently, new approaches such as stable isotope and trace element analyses have been used to help define stock structure (Doubleday et al. 2008, Hobson 1999, Rocque et al. 2006). These methods assume that a group of animals using the same resources, and inhabiting the same regions have similar isotopic signatures and elemental compositions in their tissues, allowing their differentiation from other groups (Born et al. 2003, Fontaine et al. 2007, Outridge et al. 2003). Insights from genetic studies remain limited when trying to capture population differences over periods of a few decades or less, as genetics generally assess interactions between individuals over several generations (Waples and Gaggiotti 2006). In contrast, stable isotopes and trace elements assess interactions between an individual and its environment over the individual's lifetime or a shorter period depending on the tracer and tissue (Jay et al. 2008, Outridge et al. 2003). Genetic and biogeochemical

studies therefore provide different but complementary information for stock definition. While biogeochemical tracers have been used repeatedly to better understand stock definition (Arkhipkin et al. 2009, Jay et al. 2008, Outridge and Stewart 1999, Outridge et al. 2003, Sanpera et al. 1996), few studies have combined genetic and biogeochemical markers to address this question (Clegg et al. 2003, de March et al. 2004, Stewart 2008).

In addition to providing information on stock structure, biogeochemical markers provide insights into the feeding ecology of species. Carbon and nitrogen isotope ratios provide information mainly on trophic relationships (Hobson and Welch 1992, Post 2002), but more recently on diet composition through isotopic mixing models (Ben-David et al. 1997, Phillips et al. 2005), as well as on sources of primary productivity (France 1995, Ramsay and Hobson 1991, Smith et al. 1996), and habitat use (Fontaine et al. 2007, Hobson 1999, Schell et al. 1989). This method is based on the principle that stable isotope ratios in tissues of consumers reflect that of their diet (DeNiro and Epstein 1978, 1981, Hobson et al. 1996). The relatively high (3–4‰) and predictable enrichment in ^{15}N from one trophic level to the next makes N isotopes useful indicators of trophic position (DeNiro and Epstein 1981, Minagawa and Wada 1984, Peterson and Fry 1987). The usual less pronounced trophic enrichment for ^{13}C (typically ~1‰ in marine food webs) limits the usefulness of this element as an index of trophic position, but makes it particularly suitable for delineating carbon sources (DeNiro and Epstein 1978, Peterson and Fry 1987). Trace elements are classified as essential (e.g., Cu, Zn, Se, Fe) and non-essential elements (e.g., Cd, Pb, Hg). Like the C and N isotopes, they are acquired from the environment by higher vertebrates and, to a lesser extent, fish, mainly via food ingestion (Fontaine et al. 2007, Langston and Spence 1995, Lin et al. 2007). Although the adequacy of essential elements as tracers of habitat use and diet might be debatable as they are likely under strong physiological controls (Fontaine et al. 2007), trace element biomagnification with trophic position and their relationships with regional geochemistry has been demonstrated in several instances (Campbell et al. 2005, Crawford et al. 2008, Das et al. 2003).

The beluga (*Delphinapterus leucas*) is an odontocete which is widely distributed throughout Arctic and sub-Arctic waters. In summer, Arctic beluga regularly occur in coastal regions, including estuaries, river mouths and bays to which they show a certain degree of site fidelity (Caron and Smith 1990, COSEWIC 2004, Finley et al. 1982). Beluga populations in the Canadian eastern Arctic were initially defined based on summer distribution (Finley et al. 1982, Smith and Hammill 1986), some of which were confirmed by genetic studies (de March and Postma 2003, de March et al. 2004). There are currently at least five populations in the eastern Arctic: the Canadian High Arctic, Southeast Baffin Island, Western Hudson Bay, Eastern Hudson Bay and Cumberland Sound beluga (Brown Gladden et al. 1999, COSEWIC 2004, de March and Postma 2003, de March et al. 2004). Beluga are also observed seasonally in James Bay, around the Belcher Islands, in Foxe Basin, in Ungava Bay and in Northwestern Hudson Bay. However, stock identity of these whales and seasonal migration patterns are not well understood (de March and Postma 2003, Turgeon et al. 2008). In addition, there is uncertainty concerning the location of wintering areas for beluga summering in these various locations.

Seasonal migration distances vary between populations and may lead to some overlap in distribution at certain times of the year (Bailleul et al. *Submitted*, Hammill et al. 2004). Of particular interest is the apparent overlap in seasonal migration routes of beluga from the *Endangered* Eastern Hudson Bay stock and the much healthier Western Hudson Bay stock. Whales from both stocks migrate through Hudson Strait in the fall and spring, where they are harvested by local communities both on the south and north shores. An understanding of the proportion of beluga harvested from the endangered stock is crucial for the conservation of this population.

Given the physiography of the Arctic Ocean basin, it is unlikely that the various beluga stocks occupy areas that are homogenous in terms of the characteristics of food web structure, carbon sources and geology (Powles et al. 2004). Consequently, the combination of stable isotopes and trace elements in characterizing summering or wintering

aggregations offers an opportunity to assess the composition of the seasonal harvest in Hudson Strait, as well as to identify animals likely sharing common wintering areas.

In this study, stable isotope ratios and trace element concentrations in beluga skin were examined for individuals sampled in various locations during 1989 to 2009 to gain insights into their feeding habits. Discriminant functions analysis using summer stock characteristics as end members were used to determine the contribution of Eastern Hudson Bay beluga to the fall harvest in Hudson Strait. Because skin isotopic signature likely reflects diet and habitat use over the last two to three months (e.g., St.Aubin et al. 1990), isotopic and trace element signatures of beluga harvested during the spring in Hudson Strait were examined to identify shared wintering areas. This study is innovative in that it uses mitochondrial DNA haplotypes unique to the Eastern Hudson Bay as a validation tool for the stock assignments made using discriminant function analysis.

2.3 MATERIAL AND METHODS

2.3.1 Study area

The Canadian eastern Arctic system is divided into 2 ecoregions, the Foxe Basin – Hudson Bay complex and the Baffin Bay – Davis Strait ecoregion (Figure 1) (Powles et al. 2004). They are relatively productive areas as a result of strong tidal mixing, and are also influenced by large freshwater inputs (Harvey et al. 1997, Powles et al. 2004, Tang et al. 2004). Both ecoregions are seasonally ice covered, although some polynyas persist in eastern James Bay, northwestern Hudson Bay and northwestern Foxe Basin throughout winter (Powles et al. 2004).

2.3.2 Sample collection

Skin was collected from 1070 beluga sampled between 1989 and 2009 across nine regions of the Foxe Basin – Hudson Bay complex, as well as southeast Baffin Island (the southwestern side of Baffin Bay, along the Baffin Island coast) (Figure 1). Samples were obtained mainly through the Natives subsistence harvests, with a few biopsy collections during satellite tagging studies. Hunters provided information on sex and color of harvested beluga, date and location of capture, as well as a tooth for age determination. Age was estimated by counting annual growth layer groups in the cementum of teeth, assuming the deposition of one growth layer group per year (Stewart et al. 2006). Sex was confirmed genetically in most, but not all cases.

2.3.3 Stable isotope analyses

Skin samples were preserved in a dimethyl sulfoxide (DMSO) solution ($n = 872$) or were frozen ($n = 198$) immediately or shortly after sampling. DMSO affects carbon and nitrogen isotope ratios (Hobson et al. 1997, Lesage et al. 2010). However, lipid extraction if preceded by water rinsing can restore $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values of marine mammal skin, including beluga, as if samples had been frozen directly and lipid-extracted (Lesage et al. 2010). Lipid extraction is also recommended prior to isotope ratio determination given that lipids have depleted $\delta^{13}\text{C}$ values relative to protein and may bias $\delta^{13}\text{C}$ values negatively and by a variable amount depending on lipid contents (Post et al. 2007). However, lipid-extraction also affects nitrogen isotope ratios, particularly for tissues with relatively high ($> 5\%$) lipid contents (Mintenbeck et al. 2008, Sørensen et al. 2006, Sweeting et al. 2006). Lipid extraction inflates $\delta^{15}\text{N}$ values of the skin of cetaceans, including beluga, by approximately $+0.2\%$ irrespective of $\delta^{15}\text{N}$ values (Lesage et al. 2010). Consequently, $\delta^{15}\text{N}$ values need to be corrected in order to relate beluga isotopic values to other components of the ecosystem.

DMSO-preserved and frozen skin samples were lipid extracted prior to isotope analyses following Lesage et al. (2010). Briefly, DMSO-preserved samples were rinsed three times in distilled water to eliminate some of the DMSO. All samples were then freeze-dried for 24h and grounded to a fine powder before being lipid-extracted using the Folch method (Folch et al. 1957). A sub-sample of 0.250-0.300 mg of powdered tissue was precisely weighed (± 0.005 mg) into a tin capsule, and analysed for stable isotope ratios of carbon and nitrogen using an isochrom continuous-flow stable isotope mass spectrometer coupled to a Carlo Erba elemental analyzer (CHNS-O EA1108) (Environmental Isotope Laboratory, University of Waterloo, Waterloo, Ontario). Corrections for lipid extraction effects on $\delta^{15}\text{N}$ values were made using a regression developed specifically for beluga skin (Lesage et al. 2010). By convention, ^{13}C and ^{15}N isotope abundance are expressed in delta notation (‰), as $\delta X = [(R_{\text{sample}}/R_{\text{standard}}) - 1] \times 1000$ where X is ^{13}C or ^{15}N , and R_{sample} is the corresponding ratio $^{13}\text{C}/^{12}\text{C}$ or $^{15}\text{N}/^{14}\text{N}$. R_{standard} represents the ratios for their respective standards, i.e., the Vienna Pee Dee belemnite (PDB) and atmospheric nitrogen (AIR). Replicates using laboratory standards indicated an analytical error of ± 0.2 and ± 0.3 ‰ for $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$, respectively, whereas deviations observed between replicates of skin samples ($n=102$) were on average of 0.11 ‰ for $\delta^{13}\text{C}$ and 0.15 ‰ $\delta^{15}\text{N}$.

2.3.4 Trace element analyses

DMSO affects concentrations of trace elements in an unpredictable way (Lesage et al. 2010). Therefore, the analysis of trace elements for DMSO-preserved samples was not possible and was performed only on frozen samples, all of which were also analyzed for stable isotope ratios ($n = 308$). Samples for trace element analyses were prepared in the same way as for stable isotope analysis. Approximately 0.08 g of powdered tissue and 6 ml of HNO_3 (ultrapure from Seastar Chemical, Sydney B.C.) were transferred to a tared Teflon reactor (XP-1500 plus) and heated for 30 min in a laboratory microwave oven (MARS SX, CEM corporation, Matthews NC) at 200°C. This technique uses a closed

system, which allowed reaching very high temperature to improve digestion and retain all the volatile elements. The analysis of 27 trace elements (V, Cr, Fe, Ni, Cu, Be, Na, Mg, Al, Ca, Mo, Ag, Cd, Sb, Ba, Tl, Pb, Bi, U, Mn, B, Li, K, Zn, Sn, Se, Ti) was performed using an inductively coupled plasma-mass spectrometer (ICP/MS DRC II Perkin Elmer Health Sciences Inc., Shelton Conn.) reporting concentrations as $\mu\text{g/g}$ of dry weight. Precision and accuracy of the method were assessed using certified reference materials (Bovine muscle NIST-8414, Bovine liver NIST-1577b) and duplicate analyses of 60 random skin samples. The detection limits were given by samples of low value and / or blank samples and were $0.001 \mu\text{g/g}$ for all trace elements except Mn and B ($0.002 \mu\text{g/g}$), Li and K ($0.003 \mu\text{g/g}$), Zn and Sn ($0.005 \mu\text{g/g}$), Se ($0.007 \mu\text{g/g}$) and Ti ($0.009 \mu\text{g/g}$).

2.3.5 Statistical analysis

Statistical analyses were conducted using the R software (R Development Core Team, 2008). The effect of period (1989–1999, 2000–2009), season (spring: 15 Apr–7 Jul, summer: 15 Jul–7 Sep, autumn: 15 Sep–30 Nov), sex and region on $\delta^{13}\text{C}$, $\delta^{15}\text{N}$ and the 27 trace elements, and interactions between these variables, were tested using multivariate analysis of variance (MANOVA) and the Pillai's Criterion. Multiple analyses of variance (ANOVA) were used to identify variables responsible for the observed difference, followed by student's t-tests (post-hoc) for pairwise comparisons. Variability among regions in seasonal beluga availability and harvest resulted in an unbalanced sampling design among regions, seasons or periods. Consequently, in most cases, multiple ANOVAs were not preceded by a MANOVA and were used directly to examine patterns among these independent variables, while controlling for type I error using the Bonferroni approach. In situations when assumptions for using parametric tests were not met, results were validated by repeating ANOVAs using rank values (Conover and Iman 1981).

The ability to discriminate among summer beluga stocks likely contributing animals to the fall harvest in Hudson Strait was investigated using discriminant functions analyses (procedure DISCRIM, SAS Institute 1990). Discriminant functions analysis was first performed using stable isotopes alone to maximize sample size, and was then repeated using only individuals with data available for both trace elements and stable isotopes. Prior to the latter analysis, a stepwise approach was applied to variable selection as there was a need to reduce the number of input trace element variables (Hair et al. 2006). The assumption of multinormality was not met, leading to the use of a non-parametric discriminant method, the k -nearest neighbours, to estimate group-specific probability densities. Although the choice of the number of nearest neighbors k is usually relatively uncritical (Hand 1982 cited in SAS Institute Inc. 1999. SAS Stat User's guide, version 8, p.1937), this smoothing parameter was determined by iteratively running the model with different values of k and choosing the one that minimized the overall misclassification rate, and those specific to eastern Hudson Bay and western Hudson Bay in particular, the two classes of the most interest. Misclassification rates were estimated by cross-validation, i.e., by recomputing the discriminant functions while leaving out the one observation to be classified. The eastern Hudson Bay beluga had a smaller sample size compared to some other stocks; using cutting scores weighted for sample size would have brought cutting scores closer to the eastern Hudson Bay group centroid. In order to reflect the higher costs of misclassification of eastern Hudson Bay beluga (because of their *endangered* status), and to reduce the likelihood of misclassifying eastern Hudson Bay beluga as non-eastern Hudson Bay animals, cutting scores were unweighted for differences in sample size among summering stocks when classifying observations (Hair et al. 2006).

Once summer stock characteristics were defined using the discriminant functions analysis, we applied the discriminant functions to estimate the relative contribution of the various stocks of beluga to the fall harvest in the southern Hudson Strait and the northern Hudson Strait. Because epidermis turnover time is of approximately 70-75 days in beluga (St.Aubin et al. 1990), the isotopic signature of beluga skin likely reflects the diet

integrated over the last two to three months. Given that the fall migration to the Hudson Strait is short for beluga in this area, e.g., 10 days on average for eastern Hudson Bay (Bailleul et al. *Submitted*, Lewis et al. 2009), the isotopic signature of beluga harvested during migration through Hudson Strait should still reflect their summering habitat and stock. Following this reason, isotopic signatures of summering stocks from the Belcher Islands, Eastern Hudson Bay, Foxe Basin, James Bay and Western Hudson Bay were used as sources in a discriminant functions analysis to estimate the membership of beluga in the Hudson Strait fall harvest. Ungava animals were not included in the analysis as their occurrence west of Ungava Bay was unlikely, given the general eastward movement observed at this time of the year (Bailleul et al. *Submitted*, Lewis et al. 2009). Cumberland Sound beluga were also not included as they appear to remain within this region to the northeast of Hudson Strait throughout winter (COSEWIC 2004, DFO 2008a, b).

The stock composition of the fall harvest was validated using genetic information available from individual beluga. Nuclear mitochondrial DNA analyses indicate that haplotype H17 is unique to the Eastern Hudson Bay stock whereas haplotype H18 is almost exclusively observed in Eastern Hudson Bay beluga (113/122 of cases within the Hudson Bay complex) (de March and Postma 2003, Turgeon et al. 2008). Misclassification rate of the discriminant function analysis was assessed using beluga with those haplotypes unique or almost unique to Eastern Hudson Bay individuals.

2.4 RESULTS

2.4.1 Seasonal, regional and sex variations

Stable carbon and nitrogen isotope signatures varied significantly among sex classes (two-way ANOVA on ranks: $F_{1,1014} = 19.58$ and 29.45 for $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$, respectively, both $p < 0.0001$) (Table 1). Isotopic values were generally higher in males than females for both

isotopes, but differences were statistically significant only for the Belcher Islands region (post-hoc Student's t-test pairwise comparison, $p < 0.05$). The one exception to this trend was Western Hudson Bay beluga ($F_{8,1014} = 1.63$, $p = 0.111$, although interaction was not significant), whose females showed a slightly larger, but not significant enrichment (0.04‰) in $\delta^{13}\text{C}$ relative to males. Given this slight but general trend, all subsequent statistical analyses were interpreted separately for each sex class.

For regions where beluga were sampled during both the 1990s and the 2000s (i.e., Belcher Islands spring, Eastern Hudson Bay summer and Eastern Hudson Bay summer), no significant decadal changes in carbon or nitrogen isotopic signatures were detected in either males (two-way ANOVA on ranks, $F_{1,158} = 2.96$ and 4.07 for $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$, respectively, both $p > 0.01$, p adjusted for type I error using the Bonferroni approach) or females (two-way ANOVA on ranks, $F_{1,129} = 2.21$ and 0.56 for $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$, respectively, both $p > 0.01$). As a result, data were pooled across years for each sex and region.

Isotope ratios also varied among geographical regions ($F_{8,1014} = 25.77$ and 39.70 for $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$, respectively, both $p < 0.0001$), and in a similar fashion among sex classes. Beluga carbon isotopic signatures were the lowest or most depleted in James Bay (A) and the Belcher Islands (A), intermediate in Cumberland Sound (B) and Hudson Strait North (B, C) and the most enriched in Hudson Strait South (C), Western Hudson Bay (C), Ungava Bay (C, D), Foxe Basin (C, D) and Eastern Hudson Bay (D) (Letters represent results from the post-hoc pairwise comparisons) (Figure 2, Table 1). Nitrogen isotopic signatures were significantly lower in beluga from James Bay, the Belcher Islands, Eastern Hudson Bay, Hudson Strait South and Ungava Bay, compared with those sampled in Hudson Strait North, Cumberland Sound, Western Hudson Bay and Foxe Basin (Figure 2, Table 1).

Seasonal effects could be tested statistically only for males and three regions, i.e., Belcher Islands, Eastern Hudson Bay and Ungava Bay, as seasonal beluga harvest varied

among regions. Carbon and nitrogen isotopic signatures varied significantly among these groups (two-way ANOVA on ranks, $F_{2,168} = 6.14$ and 9.63 for $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$, respectively, both $p < 0.01$) (Table 1). The three seasons were statistically different for $\delta^{13}\text{C}$. In the case of $\delta^{15}\text{N}$, beluga signatures were the most depleted during spring (A), intermediate during summer (A, B) and most enriched during autumn (B) (Letters represent results from post-hoc pairwise comparison) (Table 1). These trends were observed in each region tested, but were significant only in the Belcher Islands region. Repeating this analysis separately for each region, resulted in no significant differences being detected among seasons in either of the regions or seasons tested for the two isotopes (two-way ANOVA on ranks, $p > 0.05$ for all comparisons). In other words, although seasonal effects were detected in the global analysis of variance, these differences became insignificant when performing statistical analyses for each region separately.

Spring isotopic signatures indicated that beluga harvested at that time of the year in Cumberland Sound and the Belcher Islands were isotopically different from those harvested at the same time elsewhere (i.e., Eastern Hudson Bay, Hudson Strait North, Hudson Strait South and Ungava Bay) (Figure 3). James Bay beluga were intermediate in signature between the three groups and relatively close to beluga from Belcher Islands, but sample size was too small ($n = 1$) to test for their significance as a separate group. This trend was consistent for both isotopes and in both males (one-way ANOVA on ranks, six regions used, $F_{5,167} = 15.60$ and 10.40 for $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$, respectively, both $p < 0.001$) and females (one-way ANOVA on ranks, six regions used, $F_{5,188} = 27.54$ and 10.58 for $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$, respectively, both $p < 0.001$). Provided that the period reflected by skin tissue at the time of spring migration reflects the feeding ecology in wintering areas, the observed patterns in spring signatures among groups of beluga harvested in the various regions suggest a possible segregation of their wintering grounds (Figure 3).

2.4.2 Stock structure of the harvest

The five summering stocks considered as possible contributors to the fall harvest in Hudson Strait, i.e., Belcher Islands, Eastern Hudson Bay, Foxe Basin, James Bay and Western Hudson Bay, were entered as three sources in a discriminant functions analysis. Beluga from Belcher Islands and James Bay were generally more depleted in $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ compared to beluga from the other three regions, but were isotopically indistinguishable from one another (post-hoc pairwise comparison, $p > 0.05$ for $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$) and so, were considered as a single source (BEL&JB) (Figure 4). Similarly, beluga from Western Hudson Bay and Foxe Basin were combined in this analysis as they also shared a similar isotopic signature (post-hoc pairwise comparison, $p > 0.05$ for $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$). Beluga from Eastern Hudson Bay (EHB) and those from Western Hudson Bay and Foxe Basin looked alike carbon-wise, but the former showed lower $\delta^{15}\text{N}$ values than the western Hudson Bay & Foxe Basin (WHB&FOX) beluga and so, were considered as a distinct source. The analysis was performed separately for males and females as their isotopic signatures were significantly different (see above).

The discriminant functions analysis using five nearest neighbors to estimate probability densities and classify beluga from the various summering stocks resulted in an overall misclassification rate of 19% for both males and females (Table 2, Table 3). Misclassification rate among classes that were most likely to contribute to the fall harvest, i.e., EHB and WHB&FOX beluga, was of 7–10% depending on stock and sex classes (Table 2, Table 3). Chances of errors between EHB and WHB&FOX classes were higher for females (10–22%) than for males (6–7%). A validation of the discriminant functions developed for summering stocks of each sex, and using 15 individuals with haplotypes unique to EHB (H17) resulted in a single misclassified observation (one male as WHB&FOX). Including animals with H18, a haplotype occasionally found in Western Hudson Bay beluga (6/122 = 5%, Turgeon et al., 2008), resulted in an overall

misclassification rate of 3 out of 24 individuals (12.5%), including two males classified as WHB&FOX and one female classified as BEL&JB.

Applying these discriminant functions to calculate the contribution of the various summering stocks to the southern Hudson Strait fall harvest, it was estimated that 49% of the harvested beluga would be from Eastern Hudson Bay, including 41% of males (34/83) and 60% of females (35/58), if broken down by sex (Table 4). Using the same sample of 141 individuals, and probabilistic genetic assignments as Eastern Hudson Bay vs non-Eastern Hudson Bay (de March and Maier 2001, de March and Postma 2003, de March et al. 2002, Turgeon et al. 2008), Eastern Hudson Bay beluga would account for 18% of the harvest, a much lower proportion of the harvest, where 12% (10/83) would be males and 26% (15/58) would be females. The isotopic results are those obtained when classifying individuals to the stock with the highest probability of origin, regardless of its value, which may be, in some instances, lower than 50%. However, if a minimum threshold probability is set to accept a classification as Eastern Hudson Bay, we obtain overall proportions of 47% (or 35% and 64% for males and females, respectively), 37% (25% and 53%), 27% (20% and 36%) and 20% (14% and 28%) for threshold probabilities of 50%, 60%, 70% and 80%, respectively. These results indicate that in order to obtain results comparable to those predicted from the mtDNA, the threshold probability for accepting a classification as Eastern Hudson Bay based on isotopes would need to be raised to at least 80%.

The same discriminant analysis was applied to the northern Hudson Strait fall harvest. Based on the isotope approach, only two male Eastern Hudson Bay beluga contributed to that harvest, whereas 30 of the 33 individuals were assigned to WHB&FOX (Table 4). The last beluga harvested in the northern Hudson Strait during the fall season belonged to the BEL&JB stock.

2.4.3 Contribution from trace elements

The contribution of trace element concentrations to the study of beluga feeding ecology and discrimination among beluga groups was investigated for 308 beluga sampled only in the 2000s period for which both stable isotope ratios and trace element concentrations were determined. Trace elements were found in similar concentrations in males and females (one-way MANOVA, Pillai's criterion = 0.099, $F_{1,290} = 1.12$, $p > 0.05$). Trace element concentrations for those classes were therefore combined in subsequent analyses.

Regional and seasonal effects were tested statistically using multiple two-way ANOVAs because of the seasonal variability in beluga harvest among regions. Regional effects for K, Zn, Ti, Bi and U were observed among Cumberland Sound, Eastern Hudson Bay and Ungava Bay beluga for the two seasons tested, i.e., spring and summer (two-way ANOVA, $p < 0.002$, p adjusted for type I error using the Bonferroni approach). A regional effect was also observed for concentrations of Cr, Ti, Sb and U between Foxe Basin and Western Hudson Bay beluga when using fall and summer samples (two-way ANOVA, $p < 0.002$). No seasonal effects were observed for any element between spring and summer in the three regions tested, i.e., Cumberland Sound, Eastern Hudson Bay and Ungava Bay (two-way ANOVA, $p > 0.002$). However, a seasonal effect was observed for concentrations of Se, B, Ti and Tl, which varied significantly between summer and fall in beluga from the two regions tested, i.e., Foxe Basin and Western Hudson Bay (two-way ANOVA, $p < 0.002$). Concentrations of Ni, B, Na, K and Ti also varied significantly between fall and spring in beluga from the Belcher Islands region (two-way ANOVA, $p < 0.002$).

Combining trace element concentrations and stable isotope ratios for discriminating among beluga summering in Cumberland Sound, Eastern Hudson Bay, James Bay and Western Hudson Bay, resulted in fourteen trace elements (U, K, Mg, Li, Fe, Ti, Al, Tl, Se,

Cu, Sn, B, Cr, Be) and the two isotopes being selected through the stepwise discriminant analysis as the most significant predictors of summer group identity (Figure 5, Figure 6, Table 5). Regional patterns in these trace elements were observed. Beluga from James Bay had generally higher concentrations of Cr, Fe, Li, B, Al and lower concentrations of Cu, Se, $\delta^{13}\text{C}$, $\delta^{15}\text{N}$ in comparison to beluga from other regions (Figure 5, Figure 6, Table 5). Cumberland Sound had lower concentrations of Fe, K, Sn and higher concentrations of Mg compared to other beluga group, whereas beluga from Eastern Hudson Bay were characterized generally by relatively high values of Cu, K, U and low values of Mg. Western Hudson Bay beluga also had high concentrations of K, but lower quantities of U.

The 16 variables selected by the stepwise procedure were re-entered in a discriminant functions analysis to develop discriminant functions and estimate probability densities using 5 nearest neighbors. This classification resulted in an overall error rate of 11%. Of the six beluga sampled in Eastern Hudson Bay during summer, 4 (67%) were correctly assigned to their putative stock, while two (33%) were confounded with Western Hudson Bay beluga. Conversely, only one of 76 beluga from Western Hudson Bay was confounded with Eastern Hudson Bay beluga (Table 6). In other words, assignment to Eastern Hudson Bay was conservative as the risks of misclassifying a Western Hudson Bay (or beluga from any other stock) as Eastern Hudson Bay was less than 1.5%.

The beluga from the fall harvest in Hudson Strait North and South for which both isotopes and trace elements were determined ($n = 16$ and 9 , respectively) were then re-classified to their putative summering stocks using the preceding discriminant functions. This analysis suggested that the nine beluga hunted in Hudson Strait South belonged to the Eastern Hudson Bay population and the sixteen beluga hunted in Hudson Strait North also belonged to this population. The nine beluga forming the southern Hudson Strait fall harvest were all collected within a 3 day period in 2007 by hunters from one community (Akulivik), just north of the eastern Hudson Bay arc, i.e., where Western Hudson Bay are less likely to mix with Eastern Hudson Bay (Figure 1, Table 7). Age and sex classes were relatively uniform within a harvest event, but varied among harvest dates. For instance, one

harvest event was composed of only grey females, whereas another was composed of white male and female beluga (Table 7). Beluga harvested in Hudson Strait North also showed a tendency for homogeneity in age and sex classes during a particular harvest event, although data is lacking in many instances. However, these beluga were collected over several hunting events conducted in two separate years, and in an area where the presence of Eastern Hudson Bay is expected to be infrequent.

Assuming that trace element concentrations are integrated in tissues over longer time periods than isotopes, the discriminant functions were also applied to the spring harvest in southern Hudson Strait. Surprisingly, 40 of the 41 beluga forming the spring harvest were assigned to the Eastern Hudson Bay stock. Thirty-nine of these 41 beluga were collected in 2007 or 2008, but over several harvest events. In 9 of these events when more than one individual was sampled, a greater variation in age and sex class composition was observed within events, suggesting that the age- or sex-class segregation that appears to occur during the fall migration may not persist into the following spring (Table 8).

2.5 DISCUSSION

The analysis of stable isotope ratios and trace element concentrations provided new information on the stock structure and wintering assemblages of beluga from various locations in the Canadian eastern Arctic. These chemical tracers were also successfully used in a conservation perspective to assist genetics analyses in determining the stock composition of the beluga harvest.

2.5.1 Foraging ecology and wintering areas

Stable isotope ratios of beluga varied according to sex, geographical area and season. Males were consistently ^{13}C -enriched relative to females, a trend also observed in beluga from the Beaufort Sea and the St. Lawrence Estuary (Lesage et al. 2001, Loseto et al. 2008, Loseto et al. 2006). Some of this enrichment probably resulted from the higher trophic position of males compared with females, given that $\delta^{13}\text{C}$ increases with trophic position in marine systems, although at a lower rate than $\delta^{15}\text{N}$ (Caut et al. 2009). The enrichment of males in ^{13}C compared with females may also result from a greater dependence on benthic or nearshore resources in males compared with females (France 1995, Rubenstein and Hobson 2004). In the Arctic, the benthic system is coupled to the pelagic system through the sinking of organic material from phytoplankton cells and fecal pellets and carcasses of different animals, and is in general enriched in ^{13}C relative to the pelagic system (France 1995, Hobson and Welch 1992, Iken et al. 2005, Parsons et al. 1989). Nearshore waters are similarly ^{13}C -enriched relative to offshore waters (Ch  telat et al. 2010, France 1995, Fry 1988). Satellite telemetry data indicate that female beluga, and particularly those accompanied by calves, generally perform shallower dives than males (Kingsley et al. 2001, Martin et al. 2001, Richard et al. 2001). Independent of geographical location, these observations would either suggest more pelagic feeding in females compared with males, or if diving locations are closer to shore in females than males, more coastal and possibly more benthic feeding in females than males. The existing data on beluga foraging behaviour and habitat use does not support the hypothesis of a greater use of nearshore waters in males compared with females. The sex segregation, at least during summer time, has been documented in various beluga populations, and suggests a greater use of nearshore shallow waters in females compared to males (Barber et al. 2001, Loseto et al. 2006, Michaud 1993). Shallow waters are thought to offer more protection from predators and a greater access to food for females and the young calves and juveniles with limited diving capacities (Martin et al. 2001). In the Beaufort Sea, beluga segregate into three groups during the open-water season: females with calves and smaller males inhabit

ice-free nearshore habitats and depend on estuarine-shelf food webs; medium males and females with juveniles occupy areas near the ice edge and feed on ice-associated marine fish species such as arctic cod or other resources of the pelagic food web, while large males inhabit waters of extended sea ice cover and feed benthically in deep waters (Loseto et al. 2006). The greater dependency of large males on benthic resources compared to medium-size males and the females with juveniles in the Beaufort Sea beluga is consistent with the ^{13}C enrichment observed in males relative to females, and suggests a segregation similar to what was observed in the Beaufort Sea (Loseto et al. 2006) might also prevail in beluga from several regions of the Canadian eastern Arctic. In our study, the unavailability of data on the age and proportion of females accompanied by juveniles prevented an analysis within sex classes and likely contributed to increase the spread of values about the mean for each sex.

The higher $\delta^{15}\text{N}$ values of beluga males compared with females may indicate a greater dependence of males on prey of a larger size or of a higher trophic position. Differences in body size, diving capabilities or food handling ability (Kleiber 1961, Scholander et al. 1942) may result in animals feeding on different trophic levels (Bearhop et al. 2006, Estes et al. 2003, Werner and Gilliam 1984). Beluga are sexually dimorphic with males being larger than females (Burns and Seaman 1986, Doidge 1990, Heide-Jorgensen and Teilmann 1994, Vladykov 1944). As a result, males may consume preys that are less accessible or too large for females (Boyd and Croxall 1996, Kooyman 1989). The occurrence of prey of a larger size in digestive tracts of beluga males compared with females, and in digestive tracts of adults compared with those from juveniles support these predictions (Seaman et al. 1982, Vladykov 1946).

The regional differences observed in isotopic signatures of beluga were consistent with the current knowledge of the physiogeography of the various basins and movements of water masses in the eastern Arctic (Powles et al. 2004). The depleted $\delta^{13}\text{C}$ values of beluga from James Bay and the Belcher Islands are consistent with the strong influx of

freshwater (Bearhop et al. 1999, Hobson 1999, Peterson and Fry 1987, R.J. Smith et al. 1996) that has been documented for James Bay, and which spills into southeastern Hudson Bay and the Belcher Islands area (Harvey et al. 1997, Saucier et al. 2004, D.B. Stewart and Lockhart 2005). Freshwater inputs are not as strong in the Baffin Bay – Davis Strait ecoregion (Harvey et al. 1997, Powles et al. 2004, Saucier et al. 2004). As a result, beluga from this area, i.e., Cumberland Sound and northern Hudson Strait, had intermediate carbon isotopic signatures. The Foxe Basin – Hudson Bay complex, which also includes the Hudson Strait and Ungava Bay regions, is characterized by a higher salinity (Harvey et al. 1997, Saucier et al. 2004) and food webs that are typically more marine and ^{13}C -enriched. In accordance, the highest $\delta^{13}\text{C}$ values were observed in beluga from these regions.

The spatial variability observed in beluga nitrogen isotope ratios is harder to interpret, given that both diet and regional differences in nitrogen sources for primary producers may influence their signature and those of their prey (Rautio and Vincent 2007, Schmidt et al. 2003). The information available on zooplankton isotopic signatures for the study area revealed some inter-annual variability and spatial variability within specific regions, and no consistent trends in $\delta^{15}\text{N}$ values among regions (Pazerniuk 2007). Nitrogen isotope ratios for primary producers may vary among regions depending on environmental variables such as salinity and temperature (Harrod et al. 2005, Jennings and Warr 2003), as well as the isotopic signature and concentrations of dissolved inorganic nitrogen (Jennings and Warr 2003). $\delta^{15}\text{N}$ ratios may also vary with depth because ^{14}N is retained in the surface layer while ^{15}N is exported from the upper water column in fecal pellets by denitrification processes (Montoya et al. 2002). These processes in the euphotic zone may make ^{15}N available for phytoplankton and may be transferred to marine organisms that prey on them. $\delta^{15}\text{N}$ should be higher in more productive waters because denitrification processes are more active. The higher $\delta^{15}\text{N}$ values of beluga from Cumberland Sound, Western Hudson Bay and Foxe Basin compared to other regions suggest that these beluga likely prey on species occupying on average higher trophic positions, and which may or may not include

more benthic resources. Alternatively, beluga may all feed on similar prey, but may exploit more productive food webs in the former three regions than beluga from James Bay, the Belcher Islands, Eastern Hudson Bay, southern Hudson Strait or Ungava Bay. An overlap in $\delta^{15}\text{N}$ values among beluga from different regions does not necessarily imply similarity in diet, given that several prey species may have similar isotopic signatures. Using isotopic signatures of various fish and invertebrate species from Hudson Bay (Vincent-Chambellant 2010), and assuming a trophic enrichment factor for beluga skin of 1‰ for carbon and 1.7‰ for nitrogen (Abend and Smith 1997, Gendron et al. 2001), isotopic signatures of beluga from Eastern Hudson Bay and Western Hudson Bay, regardless of season, suggest a diet composed primarily of fish and possibly squid, with little contribution from other invertebrates.

The species entering beluga diet could not be determined given the large overlap in isotopic signatures among the various fish prey (Phillips and Gregg 2003). Very little is known about the diet of beluga in the Canadian eastern Arctic, although Arctic cod (*Boreogaidus saida*) is an important prey species for many beluga populations (Dahl et al. 2000, Hobson and Welch 1992, Loseto et al. 2009, Seaman et al. 1982, Welch et al. 1993). Beluga elsewhere have a varied diet (Heide-Jorgensen and Teilmann 1994, Hobbs et al. 2005, Seaman et al. 1982, Vladykov 1946). Greenlandic beluga populations feed on redfish (*Sebastes marinus*), halibut (*Reinhardtius hippoglossoides*), squid and several shrimp species (Heide-Jorgensen and Teilmann 1994), whereas Alaskan beluga populations feed heavily on Pacific salmon (*Oncorhynchus spp.*) (Hobbs et al. 2008, Seaman et al. 1982). In Hudson Bay, capelin (*Mallotus villosus*), *nereis* sp., squid and decapod crustaceans may be part of their diet (Sergeant 1973, Watts and Draper 1986). Accurate quantification of beluga diet is a fundamental requirement for understanding their foraging ecology. Stable isotope analyses do not easily permit individual prey species to be identified, particularly in generalist predator or in complex food webs. A large-scale sampling of different prey species in the Canadian eastern Arctic is needed to create a database of potential prey and determine whether those species can be distinguished by their stable isotope signatures.

Some information is available for sub-Arctic organisms from the Arctic food webs (Campbell et al. 2005, Iken et al. 2005, Kuzyk et al. 2010, Pazerniuk 2007), but the lack of information on isotopic signature of other components of the food web in the regions investigated in our study prevented further interpretation of the observed patterns among sex, region, season and population.

The seasonal variation in isotopic values observed in beluga from many regions was expected. As seen previously, beluga have a varied diet (Heide-Jorgensen and Teilmann 1994, Hobbs et al. 2005, Seaman et al. 1982, Vladykov 1946) which is likely to change according to the seasonal abundance and availability of prey. Beluga are also known to undertake seasonal migrations between summering and wintering areas, of an extent that varies between populations from a few tens to several thousands of kilometres (Bailleul et al. *Submitted*, DFO 2008a, b). The interpretation of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values must therefore be made in the perspective of a potential change in habitat where the base of the food web may or may not be similar isotopically.

Given that the turnover of beluga skin is between 2 to 3 mo (St.Aubin et al. 1990), stable isotope signatures from beluga sampled in the spring, summer and fall should reflect habitat use and diet acquired during the winter, spring and summer, respectively. Accordingly, the comparison of spring isotopic signatures among beluga groups suggests the existence of at least three main wintering areas. The higher $\delta^{15}\text{N}$ values in Cumberland Sound beluga, and the lower $\delta^{13}\text{C}$ values in James Bay beluga compared with the other beluga groups are consistent with satellite telemetry data, which indicate no seasonal migration in animals from these two regions (Bailleul et al. *Submitted*, DFO 2008a, b). The similarity of the Belcher Islands individuals with those of James Bay suggests proximity of their wintering grounds, most probably in southern Hudson Bay. Anecdotal ice entrapments of beluga around the Belcher Islands have been reported repeatedly during the winter and support the occurrence of beluga in this area during winter (Freeman 1967, 1968, Heide-Jørgensen et al. 2002, Lewis et al. 2009, Richard 1993). Traditional

knowledge studies also report beluga wintering at the floe edge near the Belcher Islands (Stewart and Lockhart 2005). The similarity in isotopic signatures among individuals harvested in the spring in eastern Hudson Bay and Ungava Bay, which are thought to represent mainly Eastern Hudson Bay beluga or a mixture of Ungava Bay and Eastern Hudson Bay beluga given their migration path (Bailleul et al. *Submitted*), suggest a common or adjacent wintering ground for beluga from these two summering stocks. The intermediate position of beluga from Hudson Strait South and Hudson Strait North, which are comprised of beluga from a mixture of stocks but mainly Western Hudson Bay beluga (Hammill et al. 2004, Turgeon et al. 2008) suggests that Western Hudson Bay beluga might overwinter in an area different from those used by Eastern Hudson Bay and Ungava Bay beluga. These results are consistent with observations of a large number of beluga in Hudson Strait during winter, presumably the wintering habitat for Western Hudson Bay beluga, and with recent satellite telemetry data pointing towards the Labrador Sea as the main wintering area for Eastern Hudson Bay beluga (Bailleul et al. *Submitted*, Finley et al. 1982, Lewis et al. 2009).

2.5.2 Stock structure of the harvest

The stable isotope results not only confirmed that the *Endangered* Eastern Hudson Bay beluga are harvested during their fall migration by communities from both Nunavik (Hudson Strait South) and Nunavut (Hudson Strait North), but that their contribution to the fall season might be more important than previously thought based on mitochondrial DNA analyses. Probabilistic assignments based on relatedness of haplotypes and prevalence of the various haplotypes in Eastern Hudson Bay vs other stocks suggested that Eastern Hudson Bay beluga may represent 19% to 31% of the harvest in southern Hudson Strait and Ungava Bay (de March and Maiers 2001, de March and Postma 2003, Turgeon et al. 2008). These proportions are substantially lower than the 60% and 41% estimated for females and males, respectively, using isotopic analyses. Some of the discrepancy in

Eastern Hudson Bay beluga contribution between the two approaches may arise as a result of not using the same sample for the two analyses, or from using a reduced dataset for isotope analyses. However, most of the discrepancy is probably due to the higher likelihood of classifying common haplotypes as non-Eastern Hudson Bay using the genetic approach. For instance, a haplotype such as H02, which is common to many stocks but preponderant in the Western Hudson Bay stock (66% of all occurrences) or more closely related to haplotypes typical of the Western Hudson Bay stock had no chance of being classified as an Eastern Hudson Bay beluga using the genetic approach (de March and Maiers 2001, de March and Postma 2003, Turgeon et al. 2008). In counterpart, the classification based on isotope ratios was not perfectly accurate, as misclassification error was 6–7% for males and 10–22% for females. The larger error associated with female classification may partly explain the larger discrepancy in percent contributions between the genetics (19%) and isotope (60%) approach for this class. However, our demonstration of the conservative nature of the genetics approach in assigning animals to the Eastern Hudson Bay stock (48 of 48 individuals showing disagreement in stock assignment between the two approach were classified as non-Eastern Hudson Bay by genetics) emphasize that 19% is most likely an underestimate of female Eastern Hudson Bay contribution to the harvest.

The relatively large proportion of Eastern Hudson Bay beluga in the southern Hudson Strait fall harvest and the larger proportion of Eastern Hudson Bay females taken compared to males may reflect the tendency of Eastern Hudson Bay beluga to follow the coastline when migrating (Bailleul et al. *Submitted*), and a greater tendency to do so in females with juveniles than adult males (Kingsley et al. 2001, Martin et al. 2001, Richard et al. 2001). This combined with a possible sex segregation persisting into the fall migration, may make Eastern Hudson Bay females more likely to be harvested than males. The vulnerability of Eastern Hudson Bay females with juveniles during the spring migration cannot be assessed at this time given the limit of our technique to estimate their contribution to the harvest. However, our anecdotal observations of a greater mixture among age and sex classes in spring harvest events suggest that segregation may not be as

pronounced in the spring. A more thorough analysis of the harvest composition using genetic assignments, age and sex structure broken down by harvest event date and location is needed to clarify these patterns.

Eastern Hudson Bay beluga accounted for a small portion of the northern Hudson Strait fall harvest (9%). This estimate for Eastern Hudson Bay contribution to the Hudson Strait North fall harvest is similar to the 5–11% obtained using mtDNA (March and Postma 2003, de March and Maiers 2001). The majority of the beluga hunted in the northern Hudson Strait likely comes from Western Hudson Bay or the Foxe Basin. The timing and migration route of beluga from these two regions are not well understood, but our data indicate that Western Hudson Bay beluga constitute most of the harvest in northern Hudson Strait.

2.5.3 Trace elements contribution

The use of trace elements in addition to isotope ratios for exploring the foraging ecology and stock definition of beluga emphasized the differences among beluga groups that were observed with the isotopes. Trace elements, given their variety and relationship with the environment and animal diets, are increasingly used in ecological studies to understand habitat use and trophic relationships (Born et al. 2003, Brookens et al. 2007, Caurant et al. 1993, Dietz et al. 2004, Sanpera et al. 1996). Unfortunately, little is known about the metabolisms, functions and sources of many of these elements (Morel and Price 2003), making interpretation of results difficult without prior characterization of the environment where animals evolve. In this study, both essential and non-essential trace elements were identified as useful in discriminating among beluga groups. Essential elements play a variety of roles in many biochemical pathways as they often act as a co-factor for enzymatic activities (Bryan et al. 2007) and are under strong homeostatic regulation (Kannan et al. 2007). Non-essential elements were thought to have no known

biochemical functions other than to interfere with essential elements (Anderson et al. 2010). However, this perception is changing as unsuspected biochemical functions are uncovered for many non-essential elements (Finney and O'Halloran 2003, Kraemer et al. 2005).

The concentrations of trace elements in the natural environment vary widely. In some areas unaffected by human activity, they may reach levels that elsewhere have been considered to have an effect on the ecosystem (Painter et al. 1994). Sediment is a sink for elements derived from the surrounding watershed. Trace elements, such as As, Cd, Cr, Cu, Pb, Ni and Zn, occur naturally within the bedrock, glacial sediments and soils of the watershed and are accumulate in the lake, stream and ocean sediments (Painter et al. 1994). Epidermal Se concentration in this study was highest in beluga from all regions and was also reported in epidermis of narwhal from the Canadian Arctic (Wagemann et al. 1996). As proposed by Dehn et al. 2006, Se can protect against ultraviolet induced skin damage and carcinogenesis and as beluga lose their skin pigmentation with adulthood; beluga will need more ultraviolet protection. Copper and zinc are tightly regulated, required for bone formation, tissue growth, immune function and protects against ultraviolet radiation in the epidermis (Dehn et al. 2006). Sr is known to be an element with chemical behaviour similar to that of calcium (Ca), and thus acts also as a bone-seeking element. Trace element deposition in animal tissues is strongly dependent on numerous physical and biological factors such as wintering or migration sites, sex, age, health status and body condition (Dehn et al. 2005, Wagemann et al. 1996). The different concentrations in essential and non-essential elements among regions may be due to the fact that they represent distinct genetic and demographic populations (Caron and Smith 1990, de March and Postma 2003) which have different nutritional characteristics. The seasonal and regional variability in these trace elements could potentially be explained by diet. The beluga populations are presumably exposed to different dietary levels of these elements as a result of different man-made and natural inputs in the geographical areas and other factors that modulate the distribution of these elements in the marine food chain. However, further research is

needed to determine the relationship between beluga element concentrations and feeding ecology before this conclusion can be made.

The combined use of several trace element concentrations and C and N isotope ratios appeared as a more effective means to discriminate among stocks than the use of isotopes alone. The discriminant functions developed by cross-validation were proven to be conservative in estimating the number of beluga that belonged to the Eastern Hudson Bay stock, as only one out of 76 Western Hudson Bay beluga was mistakenly assigned to the Eastern Hudson Bay stock. However, the high percent contribution of Eastern Hudson Bay to the Hudson Strait North harvest, where few Eastern Hudson Bay are normally expected to be taken given their migration patterns (Bailleul et al. *Submitted*), calls for caution and further testing before implementing this technique to discriminate among stocks. Trace element signatures for summering stocks, which were used to assign beluga from the fall harvest, were based on a small number of individuals for all but the Western Hudson Bay summering stock and so, might have been unrepresentative of the summering stocks or their variance.

This study employed a relatively new approach to investigate beluga feeding ecology and population substructure by examining the variation in stable carbon and nitrogen isotope ratios and concentrations of certain trace elements in beluga skin from across the Canadian eastern Arctic. The use of stable isotope ratios provided some evidence for spatial segregation as well as trophic niche separation between sexes in beluga, at least during summer, as well as for the exploitation of different food webs in the Canadian eastern Arctic. The chemical signatures of summering stocks of beluga were used to determine the composition of the fall harvest. The validation of these results against genetic data added to the novelty of this approach, and showed how these tracers and techniques can be applied to highly important conservation issues.

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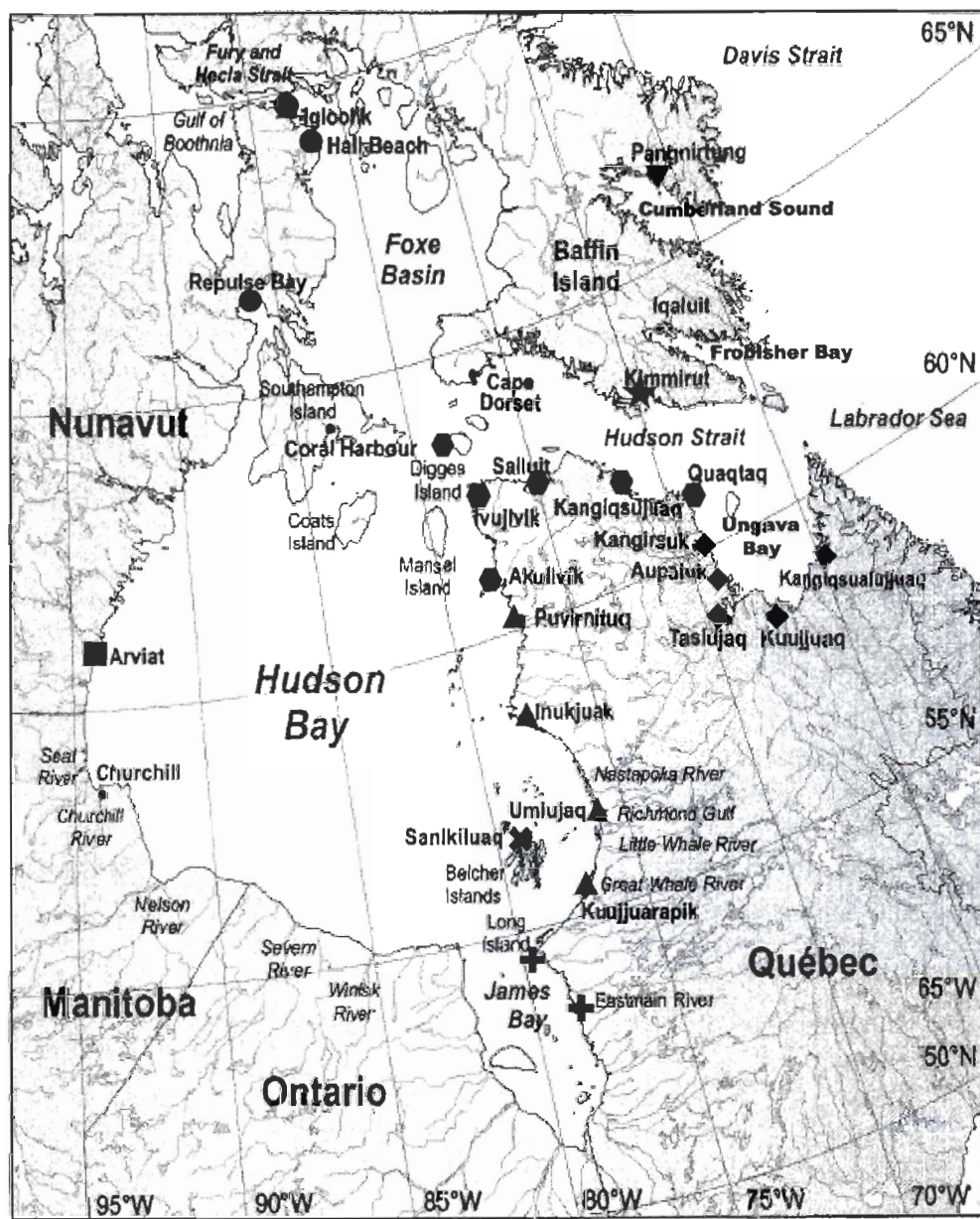


Figure 1. Study area map with names of regions and communities where beluga were captured and sampled (code for study region: x = Belcher Islands, ▼ = Cumberland Sound, ▲ = Eastern Hudson Bay, ● = Foxe Basin, ★ = Hudson Strait North, ◆ = Hudson Strait South, + = James Bay, ◆ = Ungava Bay and ■ = Western Hudson Bay) (Map modified from de March et al., 2003).

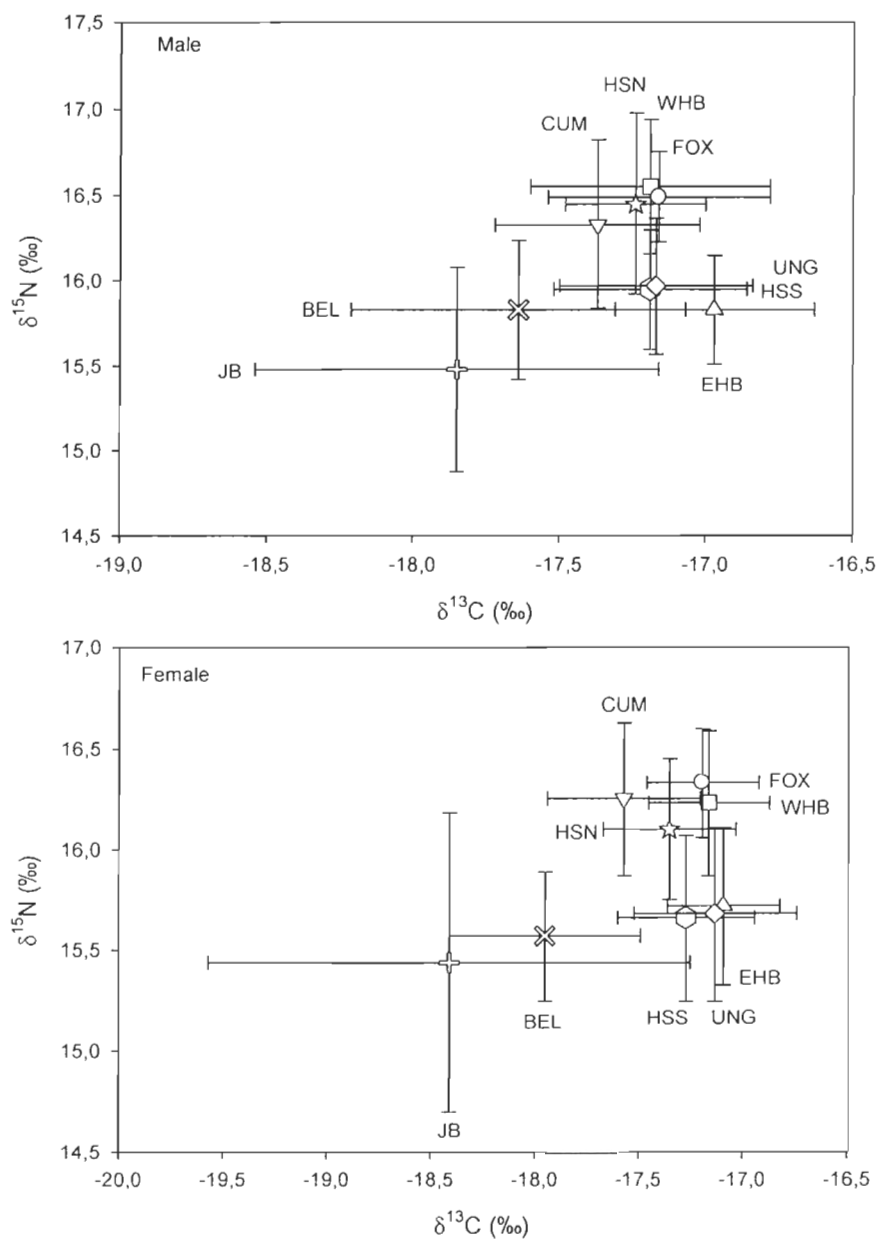


Figure 2. Mean isotopic signatures ($\pm$ SD) of beluga males and females harvested in various locations (BEL = Belcher Islands = ✕, CUM = Cumberland Sound = ▼, EHB = Eastern Hudson Bay = ▲, FOX = Foxe Basin = ●, HSN = Hudson Strait North = ★, HSS = Hudson Strait South = ●, JB = James Bay = +, UNG = Ungava Bay = ◆ and WHB = Western Hudson Bay = ■) in the Canadian eastern Arctic.

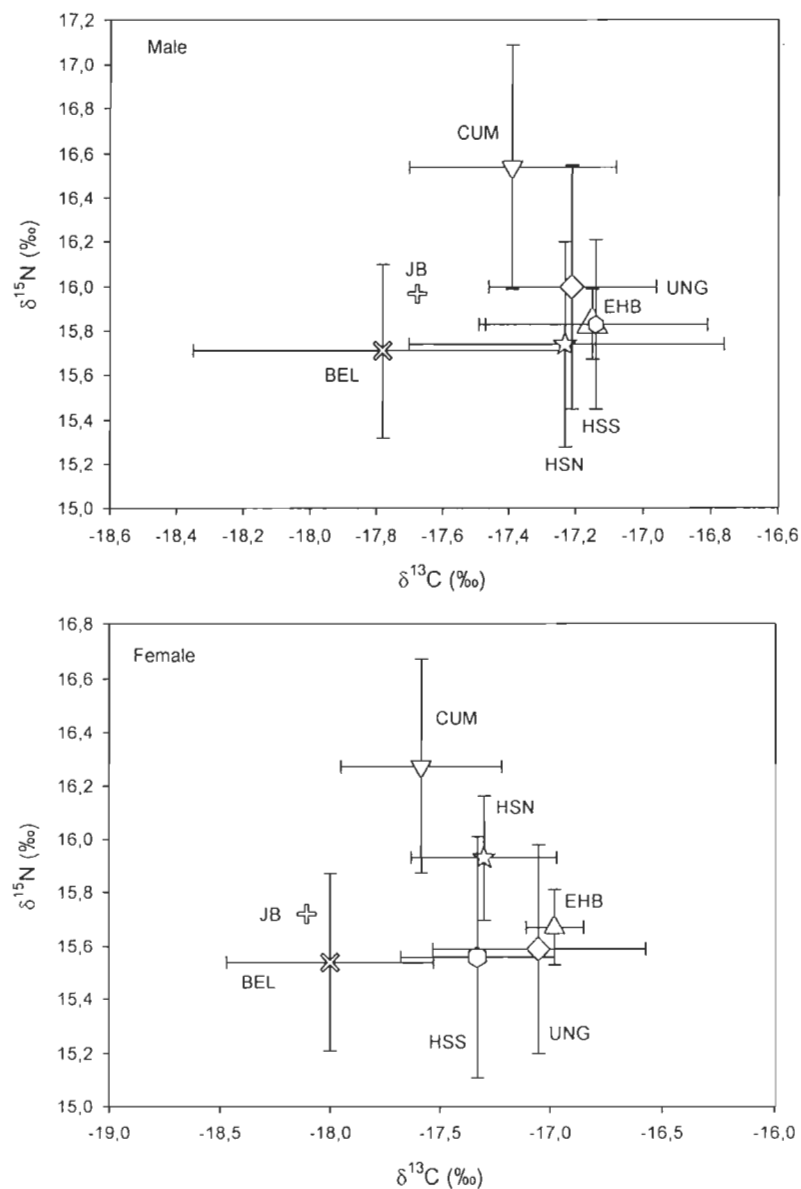


Figure 3. Mean isotopic signatures ($\pm$ SD) of beluga males and females harvested in the spring in various locations (BEL = Belcher Islands = ✕, CUM = Cumberland Sound = ▼, EHB = Eastern Hudson Bay = ▲, HSN = Hudson Strait North = ★, HSS = Hudson Strait South = ●, JB = James Bay = ⊕ and UNG = Ungava Bay = ◆). For males: BEL n=65, CUM n=15, EHB n=3, HSN n=5, HSS n=60, JB n=1 and UNG n=6 and for females: BEL n=62, CUM n=12, EHB n=5, HSN n=20, HSS n=88, JB n=1 and UNG n=12.

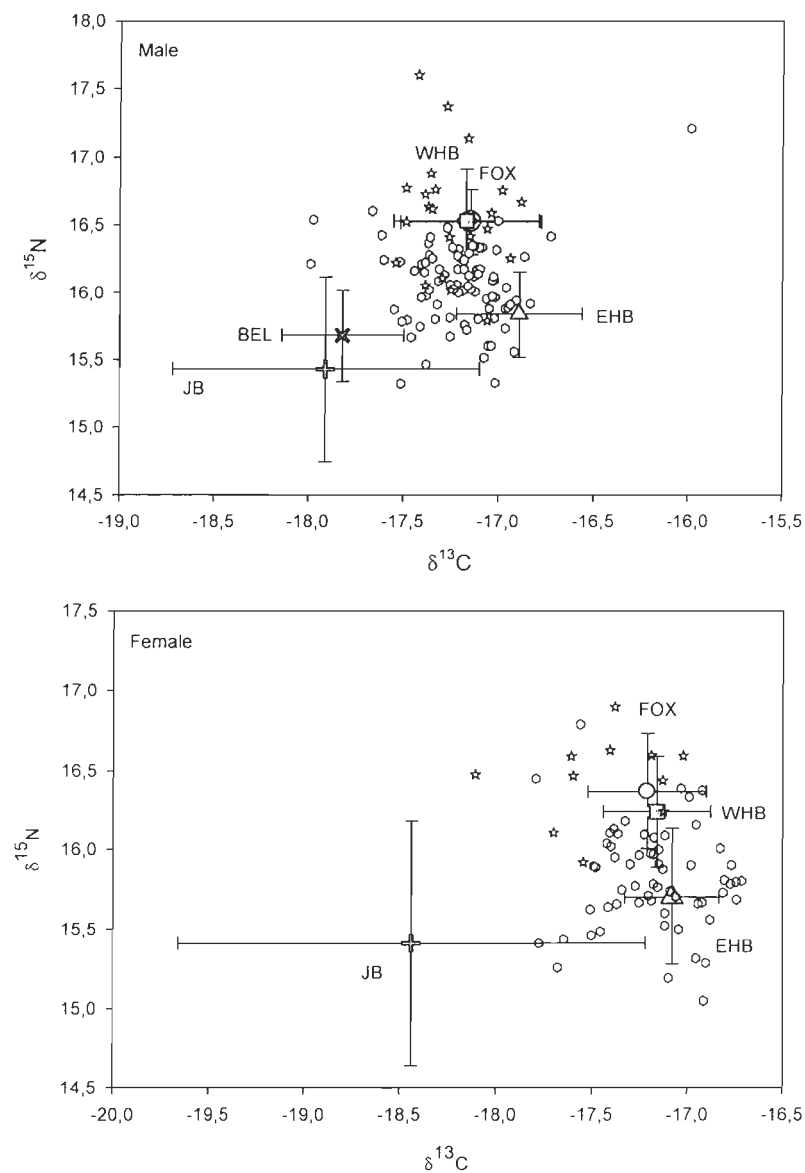


Figure 4. Biplots of mean stable isotopic ratios of carbon and nitrogen ($\pm$ SD) for the fall harvest (southern Hudson Strait = $\circ$ and northern Hudson Strait = $\star$) and summering sources (BEL = Belcher Islands = $\times$, EHB = Eastern Hudson Bay = $\blacktriangle$, FOX = Foxe Basin = $\bullet$, JB = James Bay = $+$ and WHB = Western Hudson Bay = $\blacksquare$). For males: BEL $n=5$, EHB $n=41$, FOX $n=19$, JB $n=17$ and WHB $n=49$ and for females: EHB $n=32$, FOX $n=9$, JB $n=14$ and WHB $n=38$.

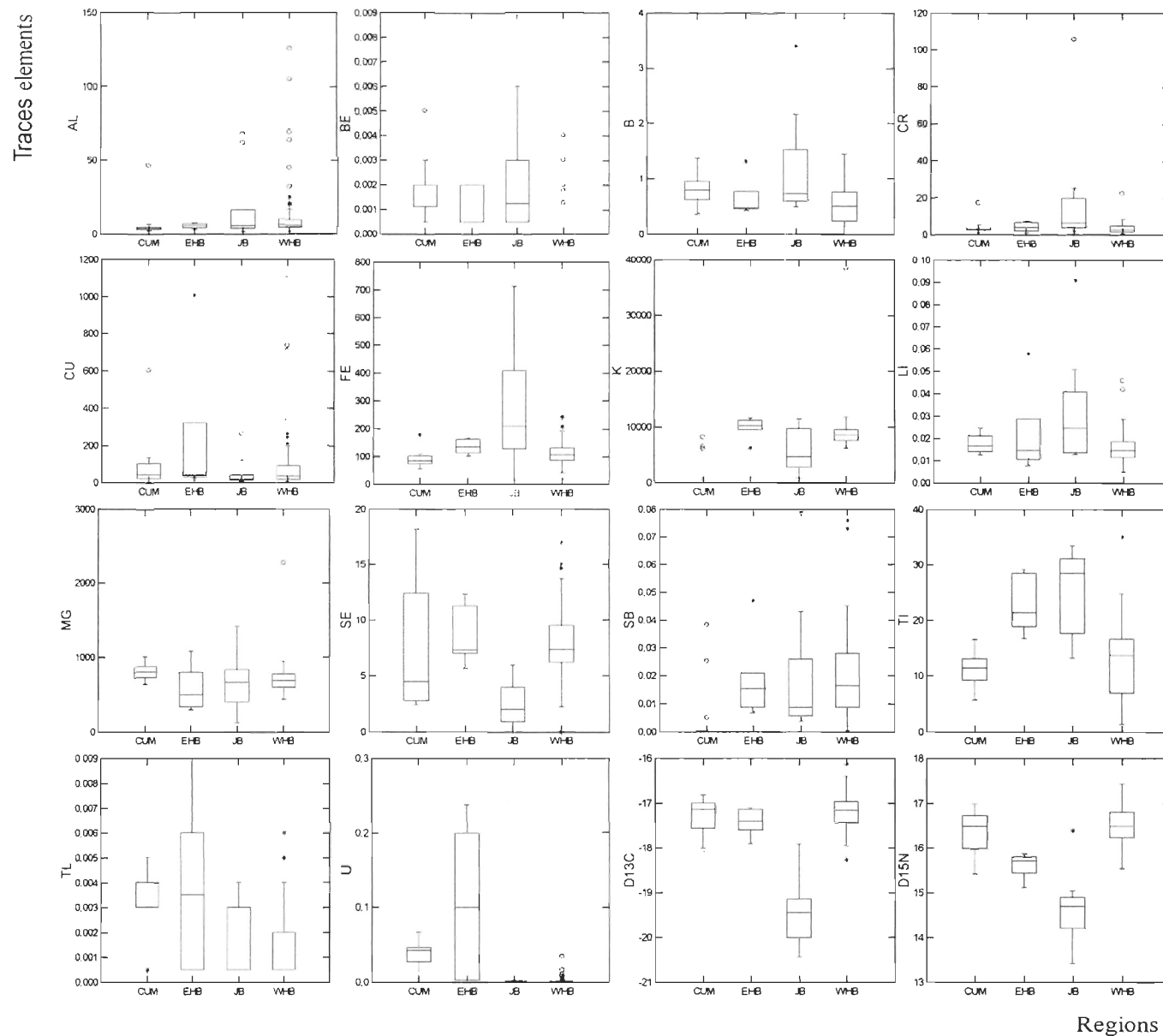


Figure 5. Trace element concentrations ($\mu\text{g/g}$ dry weight) and stable isotope ratios in beluga skin in summer from various regions (Mean, 50% and 95%). Only those elements contributing to the differentiation among regions, as determined from a stepwise discriminant analysis, are presented.

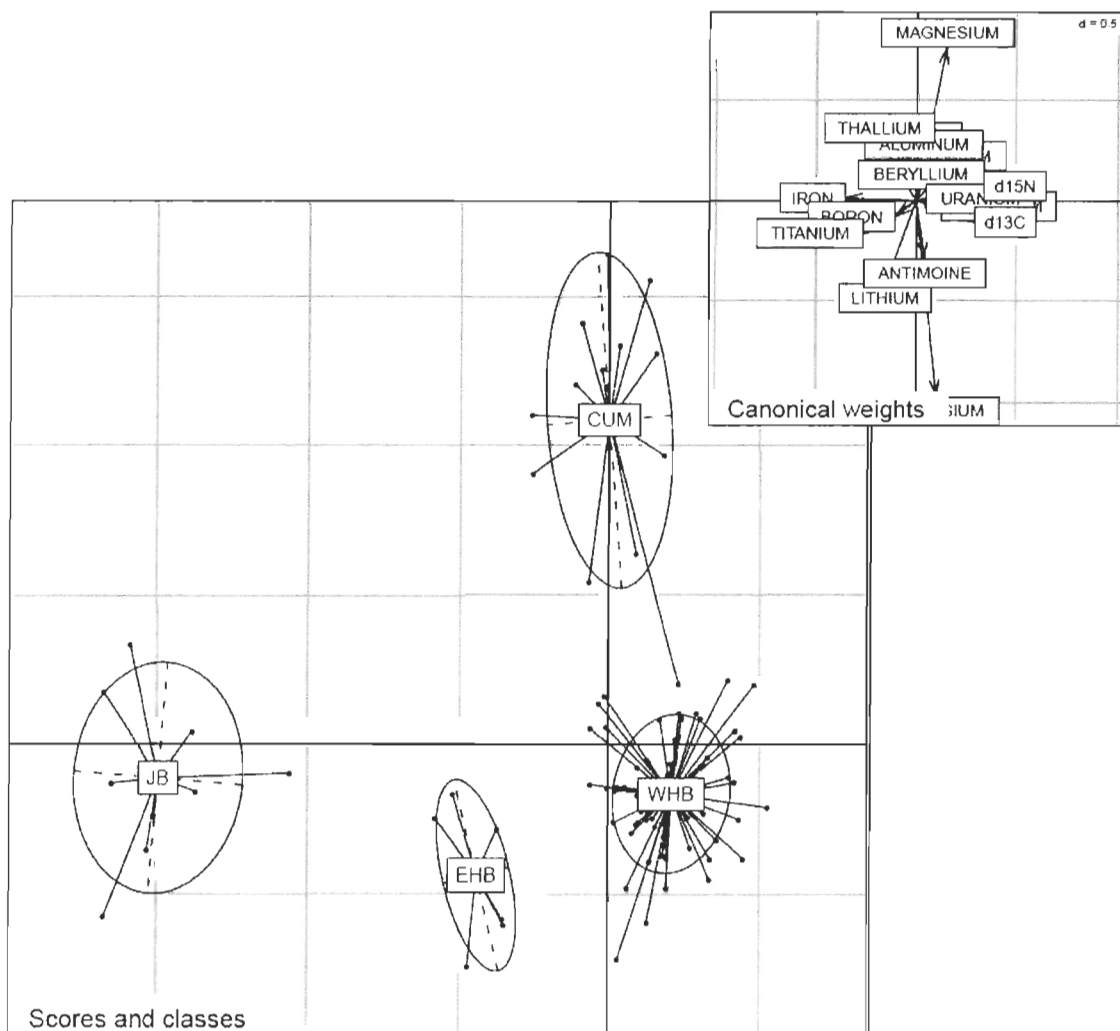


Figure 6. Discriminant function scores for beluga hunted during summer in James Bay (JB), Eastern Hudson Bay (EHB), Western Hudson Bay (WHB) and Cumberland Sound (CUM) plotted on the two canonical axis. The expanded view shows the canonical weight and direction for the 14 trace elements and 2 stable isotopes.

Table 1. Stable isotope values of carbon $\delta^{13}\text{C}$ and nitrogen $\delta^{15}\text{N}$ in the skin of male and female beluga from various regions and seasons (mean $\pm$ SD).

Regions	Seasons	Female			Male		
		N	$\delta^{13}\text{C}$	$\delta^{15}\text{N}$	N	$\delta^{13}\text{C}$	$\delta^{15}\text{N}$
BEL	Spring	63	-18.00 ± 0.47	15.54 ± 0.33	70	-17.78 ± 0.57	15.71 ± 0.39
	Summer	2	-17.85 ± 0.18	15.72 ± 0.20	5	-17.82 ± 0.32	15.68 ± 0.34
	Fall	1	-17.24	15.74	18	-17.37 ± 0.46	16.12 ± 0.26
	Global	75	-17.95 ± 0.46	15.57 ± 0.32	113	-17.64 ± 0.57	15.83 ± 0.41
CUM	Spring	12	-17.59 ± 0.37	16.27 ± 0.40	15	-17.39 ± 0.31	16.54 ± 0.55
	Summer	11	-17.47 ± 0.35	16.31 ± 0.37	25	-17.35 ± 0.38	16.23 ± 0.41
	Fall	0	-	-	0	-	-
	Global	25	-17.57 ± 0.37	16.25 ± 0.38	41	-17.37 ± 0.35	16.33 ± 0.49
EHB	Spring	4	-16.98 ± 0.13	15.67 ± 0.14	4	-17.15 ± 0.34	15.83 ± 0.16
	Summer	31	-17.08 ± 0.25	15.70 ± 0.43	42	-16.89 ± 0.33	15.84 ± 0.32
	Fall	2	-17.16 ± 0.38	15.91 ± 0.36	8	-17.25 ± 0.23	15.94 ± 0.37
	Global	42	-17.09 ± 0.27	15.72 ± 0.39	59	-16.97 ± 0.34	15.83 ± 0.32
FOX	Spring	0	-	-	0	-	-
	Summer	9	-17.21 ± 0.31	16.37 ± 0.36	19	-17.15 ± 0.37	16.52 ± 0.24
	Fall	8	-17.16 ± 0.24	16.30 ± 0.09	33	-17.16 ± 0.39	16.46 ± 0.27
	Global	17	-17.19 ± 0.27	16.33 ± 0.27	53	-17.16 ± 0.38	16.49 ± 0.26
HSN	Spring	21	-17.30 ± 0.33	15.93 ± 0.23	4	-17.23 ± 0.47	15.74 ± 0.46
	Summer	0	-	-	0	-	-
	Fall	11	-17.44 ± 0.32	16.45 ± 0.27	22	-17.25 ± 0.19	16.58 ± 0.43
	Global	33	-17.35 ± 0.32	16.10 ± 0.35	26	-17.24 ± 0.24	16.45 ± 0.53
HSS	Spring	83	-17.33 ± 0.35	15.56 ± 0.45	71	-17.14 ± 0.33	15.83 ± 0.38
	Summer	10	-17.21 ± 0.33	15.47 ± 0.22	7	-17.24 ± 0.39	15.90 ± 0.38
	Fall	61	-17.18 ± 0.27	15.82 ± 0.32	87	-17.20 ± 0.26	16.07 ± 0.30
	Global	166	-17.27 ± 0.33	15.66 ± 0.41	184	-17.19 ± 0.33	15.95 ± 0.35
JB	Spring	1	-18.11	15.72	1	-17.68	15.97
	Summer	11	-18.44 ± 1.22	15.41 ± 0.77	20	-17.91 ± 0.81	15.43 ± 0.69
	Fall	5	-17.76 ± 0.14	15.46 ± 0.14	6	-17.78 ± 0.14	15.46 ± 0.13
	Global	12	-18.41 ± 1.16	15.44 ± 0.74	28	-17.85 ± 0.69	15.48 ± 0.60
UNG	Spring	11	-17.05 ± 0.48	15.59 ± 0.39	9	-17.21 ± 0.25	16.00 ± 0.55
	Summer	7	-17.23 ± 0.42	15.72 ± 0.54	19	-17.09 ± 0.27	16.03 ± 0.32
	Fall	0	-	-	2	-16.97 ± 0.75	15.66 ± 0.47
	Global	25	-17.13 ± 0.39	15.68 ± 0.43	33	-17.17 ± 0.33	15.97 ± 0.40
WHB	Spring	0	-	-	0	-	-
	Summer	41	-17.16 ± 0.28	16.24 ± 0.35	53	-17.17 ± 0.38	16.53 ± 0.38
	Fall	1	-16.80	15.77	2	-17.96 ± 1.02	16.68 ± 0.23
	Global	42	-17.16 ± 0.29	16.23 ± 0.36	58	-17.19 ± 0.41	16.55 ± 0.39

Table 2. Cross-validated classification for female beluga harvested during summer using linear discrimination functions based on their stable carbon and nitrogen isotope signatures.

Sex	Observed group	Assigned group		
		EHB	BEL&JB	WHB&FOX
Female	EHB	87% (27)	3% (1)	10% (3)
	BEL&JB	0% (0)	85% (11)	15% (2)
	WHB&FOX	22% (11)	8% (4)	70% (35)

Table 3. Cross-validated classification for male beluga harvested during summer using linear discrimination functions based on their stable carbon and nitrogen isotope signatures.

Sex	Observed group	Assigned group		
		EHB	BEL&JB	WHB&FOX
Male	EHB	81% (35)	12% (5)	7% (3)
	BEL&JB	8% (2)	80% (20)	12% (3)
	WHB&FOX	6% (4)	8% (7)	85% (61)

Table 4. Contribution of the various summering stocks to the Hudson Strait fall harvest as determined from linear discrimination function based on stable carbon and nitrogen isotope signatures.

		Assigned group			
		EHB	BEL&JB	WHB&FOX	TOTAL
HSS	Female	61% (37)	1% (1)	38% (23)	100% (61)
	Male	40% (35)	9% (8)	51% (44)	100% (87)
HSN	Female	0% (0)	9% (1)	91% (10)	100% (11)
	Male	9% (2)	0% (0)	91% (20)	100% (22)

Table 5. Trace element concentrations ($\mu\text{g/g}$ dry weight) in beluga skin from various regions and seasons (mean $\pm$ SD). Only those elements contributing to the differentiation among regions and seasons, as determined from a stepwise discriminant analysis, are presented.

REGION	SEASON	N	CHROMIUM	IRON	COPPER	SELENIUM	LITHIUM	BERYLLIUM	BORON
BEL	Spring	60	3.425 $\pm$ 2.217	82.597 $\pm$ 47.157	116.585 $\pm$ 200.316	6.597 $\pm$ 2.578	0.019 $\pm$ 0.006	0.007 $\pm$ 0.005	1.138 $\pm$ 0.52
	Summer	1	7.614	124.806	1 429.210	7.837	0.025	0.001	0.4
	Fall	5	7.389 $\pm$ 5.449	120.437 $\pm$ 40.209	96.964 $\pm$ 96.281	5.571 $\pm$ 1.739	0.015 $\pm$ 0.005	0.009 $\pm$ 0.015	0.224 $\pm$ 0.091
CUM	Global	66	3.789 $\pm$ 2.763	86.103 $\pm$ 47.361	134.987 $\pm$ 251.369	6.538 $\pm$ 2.514	0.019 $\pm$ 0.006	0.007 $\pm$ 0.006	1.057 $\pm$ 0.559
	Spring	7	2.887 $\pm$ 1.196	86.35 $\pm$ 14.466	77.893 $\pm$ 62.747	7.259 $\pm$ 4.865	0.016 $\pm$ 0.003	0.002 $\pm$ 0.001	0.934 $\pm$ 0.296
	Summer	15	3.98 $\pm$ 3.748	93.017 $\pm$ 28.12	94.755 $\pm$ 146.945	7.186 $\pm$ 5.428	0.018 $\pm$ 0.004	0.002 $\pm$ 0.001	0.8 $\pm$ 0.246
EHB	Fall	0	-	-	-	-	-	-	-
	Global	22	3.632 $\pm$ 3.169	90.896 $\pm$ 24.435	89.39 $\pm$ 124.839	7.209 $\pm$ 5.139	0.017 $\pm$ 0.004	0.002 $\pm$ 0.001	0.843 $\pm$ 0.263
	Spring	2	6.673 $\pm$ 3.69	469.616 $\pm$ 554.723	449.849 $\pm$ 591.233	5.475 $\pm$ 5.609	0.04 $\pm$ 0.016	0.001 $\pm$ 0.001	1.204 $\pm$ 1.33
FOX	Summer	6	4.425 $\pm$ 2.71	136.402 $\pm$ 25.43	245.931 $\pm$ 390.866	8.501 $\pm$ 2.656	0.023 $\pm$ 0.019	0.001 $\pm$ 0.001	0.665 $\pm$ 0.341
	Fall	0	-	-	-	-	-	-	-
	Global	8	4.987 $\pm$ 2.876	219.705 $\pm$ 261.179	296.91 $\pm$ 409.845	7.744 $\pm$ 3.39	0.027 $\pm$ 0.019	0.001 $\pm$ 0.001	0.799 $\pm$ 0.631
HSN	Spring	0	-	-	-	-	-	-	-
	Summer	2	12.972 $\pm$ 4.834	220.705 $\pm$ 89.117	459.503 $\pm$ 630.62	6.095 $\pm$ 0.489	0.02 $\pm$ 0.011	0.003 $\pm$ 0.001	0.815 $\pm$ 0.196
	Fall	15	4.443 $\pm$ 3.29	128.247 $\pm$ 31.392	164.911 $\pm$ 301.26	4.888 $\pm$ 1.841	0.029 $\pm$ 0.029	0.001 $\pm$ 0.001	1.079 $\pm$ 0.283
HSS	Global	17	5.446 $\pm$ 4.353	139.124 $\pm$ 47.974	199.569 $\pm$ 337.402	5.03 $\pm$ 1.772	0.028 $\pm$ 0.027	0.001 $\pm$ 0.001	1.048 $\pm$ 0.283
	Spring	2	3.347 $\pm$ 2.685	114.211 $\pm$ 29.83	14.118 $\pm$ 3.07	8.614 $\pm$ 1.024	0.014 $\pm$ 0.004	0.003 $\pm$ 0.001	1.031 $\pm$ 0.129
	Summer	0	-	-	-	-	-	-	-
JB	Fall	16	7.095 $\pm$ 9.066	172.677 $\pm$ 88.321	126.353 $\pm$ 169.644	4.651 $\pm$ 2.003	0.019 $\pm$ 0.008	0.002 $\pm$ 0.001	0.918 $\pm$ 0.328
	Global	18	6.679 $\pm$ 8.627	166.181 $\pm$ 85.397	113.883 $\pm$ 163.436	5.091 $\pm$ 2.29	0.019 $\pm$ 0.008	0.002 $\pm$ 0.001	0.931 $\pm$ 0.311
	Spring	43	4.362 $\pm$ 3.85	111.64 $\pm$ 49.89	167.653 $\pm$ 267.734	13.794 $\pm$ 5.115	0.039 $\pm$ 0.02	0.052 $\pm$ 0.064	1.136 $\pm$ 0.504
UNG	Summer	3	4.178 $\pm$ 2.425	121.979 $\pm$ 17.061	537.976 $\pm$ 899.48	17.52 $\pm$ 3.84	0.033 $\pm$ 0.013	0.001 $\pm$ 0.000	1.018 $\pm$ 0.288
	Fall	9	4.021 $\pm$ 1.849	95.202 $\pm$ 31.356	121.483 $\pm$ 236.165	8.76 $\pm$ 2.421	0.031 $\pm$ 0.007	0.020 $\pm$ 0.020	0.968 $\pm$ 0.217
	Global	55	4.296 $\pm$ 3.503	109.514 $\pm$ 46.246	180.298 $\pm$ 319.048	13.174 $\pm$ 5.135	0.038 $\pm$ 0.018	0.044 $\pm$ 0.059	1.102 $\pm$ 0.461
WHB	Spring	0	-	-	-	-	-	-	-
	Summer	9	21.168 $\pm$ 32.878	282.164 $\pm$ 218.687	57.167 $\pm$ 85.925	2.465 $\pm$ 1.926	0.033 $\pm$ 0.025	0.003 $\pm$ 0.003	1.25 $\pm$ 0.975
	Fall	0	-	-	-	-	-	-	-
WHB	Global	9	21.168 $\pm$ 32.878	282.164 $\pm$ 218.687	57.167 $\pm$ 85.925	2.465 $\pm$ 1.926	0.033 $\pm$ 0.025	0.003 $\pm$ 0.003	1.25 $\pm$ 0.975
	Spring	4	2.918 $\pm$ 1.22	138.153 $\pm$ 36.803	19.493 $\pm$ 7.677	11.089 $\pm$ 4.249	0.027 $\pm$ 0.015	0.002 $\pm$ 0.003	0.918 $\pm$ 0.335
	Summer	5	2.949 $\pm$ 1.207	126.068 $\pm$ 36.689	93.944 $\pm$ 145.78	10.9 $\pm$ 2.083	0.025 $\pm$ 0.02	0.001 $\pm$ 0.001	0.498 $\pm$ 0.366
WHB	Fall	0	-	-	-	-	-	-	-
	Global	9	2.935 $\pm$ 1.134	131.439 $\pm$ 34.95	60.855 $\pm$ 110.398	10.984 $\pm$ 2.992	0.026 $\pm$ 0.017	0.001 $\pm$ 0.002	0.685 $\pm$ 0.398
	Spring	0	-	-	-	-	-	-	-
WHB	Summer	76	3.732 $\pm$ 2.819	114.393 $\pm$ 38.748	94.07 $\pm$ 170.924	8.184 $\pm$ 2.927	0.016 $\pm$ 0.008	0.001 $\pm$ 0.001	0.57 $\pm$ 0.354
	Fall	3	3.482 $\pm$ 1.43	108.098 $\pm$ 19.857	44.973 $\pm$ 18.241	4.64 $\pm$ 4.039	0.013 $\pm$ 0.002	0.014 $\pm$ 0.020	0.55 $\pm$ 0.305
	Global	79	3.723 $\pm$ 2.774	114.154 $\pm$ 38.148	92.206 $\pm$ 167.896	8.049 $\pm$ 3.02	0.016 $\pm$ 0.007	0.001 $\pm$ 0.004	0.569 $\pm$ 0.35

Table 5 (continued).

REGION	SEASON	N	MAGNESIUM	ALUMINUM	POTASSIUM	TITANIUM	TIN	THALLIUM	URANIUM
BEL	Spring	60	781.342 ± 140.074	5.365 ± 3.944	6 712.950 ± 3 320.254	5.109 ± 2.519	16.484 ± 16.413	0.005 ± 0.003	0.026 ± 0.017
	Summer	1	583	2.057	6.969	6.268	78.187	0.003	0.048
	Fall	5	593.6 ± 72.831	3.229 ± 0.9	1 567.597 ± 3 489.050	9.576 ± 3.783	15.266 ± 14.12	0.005 ± 0.004	0.045 ± 0.009
	Global	66	764.114 ± 145.435	5.153 ± 3.827	6 221.545 ± 3 638.513	5.465 ± 2.84	17.327 ± 17.742	0.005 ± 0.003	0.027 ± 0.017
CUM	Spring	7	811.571 ± 101.885	4.02 ± 2.591	8.559 ± 1.808	10.825 ± 1.031	7.974 ± 7.05	0.003 ± 0.001	0.041 ± 0.010
	Summer	15	796.267 ± 107.923	6.826 ± 10.876	1 399.167 ± 2 907.588	11.3 ± 2.735	7.108 ± 8.443	0.004 ± 0.001	0.038 ± 0.017
	Fall	0	-	-	-	-	-	-	-
	Global	22	801.136 ± 103.846	5.933 ± 9.087	956.701 ± 2 464.862	11.149 ± 2.311	7.383 ± 7.867	0.003 ± 0.001	0.039 ± 0.015
EHB	Spring	2	822 ± 82.024	25.938 ± 23.373	8 637.000 ± 3 395.527	26.358 ± 10.569	29.373 ± 26.527	0.002 ± 0	0.001 ± 0.000
	Summer	6	581.667 ± 297.28	5.705 ± 1.569	9 881.667 ± 1 940.731	22.704 ± 5.053	28.996 ± 33.809	0.004 ± 0.003	0.107 ± 0.115
	Fall	0	-	-	-	-	-	-	-
	Global	8	641.75 ± 276.521	10.763 ± 12.943	9 570.500 ± 2 160.872	23.618 ± 6.088	29.09 ± 30.283	0.003 ± 0.003	0.080 ± 0.109
FOX	Spring	0	-	-	-	-	-	-	-
	Summer	2	717.5 ± 7.778	5.886 ± 3.126	11 112.500 ± 1 293.298	2.231 ± 0.218	39.839 ± 50.749	0.003 ± 0.001	0.001 ± 0.001
	Fall	15	749.8 ± 123.36	11.632 ± 22.158	8 393.200 ± 686.647	2.386 ± 1.528	14.992 ± 20.037	0.002 ± 0.001	0.001 ± 0.001
	Global	17	746 ± 115.906	10.956 ± 20.829	8 713.118 ± 8 713.118	2.367 ± 1.431	17.916 ± 24.091	0.002 ± 0.001	0.001 ± 0.001
HSN	Spring	2	845.5 ± 252.437	8.117 ± 7.129	10 917.750 ± 1 207.385	3.192 ± 1.598	4.225 ± 0.98	0.003 ± 0.001	0.001 ± 0.001
	Summer	0	-	-	-	-	-	-	-
	Fall	16	893.656 ± 779.323	7.141 ± 8.454	11 428.313 ± 13 691.114	2.962 ± 1.878	12.969 ± 11.535	0.003 ± 0.001	0.001 ± 0.000
	Global	18	888.306 ± 734.768	7.25 ± 8.133	11 371.583 ± 12 864.955	2.988 ± 1.808	11.997 ± 11.2	0.003 ± 0.001	0.001 ± 0.000
HSS	Spring	43	763.837 ± 192.487	19.967 ± 72.464	10 398.307 ± 2 506.135	27.125 ± 6.093	20.451 ± 19.561	0.025 ± 0.025	0.489 ± 0.543
	Summer	3	682.333 ± 69.176	6.334 ± 3.318	11 778.667 ± 1 987.441	22.71 ± 1.844	34.488 ± 48.261	0.008 ± 0.002	0.231 ± 0.007
	Fall	9	691.5 ± 103.521	7.841 ± 7.534	11 222.944 ± 1 302.457	26.834 ± 3.205	13.434 ± 8.926	0.021 ± 0.018	0.372 ± 0.358
	Global	55	747.555 ± 177.633	17.239 ± 64.189	10 608.540 ± 2 335.976	26.837 ± 5.615	20.068 ± 20.364	0.023 ± 0.023	0.456 ± 0.503
JB	Spring	0	-	-	-	-	-	-	-
	Summer	9	671.667 ± 384.687	19.641 ± 25.863	5 771.056 ± 4 027.869	25.049 ± 7.516	18.682 ± 17.139	0.002 ± 0.001	0.001 ± 0.001
	Fall	0	-	-	-	-	-	-	-
	Global	9	671.667 ± 384.687	19.641 ± 25.863	5 771.056 ± 4 027.869	25.049 ± 7.516	18.682 ± 17.139	0.002 ± 0.001	0.001 ± 0.001
UNG	Spring	4	651.375 ± 165.5	34.832 ± 26.7	9 495.375 ± 1 242.657	18.13 ± 8.341	6.181 ± 2.532	0.016 ± 0.017	0.339 ± 0.326
	Summer	5	616.6 ± 165.941	12.882 ± 6.696	10 637.200 ± 1 081.044	23.258 ± 4.664	16.567 ± 18.453	0.006 ± 0.003	0.176 ± 0.104
	Fall	0	-	-	-	-	-	-	-
	Global	9	632.056 ± 156.126	22.638 ± 20.581	10 129.722 ± 1 235.135	20.979 ± 6.654	11.951 ± 14.235	0.01 ± 0.012	0.248 ± 0.229
WHB	Spring	0	-	-	-	-	-	-	-
	Summer	76	704.625 ± 215.419	13.004 ± 20.616	9 021.684 ± 3 650.034	12.329 ± 6.385	26.13 ± 14.198	0.001 ± 0.001	0.002 ± 0.005
	Fall	3	599.333 ± 68.413	6.576 ± 2.078	7 128.000 ± 201.859	12.533 ± 9.076	22.339 ± 6.035	0.009 ± 0.012	0.165 ± 0.285
	Global	79	700.627 ± 212.487	12.76 ± 20.256	8 949.772 ± 3 597.786	12.337 ± 6.428	25.986 ± 13.974	0.002 ± 0.003	0.009 ± 0.056

Table 6. Cross-validated classification of the beluga from various summering stocks as determined from a stepwise linear discrimination functions analysis using $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values and 27 trace elements. Isotope ratios of both C and N, as well as 14 trace elements (see Table 3) were selected to develop discriminant functions for this dataset.

Observed group	Assigned group			
	CUM	EHB	JB	WHB
CUM	93% (14)	0% (0)	0% (0)	7% (1)
EHB	0% (0)	67% (4)	0% (0)	33% (2)
JB	0% (0)	0% (0)	100% (9)	0% (0)
WHB	1,5% (1)	1,5% (1)	0% (0)	97% (74)

Table 7. Beluga harvested in southern Hudson Strait (N=9) and northern Hudson Strait (N = 16) during the fall and classified as being from the EHB stock using the discriminant functions analysis developed from stable isotope ratios and trace element concentrations. Grey color indicate harvest events when more than one individual was sampled.

SAMPLE	MM	DD	SEASON	YEAR	REGION	COMMUNITY	SEX	AGE	COLOUR
DL-9075	9	17	Autumn	2007	hss	Akulivik	M	23	W
DL-9065	9	18	Autumn	2007	hss	Akulivik	F	-	G
DL-9077	9	18	Autumn	2007	hss	Akulivik	F	13	G
DL-9078	9	18	Autumn	2007	hss	Akulivik	F	8	G
DL-9079	9	18	Autumn	2007	hss	Akulivik	F	-	G
DL-9066	9	19	Autumn	2007	hss	Akulivik	M	32	W
DL-9068	9	19	Autumn	2007	hss	Akulivik	F	24	W
DL-9076	9	19	Autumn	2007	hss	Akulivik	F	20	W
DL-9080	9	19	Autumn	2007	hss	Akulivik	M	37	W
ARLH-02-1050	10	26	Autumn	2001	hsn	Kimmirut	F	26	-
ARLH-01-1009	11	2	Autumn	2001	hsn	Kimmirut	M	26	-
ARLH-01-1042	11	2	Autumn	2001	hsn	Kimmirut	M	48	-
ARLH-01-1006	11	8	Autumn	2001	hsn	Kimmirut	M	16	-
ARLH-01-1041	11	8	Autumn	2001	hsn	Kimmirut	F	38	-
ARLH-01-1003	11	9	Autumn	2001	hsn	Kimmirut	-	23	-
ARLH-01-1008	11	9	Autumn	2001	hsn	Kimmirut	M	28	-
ARLH-01-1036	11	9	Autumn	2001	hsn	Kimmirut	M	11	-
ARLH-01-1040	11	9	Autumn	2001	hsn	Kimmirut	M	31	-
ARLH-01-1007	11	15	Autumn	2001	hsn	Kimmirut	M	11	-
ARLH-01-1017	11	18	Autumn	2001	hsn	Kimmirut	M	29	-
ARLH-01-1043	11	20	Autumn	2001	hsn	Kimmirut	F	48	-
ARLH-01-1047	11	20	Autumn	2001	hsn	Kimmirut	-	34	-
ARLH-02-1035	10	29	Autumn	2002	hsn	Kimmirut	F	19	-
ARLH-02-1176	10	29	Autumn	2002	hsn	Kimmirut	F	15	-
ARLH-02-1198	10	-	Autumn	2002	hsn	Kimmirut	F	28	-

Table 8. Beluga from the southern Hudson Strait spring harvest (N=41) and classified as coming from the EHB stock in the discriminant functions analysis. Grey color represents harvest events when more than one individual was sampled.

SAMPLE	MM	DD	SEASON	YEAR	REGION	COMMUNITY	SEX	AGE	COLOUR
DL-9122	6	7	Spring	2007	hss	Kangiqsujaq	M	28	W
DL-9155	6	17	Spring	2007	hss	Airaqtukallak	M	30	W
DL-9151	6	21	Spring	2007	hss	Airaqtukallak	M	16	W
DL-9153	6	21	Spring	2007	hss	Airaqtukallak	F	34	W
DL-9157	6	21	Spring	2007	hss	Airaqtukallak	M	10	G
DL-9158	6	21	Spring	2007	hss	Airaqtukallak	F	12	W
DL-9102	6	22	Spring	2007	hss	Nanurtuvik	F	27	W
DL-9145	6	22	Spring	2007	hss	Nuvuk	M	20	W
DL-9156	6	22	Spring	2007	hss	Nuvuk	F	21	W
DL-9236	6	22	Spring	2007	hss	Imilik	F	18	W
DL-9135	6	23	Spring	2007	hss	Itiviq	F	31	W
DL-9143	6	24	Spring	2007	hss	Nuvuk	F	28	W
DL-9111	6	25	Spring	2007	hss	Nanurtuvik	F	13	G
DL-9134	6	27	Spring	2007	hss	Kangiqsuapik	M	39	W
DL-9140	6	27	Spring	2007	hss	Itiviani	F	37	W
DL-9121	6	29	Spring	2007	hss	Tulakvik	M	24	W
DL-9105	6		Spring	2007	hss	NA	M	36	W
DL-9136	7	1	Spring	2007	hss	Itiviq	F	44	W
DL-9123	7	3	Spring	2007	hss	Kangiqsujaq	M	51	W
DL-9132	7	6	Spring	2007	hss	Kangiqsujaq	F	20	W
DL-10007	6	6	Spring	2008	hss	Naujaat	M	12	W
DL-10001	6	9	Spring	2008	hss	Naujaat	F	41	W
DL-10009	6	9	Spring	2008	hss	Naujaat	F	29	W
DL-10085	6	9	Spring	2008	hss	Ivujivik	F	-	W
DL-10008	6	10	Spring	2008	hss	Naujaat	F	17	G
DL-10012	6	10	Spring	2008	hss	Naujaat	F	17	G
DL-10002	6	11	Spring	2008	hss	Naujaat	F	16	G
DL-10006	6	12	Spring	2008	hss	Naujaat	M	13	G
DL-10011	6	13	Spring	2008	hss	Naujaat	F	-	G
DL-10015	6	13	Spring	2008	hss	Naujaat	M	15	W
DL-10004	6	15	Spring	2008	hss	Nuvukalak	F	22	G
DL-10005	6	15	Spring	2008	hss	Nuvukalak	F	19	G
DL-10014	6	15	Spring	2008	hss	Nuvukalak	F	14	G
DL-10104	6	18	Spring	2008	hss	Nunatuuvik	M	-	W
DL-9116	6	18	Spring	2008	hss	Nunatuuvik	F	26	W
DL-10100	6	19	Spring	2008	hss	Nunatuuvik	M	16	W
DL-10101	6	19	Spring	2008	hss	Nunatuuvik	M	31	W
DL-10105	6	19	Spring	2008	hss	Nunatuuvik	F	-	W
DL-10103G	6	23	Spring	2008	hss	Nunatuuvik	F	19	G
DL-17-06-2009-01-F	6	17	Spring	2009	hss	Quartaq	F	-	W
DL-17-06-2009-01-Foetus	6	17	Spring	2009	hss	Quartaq	F	0	DG

CHAPITRE 3 - CONCLUSION GÉNÉRALE

Cette étude avait pour objectif de déterminer si l'analyse des isotopes stables et des éléments traces peut aider à discriminer les populations et à estimer la proportion de bélugas de l'est de la baie d'Hudson dans la chasse d'automne du détroit d'Hudson. Les isotopes stables de carbone et d'azote, les éléments traces ainsi que les analyses discriminantes se sont avérés être de bons outils, en complément à la génétique, afin de mieux définir les populations de bélugas de l'est de l'Arctique canadien et ainsi promouvoir leur conservation. Cette étude a aussi permis de mieux comprendre l'écologie alimentaire et les mouvements saisonniers des bélugas ainsi que la ségrégation des niches entre les sexes.

Il a cependant été difficile d'interpréter les patrons isotopiques et d'éléments traces entre les saisons et les régions étant donné le peu de connaissance disponible concernant leur concentration dans les autres composantes de l'écosystème et leur patron de variabilité spatiale et temporelle. Cette contrainte a été exacerbée lors de l'interprétation des patrons d'éléments traces puisque le métabolisme, les fonctions et la provenance de plusieurs d'entre eux sont encore peu compris. Ces analyses ont également été limitées par la méconnaissance des proies ingérées par les bélugas dans ces régions, ce qui a prévenu l'emploi de modèles mixtes isotopiques pour déterminer leur importance relative (Inger et al. 2010, Parnell et al. 2010, Phillips and Gregg 2001, 2003, Semmens et al. 2009).

Néanmoins, cette étude a permis de démontrer que les mâles et les femelles béluga semblent exploiter des niches écologiques distinctes. Cette ségrégation de l'utilisation des ressources alimentaires est attendue chez des espèces sympatriques ou ayant un dimorphisme sexuel, comme c'est le cas pour le béluga. D'autre part, elle souligne également que les bélugas mâles et femelles ne sont pas également vulnérables aux modifications de leur environnement, les mâles semblant être plus hauturiers et dépendants des ressources benthiques et les femelles plus côtières, du moins durant l'été. Dans le

contexte d'un climat changeant et d'une accélération du développement côtier et extracôtier, une meilleure compréhension des préférences alimentaires du béluga et des contraintes à l'utilisation de l'habitat s'avèrera un atout afin de prédire les effets de ces facteurs sur les diverses composantes de ces populations.

Cette étude a également permis de bonifier les informations obtenues à l'aide de la génétique quant à la contribution des bélugas de diverses populations à la chasse de subsistance menée par les Inuits. La distinction des populations de bélugas dans l'est de l'Arctique canadien est primordiale à la gestion de cette chasse puisque certaines populations sont en péril. Les résultats basés sur les isotopes stables suggèrent que la contribution des bélugas de l'est de la baie d'Hudson dans la chasse d'automne du détroit d'Hudson est plus élevée que celle estimée par la génétique. Si ces résultats sont exacts, et si les prises sont plus importantes pour les femelles que pour les mâles, il peut s'avérer nécessaire de revoir la stratégie de gestion et les impacts appréhendés de la chasse sur les bélugas de l'est de la baie d'Hudson. Néanmoins, des analyses plus approfondies sont nécessaires afin de valider ces résultats, notamment, effectuer la classification génétique et isotopique en utilisant le même jeu de données. Également, il faudrait examiner l'appartenance des bélugas aux diverses populations en n'utilisant qu'un seul animal par événement de chasse. De cette manière, il serait possible de mieux évaluer les probabilités de tuer un groupe de bélugas provenant de la population en danger de disparition.

Les analyses discriminantes basées sur les isotopes stables et les éléments traces ont classifié les bélugas de la chasse d'automne avec un taux d'erreur plus faible qu'avec les isotopes stables seuls. Cette méthode semble être l'approche à préconiser pour le futur. Toutefois, la faible taille d'échantillon (isotopes stables et éléments traces combinés) pour la plupart des aires d'été rend prématuré l'établissement des proportions de chasse attribuables aux diverses populations à partir de cette approche. Il est donc nécessaire de mieux caractériser les populations d'été pour l'ensemble de celles qui contribuent à la chasse d'automne ou de printemps.

Il aurait aussi été intéressant d'analyser la composition de la chasse de printemps, mais le manque d'échantillons pour les bélugas sur les aires d'hivernage prévient cette analyse. Une meilleure caractérisation des aires d'hivernage des bélugas et un meilleur échantillonnage tant au niveau génétique qu'isotopique pourrait aider à déterminer la proportion de bélugas de l'est de la baie d'Hudson présent dans la chasse printanière. La chasse tend à s'effectuer principalement au printemps, car selon la génétique, les chances de récolter un béluga de la population en danger de l'est de la baie d'Hudson sont plus faibles qu'à l'automne (MPO 2009). Cependant, il faut aussi mentionner que c'est à cette période que les moyens d'établir la contribution des bélugas de l'est de la baie d'Hudson sont les plus limités.

En dépit de ces difficultés et considérant le nombre important d'individus que nous avons analysés, nous sommes confiants que les patrons observés sont fidèles à l'écologie alimentaire et à la structure des populations de béluga de l'est de l'Arctique canadien. De nombreux outils sont aujourd'hui disponibles, tels que ceux utilisés ici (analyse d'isotopes stables et d'éléments traces), de même que l'analyse des acides gras et des contenus stomacaux, la télémétrie et les connaissances traditionnelles des Inuits. Une approche préconisant l'utilisation combinée de ces outils permettra de parfaire nos connaissances sur l'écologie alimentaire du béluga et des autres prédateurs marins.

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