

RESEARCH NOTE

Greenland sharks (*Somniosus microcephalus*) scavenge offal from minke (*Balaenoptera acutorostrata*) whaling operations in Svalbard (Norway)

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Abstract

Minke whale (*Balaenoptera acutorostrata*) tissue (mainly blubber) was found in the gastrointestinal tracks of Greenland sharks (*Somniosus microcephalus*) collected in Kongsfjorden, Svalbard, Norway. In order to determine whether the sharks were actively hunting the whales, finding naturally dead whales or consuming offal from whaling, we checked the genetic identity of the whale tissue found in the sharks against the DNA register for minke whales taken in Norwegian whaling operations. All of the minke whale samples from the sharks that had DNA of sufficient quality to perform individual identifications were traceable to the whaling DNA register. During whaling operations, the blubber is stripped from the carcass and thrown overboard. The blubber strips float on the surface and are available for surface-feeding predators. This study revealed that Greenland sharks are scavenging this material; additionally, it demonstrates the capacity of this 'benthic-feeding' shark to utilize the whole water column for foraging.

Cold-water adapted sharks that inhabit the High Arctic belong to the genus *Somniosus* and include the Pacific sleeper shark (*Somniosus pacificus*) in the North Pacific and the Greenland shark (*Somniosus microcephalus*) in the North Atlantic (Benz et al. 2004). These slow-swimming sharks feed on a wide variety of prey but their diet is primarily comprised of fish and seals (Yano et al. 2007). However, they have also been reported to occasionally feed on cetaceans such as common porpoises (*Phocoena phocoena*) and grey whales (*Eschrichtius robustus*) (Williamson 1963; Sigler et al. 2006). It is generally assumed that much of the cetacean tissue in these sharks' stomachs is derived from carrion from natural mortalities of large cetacean species (Smith & Baco 2003) or offal from whaling operations (Compagno 1984).

In 2008, we collected 32 Greenland sharks in Kongsfjorden, on the west coast of Spitsbergen, Norway (Fig. 1) as part of a harbour seal (*Phoca vitulina*) ecology study. Six of the Greenland sharks' gastrointestinal tracts (GITs)

contained cetacean tissue. Chunks of whale blubber with the skin attached and in one case some muscle tissue (ranging from 210 to 750 g) were found in the stomachs of the sharks, while small skin pieces (0.5–1 cm in length) were found in the pyloric cecum, proximal intestine and the spiral intestine in a few individuals. In total, 10 samples, thought to be minke whale tissue, were taken from the six sharks and placed in 70% ethanol for genetic analysis (Table 1).

The Norwegian authorities established a DNA register for all minke whales harvested in commercial whaling operations in 1996. The register contains individual DNA profiles for all whales hunted since that time (Olaisen 1997; Haaland & Skaug 2007). This provided us with the opportunity to examine whether the tentatively identified tissues consumed by the Greenland sharks captured in Svalbard were from minke whales and whether the material originated from whaling offal or alternative sources.

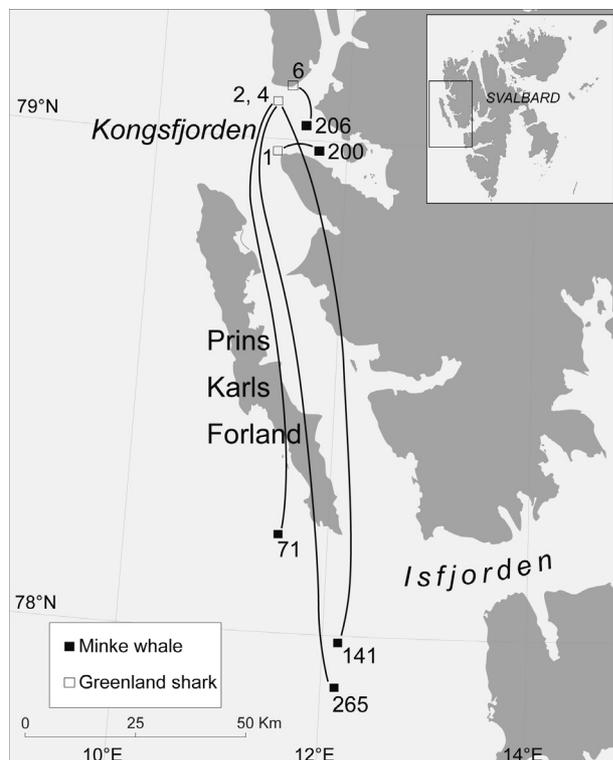


Fig. 1 Locations where the minke whales and the Greenland sharks were collected between 18 May and 12 June 2008. The numbers refer to the whale numbers from the DNA registry and the shark numbers refer to individuals described in Table 1.

Genetic identification of species is usually conducted by sequencing mitochondrial DNA genes and matching the sequence to databases such as the Barcode of Life initiative (e.g., Hebert et al. 2003). However, due to potential contamination from the sharks themselves and other prey items present in the stomachs, this study screened for microsatellite markers that are used in the Norwegian minke whale DNA register (Glover et al. 2010). If amplifiable, these markers identify the samples to individual whales in the DNA register, thus automatically providing species identification. Alternatively, if a given sample does not match a single whale in the DNA register directly but the alleles fit with the calibrated allele sizing system established for minke whales (Glover et al. 2010), a tentative or robust species identification is made depending on the number of markers amplified. An earlier study demonstrated that seven microsatellite loci give a probability of false individual match of 0.0054 for a sub-set of 2676 individual minke whales in the DNA register (Palsbøll et al. 2006).

DNA for each of the 10 samples was isolated twice using the DNeasy blood and tissue kit in 96-well format (Qiagen, Venlo, Netherlands). Following DNA isolation,

10 microsatellite loci and a single sex determinant locus were analysed in three polymerase chain reactions (PCR): multiplex 1 = *GT509* (Berube et al. 2000), *GATA098* (Palsbøll et al. 1997), *EV001PmG09074* (Valsecchi & Amos 1996), *EV037MnG09081* (Valsecchi & Amos 1996) and *GT310* (Berube et al. 2000); multiplex 2 = *GT211* (Berube et al. 2000) and *GT575* (Berube et al. 2000); multiplex 3 = *GATA417* (Palsbøll et al. 1997), *GATA028* (Palsbøll et al. 1997) and *GT023* (Berube et al. 2000) and a sex determining marker (Palsbøll et al. 1998). Amplification conditions for these markers are described by Glover et al. (2010). All DNA isolates were genotyped twice, giving four independent genotyping attempts per sample. The PCR fragments were identified and sized in a capillary-based DNA analyser (ABI 3730xl, Life Technologies Corporation, Carlsbad, CA, USA). Genotypes were first automatically determined and then manually checked by two independent observers before exporting the data. To check for potential genotyping errors, cross-validation of up to four runs per sample were performed but no errors were found. For samples where genotypic data could be resolved, available data were then compared to the Norwegian DNA register for minke whales in order to attempt to identify them.

Because of tissue degradation, genotyping failed to resolve genetic data for three of the samples, all of which were from shark 3 (Table 1). Consequently, species identification was not confirmed for any of these samples, although the thickness and colour of these bits of skin were consistent with that of minke whales. Sample 5 displayed genetic data at 3 of the 11 microsatellite loci. The resultant genetic profile of this sample was not sufficient to provide an unambiguous identification to a specific whale in the DNA register. But the alleles for this sample were in the size bins calibrated for this species and the profile closely matched six whales (of the 525 profiles from the 2008 catch) in the register, which strongly suggests that it was minke whale tissue. Based upon successfully genotyping 3 to 11 loci, the remaining six samples collected from four sharks (1, 2, 4 and 6) were all unambiguously identified (i.e., unique match) to individual animals in the DNA register for minke whales caught in 2008 (DNA register numbers 71, 141, 200, 206 and 265). Shark 4 had consumed tissues from two different whales (Table 1).

The five minke whales identified within the shark GITs had all been killed in Svalbard between 18 May and 1 June 2008 in the vicinity of Kongsfjorden. Whales 200 and 206 were both taken within this fjord, while whales 71, 141 and 265 were taken south of Prins Karls Forland (Fig. 1). The sharks containing the whale tissues were

Table 1 Information on cetacean tissue collected in the gastrointestinal tracts (GITs) of Greenland sharks in 2008 on the west coast of Spitsbergen, Svalbard (Norway) for genetic investigations of shark diet.

Whale sample number	Shark number	Tissue type found in the shark's GIT	Total number of loci successfully genotyped (of 11 possible)	Whale number from the DNA register	Harvest date (whale)	Harvest date (shark)
1	1	skin	10	200	24 May	7 Jun
2	1	skin	4	200		
3	2	blubber + skin	3	71	18 May	8 Jun
4	3	blubber + skin	–	–	–	8 Jun
5	3	skin	–			
6	3	skin	–			
7	4	muscle	11	265	26 May	8 Jun
8	4	skin	11	141	25 May	8 Jun
9	5	skin	3	–	–	9 Jun
10	6	blubber + skin	11	206	1 Jun	12 Jun

collected 12–22 days after the whales had been killed. Although it is not known precisely where the sharks consumed the blubber, the shortest straight-line distance between the whale harvesting points and the shark collection points varied between 8 and 108 km (Fig. 1).

During Norwegian minke whaling operations, the blubber is stripped from the carcass and thrown overboard, the entrails are removed and then the meat (muscle) is taken from the whale and finally the rest of the carcass, which is mostly bones, is discarded into the ocean. These whale carcasses, which sink to the bottom, represent relatively little potential food for sharks. But the floating blubber strips are high energy food for Greenland sharks and other animals. The sharks must swim quickly to the surface to access this potential food source because the blubber strips are immediately attacked upon their release from the boats by large flocks of birds, mainly fulmars (*Fulmarus glacialis*). Observations of Greenland sharks attracted to the surface by whaling and sealing operations have previously been described in the literature (Jensen 1914; Nansen 1924; Beck & Mansfield 1969; Compagno 1984). Greenland sharks from the study area equipped with pop-up satellite tags that record swimming depths of these fish show a depth range from deeper than 1500 m up to the surface (Fisk, Kovacs & Lydersen, unpubl. data) with some sharks routinely showing vertical movements up through the water column. Such movements have been associated with prey searching in other shark species (e.g., Hulbert et al. 2006). Given the relatively limited number of whales taken in current whaling operations, the broad geographic spread of the catch and the competition for this food from birds, it is unlikely that this potential food source has much impact on Greenland sharks at the population level.

In conclusion, all minke whale samples found in Greenland shark GITs that had sufficient DNA quality

to perform individual identifications were traceable to the Norwegian minke whale DNA harvest registry. This demonstrated that the sharks were surface-feeding on offal from the whaling operation that took place near Kongsfjorden at the end of May 2008.

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