

# Information of relevance on Evaluation Trials for West Greenland minke whales

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## ABSTRACT

The development of a Strike Limit Algorithm (SLA) for minke whales off West Greenland would naturally be done on Evaluation Trials constructed by an extension or modification of the current RMP Implementation Simulation Trials developed for North Atlantic minke whales (IWC 1993, 2004). These trials consider three stocks of minke whales in the North Atlantic; a western, a central and a eastern stock. I summaries what is known on the stock structure of North Atlantic minke whales with a focus on the western and central part of the region. I consider the assumed dynamics in the RMP trials, and provide information and discussions for the construction of Evaluation Trials for an SLA for the harvest of minke whales in West Greenland.

## STOCK STRUCTURE

The selection of abstract below summarise what is known about the stock structure in western and central North Atlantic minke whales. Some studies find large-scale differentiation indicating some degree of separation between minke whales summering in the western, central and eastern North Atlantic, while other studies find no evidence of geographical structure. A recent model study (Anderwald et al. 2011) indicates the possibility of two breeding stocks that mix in more or less similar proportions in all summer feeding areas. The overall conclusion seem be that minke whales range extensively across the North Atlantic, and that the degree to which North Atlantic minke whales aggregated into discrete breeding units is unclear.

The underlying analysis behind the recent hypothesis of two breeding stocks that distribute themselves in more or less similar proportions in the different summer aggregations (Anderwald et al. 2011) needs to be discussed in detail before its relevance to North Atlantic minke whales can be concluded. In this paper I make no attempt to include this hypothesis into the suggested structure of the Evaluation Trials for West Greenland minke whales.

## **Andersen et al. 2003: Genetic population structure of minke whales *Balaenoptera acutorostrata* from Greenland, the North East Atlantic and the North Sea probably reflects different ecological regions**

*Abstract:* A genetic study to determine the population structure of minke whales *Balaenoptera acutorostrata* in Greenland, the Central and NE Atlantic and the North Sea was carried out on a sample of 306 individuals. Samples were analysed by sequencing the D-loop in mtDNA and

using 16 polymorphic nuclear microsatellite markers. Muscle samples from a total of 154 minke whales, caught between 6 May and 31 October 1998 by Greenland and Norwegian licensed whalers within 6 areas of the North Atlantic, were analysed (West Greenland,  $n = 44$ ; Jan Mayen,  $n = 24$ ; Svalbard,  $n = 16$ ; the Barents Sea,  $n = 33$ ; Vesterålen/Lofoten on the coast of northwestern Norway,  $n = 14$ , and the North Sea,  $n = 23$ ). In addition, 30 minke whales sampled in East Greenland during 1996, 1997 and 1999 were included. Furthermore, 122 minke whales caught in West Greenland in 3 different years (1982, 1996 and 1997) were analysed to determine potential inter-annual variation within a sampling area. The lack of inter-annual variation in West Greenland suggests that the minke whales summering in the area year after year belong to the same sub-population. The study indicated the existence of 4 genetically differentiated sub-populations: (1) West Greenland, (2) Central North Atlantic-East Greenland-Jan Mayen area, (3) NE Atlantic (Svalbard, the Barents Sea and northwestern Norway), and (4) North Sea. It is suggested that these sub-populations have been isolated by discontinuities between regions, i.e. each of the sub-populations has evolved in response to regional differences in ecological conditions (oceanography, ice cover, prey type and prey availability).

**Born et al. 2003: Population substructure of North Atlantic minke whales (*Balaenoptera acutorostrata*) inferred from regional variation of elemental and stable isotopic signatures in tissues**

*Abstract:* Information on population structure is essential for estimating population demographics and managing the impacts of exploitation of North Atlantic minke whales (*Balaenoptera acutorostrata*). New approaches including assessment of geochemical signatures in tissues can assist in defining such structure.

This study determined regional variations in long-term elemental diagnostics of stock differences among 159 minke whales harvested in West Greenland, the Northeast Atlantic Ocean and the North Sea in 1998. The diagnostics tested included mercury (Hg), selenium (Se) and cadmium (Cd) in various tissues, and the trace and major element composition of baleen. Supporting data was also gathered on  $\delta^{15}\text{N}$  and  $\delta^{13}\text{C}$  and stable lead isotope ratios.

For female whales, significant differences in at least one long-term diagnostic element occurred between several areas. Existence of the following population substructure was inferred: (a) West Greenland, (b) a central group represented by whales from Jan Mayen, (c) a northeastern stock encompassing the Barents Sea, Svalbard and coastal Norway, and (d) the North Sea. These groups were consistent with those defined genetically by Andersen et al. [Mar. Ecol., Prog. Ser. 247 (2003) 263]. Males appeared to fall into similar groupings to females but because of smaller sample sizes fewer significant differences occurred between areas.

Stable-isotopic values in minke whales suggested lower trophic-level feeding in this species than hitherto suspected, with significant dietary differences between areas. Variations in feeding habits appeared to explain part of the geographical variation in tissue Cd, but not tissue Hg or Se.

**Born et al. 2007: A multi-elemental approach to identification of subpopulations of North Atlantic minke whales *Balaenoptera acutorostrata***

*Abstract:* A combination of heavy metals, organochlorines (OC) and fatty acids (FA) that reflect long-term deposition (1+ year) in tissues was used in a Canonical Discriminant Analysis (CDA) exploring population substructure in 104 minke whales *Balaenoptera acutorostrata* that were sampled in West Greenland, the Central and Northeast Atlantic Sea and in the North Sea in 1998. Using a CDA that included mercury and cadmium in muscle, liver and kidney, and eight OCs and four subpopulations: 1) a West Greenland group, 2) a Central Atlantic group represented by whales from Jan Mayen, 3) a Northeast Atlantic group (Svalbard, Barents Sea and northwestern Norway), and 4) a North Sea group. During an assignment test based on the data transformation developed by the CDA, about 84% of the individuals were correctly assigned to the area where they had been caught. The highest degree of misassignment was between Jan Mayen and the Northeast Atlantic groups. The differences among the four groups likely reflected regional differences (i.e. sea water chemistry, prey type and prey availability) among the marine ecosystems within the range studied. The study indicated that a multi-elemental approach based on long-term deposited compounds with different ecological and physiological pathways can be used for identification of subpopulations of marine mammals.

**SC/60/PFI10, Pampoulie et al. 2008: Genetic structure of the North Atlantic common minke whale (*Balaenoptera acutorostrata*) at feeding grounds: a microsatellite loci and mtDNA analysis**

*Abstract:* The common minke whale (*Balaenoptera acutorostrata*) is widely distributed in the North Atlantic and is frequently observed along the Icelandic, Norwegian and Portugal coasts, in eastern Canada, North Sea and Greenland, and around Jan Mayen and Svalbard islands. Traditionally, the management of the North Atlantic common minke whales has been based on four geographical subdivisions partitioned by the international Whaling Commission, namely the Canadian East coast stock, the West Greenland stock, the Central stock (Iceland) and the Northeastern stock (Norway). These management regions have been primarily established through studies based on catch statistics, biological characteristics and tagging. Lately, genetic studies tend to confirm the established subdivisions.

The primary goal of the present study was to assess the genetic variation of North Atlantic common minke whales collected at different geographical regions using 16 microsatellite loci and mtDNA sequencing. Both genetic markers gave congruent results and did not show significant genetic signals among the samples collected. In addition, two distinct groups of haplotypes were detected and there was a lack of concordance between geographic and phylogenetic position of mtDNA haplotypes. Together these results suggested the presence of two breeding sites based on the two haplotypes groups detected but a lack of genetic structure of the North Atlantic minke whale at feeding grounds.

## **Anderwald et al. 2011: Possible cryptic stock structure for minke whales in the North Atlantic: Implications for conservation and management**

*Abstract:* The minke whale is the last of the great whale species to be hunted in significant numbers. Effective management must include an understanding of how genetic diversity is divided and distributed among putative local populations, and as for many migratory species, this is complicated for the minke whale by large-scale seasonal movement among geographic regions. The problem is that the geographic identity of breeding populations is not known, and instead these whales are predictably found and hunted where different breeding stocks may mix on seasonal feeding grounds. Here we use microsatellite DNA and mtDNA markers to investigate minke whale population structure across the species range in the North Atlantic. We found no evidence of geographic structure comparing putative populations in recognized management areas, though some limited structure had been indicated in earlier studies. However, using individual genotypes and likelihood assignment methods, we identified two putative cryptic stocks distributed across the North Atlantic in similar proportions in different regions. Some differences in the proportional representation of these populations may explain some of the apparent differentiation between regions detected previously. The implication would be that minke whales range extensively across the North Atlantic seasonally, but segregate to some extent on at least two breeding grounds. This means that established stock boundaries in the North Atlantic, currently used for management, should be re-considered to ensure the effective conservation of genetic diversity.

## **SC/57/O9, Vikingsson and Heide-Jørgensen 2005: A note on the movements of minke whales tracked by satellite in Icelandic waters in 2001 - 2004**

*Abstract:* This note gives a brief account of experiments to track the movements of common minke whales in Icelandic waters during 2001-2004. We were able to track the movements of three individuals out of Icelandic waters during autumn. Signals were received from one minke whale off the west coast of Africa in early December 2004, 101 days after tagging and 377km from the tagging site off SW Iceland.

## **ASSESSMENT**

Owing to the issue with female biased catches there is so far no accepted method for the assessment of minke whales in West Greenland.

## **ABUNDANCE DATA**

Agreed abundance estimates for West Greenland minke whales are listed in Table 1. Other abundance information include a 2007 estimate of 5,675 (CV:0.24) minke whales in Canadian waters (NAMMCO 2010, 2011).

Year	$N$	$I$
1984	–	446 (36)
1985	–	198 (38)
1987	–	297 (31)
1988	–	1841 (37)
1987/8	3,266 (31)	–
1989	–	636 (37)
1993	8,371 (43)	1055 (86)
2005	10,792 (59)	663 (33)
2007	16,610 (43)	1365 (25)

Table 1: **Abundance** estimates from West Greenland with CV in parenthesis (given in %).  $N$  absolute estimates; 1987/88, 1993 and 2005 cue count estimates; 2007: fully corrected line-transect estimate.  $I$  time series of relative abundance. Data from Larsen (1995), Heide-Jørgensen and Laidre (2008), Heide-Jørgensen et al. (2008), and Heide-Jørgensen et al. (2010).

## TRIAL STRUCTURE

### RMP trial structure

The sub-areas (small areas) applied in the RMP Implementation Trials for North Atlantic minke whales are shown in Figures 1 and 2. Following the recommendations from IWC (2004), minke whales in the North Atlantic are assumed to belong to three stocks; a western, central and eastern stock. The western stock is divided into two small areas (WC and WG), the central stock into four small areas (CG, CIP, CIC and CM), and the eastern stock into the four small areas ES, EB, EW and EN.

Relating to the underlying structure of the catch mixing matrix ( $V$ ) for West Greenland (small area WG), the standard catch mixing matrix from IWC (1993) assumes that only 24% of the minke whales that belong to the WG sub-stock are exposed to hunting in the WG sub-area, while 33% are exposed to hunting in the Canadian WC sub-area, 10% in the CIP sub-area, and the remaining 33% to hunting in the CG sub-area. For the minke whales that belong to the WC sub-stock, 50% are assumed to be exposed to hunting in the WG sub-area, while the remaining 50% are hunted in the WC sub-area. Furthermore, 10% of the CIP sub-stock and 6% of the CG sub-stock are assumed hunted in WG.

The sighting survey mixing matrix ( $W$ ) in IWC (1993) assumed that all the whales that belong to the WG sub-stock are counted in the WG sub-area. It is also assumed that 50% of the whales that belong to the WC sub-stock, and 10% of the whales that belong to the CG sub-stock, are counted in the WG management sub-area.

It is unclear why it has been assumed that all WG whales are in the WG sub-area when they are surveyed, while only 24% of them are assumed to be in the same area when they are hunted. Given the general lack of evidence on the possible presence of discrete stock boundaries in North Atlantic minke whales, and the lack of evidence on the possible geographical locations of such postulated boundaries, it seems difficult, if not impossible, to comment on the relevance and completeness of the assumption that West Greenland minke whales belong to a common breeding

stock with Canadian minke whales, while East Greenland minke whales belong to another central Atlantic breeding stock. It would instead be much easier and more informative to comment on a model that is based on summer aggregations only, without additional hypothetical assumptions on the underlying breeding structure.

### Summer aggregations

A transition to a summer aggregation model should be relatively easily done within the present framework; the main requirement being that the underlying population dynamic models are constructed for each of the summer aggregations. The default assumption on the survey and catch mixing matrixes would be the unitary matrix, or a close approximation of it, to reflect that surveys are carried out, and catches taken, during the summer feeding period. If no dispersal is assumed, this model would in effect resemble a model with different isolated stocks. It is, however, recommended that the stock term is not associated with these units, and this is because we want to make no explicit assumptions on breeding structure. In our absence of knowledge of unique breeding units to preserve, our management model need only reflect, in the best way possible, the population dynamics of our management units.

While generally being a conservative approach, an assumption of no permanent dispersal between summer aggregations is likely not completely true, and the allowance of density dependent dispersal between summer aggregations may have to be added, e.g., between West Greenland and East Greenland. Furthermore, as the birth sex ratio in minke whales is even, a sex biased redistribution of individuals when they become independent of their mothers may have to be included in order to make models that are consistent with the often uneven occurrence of males and females in the different management areas. To illustrate this in relation to West Greenland, let density regulation affect the birth rate and let it be defined at the sub-area level

$$b_t^k = b^* + [b_{\max} - b^*][1 - (d_t^k)^\gamma] \quad (1)$$

where  $b_t^k$  is the birth rate in year  $t$  in sub-area  $k$ ,  $b^*$  is the birth rate at carrying capacity,  $b_{\max}$  the maximal birth rate, and  $d_t^k$  the depletion ratio in sub-area  $k$  at time  $t$ . The number of age-class zero individuals (newborns) in sub-area  $k$  at time  $t$  is then

$$N_{0,t}^k = b_t^k N_{m,t}^{k,f} \quad (2)$$

where  $N_{m,t}^{k,f}$  is the number of mature ( $m$ ) females ( $f$ ) in sub-area  $k$ . Assume an even sex ratio at birth so that  $N_{0,t}^{k,f} = N_{0,t}^k/2$  and  $N_{0,t}^{k,m} = N_{0,t}^k - N_{0,t}^{k,f}$ , with superscript  $m$  denoting males.

Now let  $\vartheta$  be a constant that defines the equilibrium (all relevant sub-areas at carrying capacity) fraction of females in the 1+-component of the whales in the West Greenland sub-area. Given the historical catches in West Greenland we expect that  $\vartheta$  will have a value round 0.7. Above it is assumed that age-class zero individuals stay with their mothers, and now let us make the assumption that offspring redistribute themselves at the age of one in relation to the constant  $\vartheta$  and the relative densities of individuals in the different areas. If we assume that no age-class zero individuals are harvested, the total number of age class one individuals at time

$t + 1$  of the female or male gender ( $g$ ) is

$$N_{1,t+1}^g = \sum_k s_0^k N_{0,t}^{k,g} \quad (3)$$

where  $s_0^k$  is the survival rate of age-class zero individuals in sub-area  $k$ , with the total number of age-class one individuals being  $N_{1,t+1} = N_{1,t+1}^f + N_{1,t+1}^m$ . These may distribute themselves in accordance with the relative abundance of the 2+ individuals in the different sub-areas, so that the number of age-class one individuals in sub-area  $\dot{k}$  is

$$N_{1,t+1}^{\dot{k}} = N_{1,t+1} \frac{N_{2+,t+1}^{\dot{k}}}{\sum_k N_{2+,t+1}^k} \quad (4)$$

Hence the number of age-class one females in sub-area WG, denoted  $w$  for simplicity here, is

$$N_{1,t+1}^{w,f} = \vartheta N_{1,t+1}^w \quad (5)$$

and the number of males  $N_{1,t+1}^{w,m} = N_{1,t+1}^w - N_{1,t+1}^{w,f}$ . The number of age-class one females in any other sub-area is then

$$N_{1,t+1}^{k \neq w,f} = \frac{N_{1,t+1}^f - N_{1,t+1}^{w,f}}{N_{1,t+1} - N_{1,t+1}^{w,f} - N_{1,t+1}^{w,m}} N_{1,t+1}^k \quad (6)$$

and the number of males  $N_{1,t+1}^{k \neq w,m} = N_{1,t+1}^k - N_{1,t+1}^{k,f}$ .

So far, offspring follow their mothers, and age-class one individuals re-distribute themselves according to the relative abundance in the different areas, and the equilibrium female fraction in West Greenland. For 2+ individuals we assume that they stay in the same sub-area unless they disperse to another sub-area, with the number of dispersing individuals being determined by the sex specific depletion in each area. Hence, the number of age-class  $a$  individuals ( $a > 2$ ) of a gender  $g$  in sub-area  $\dot{k}$  can be given as

$$N_{t+1,a}^{g,\dot{k}} = \left( 1 - \sum_{k \neq \dot{k}} D_t^{g,k \rightarrow \dot{k}} \right) \left( N_{t,a-1}^{g,\dot{k}} - C_{t,a-1}^{g,\dot{k}} \right) s_{a-1}^{\dot{k}} + \sum_{k \neq \dot{k}} D_t^{g,k \rightarrow \dot{k}} \left( N_{t,a-1}^{g,k} - C_{t,a-1}^{g,k} \right) s_{a-1}^k \quad (7)$$

where  $D_t^{g,k \rightarrow \dot{k}}$  is the dispersal of gender  $g$  individuals from sub-area  $k$  into sub-area  $\dot{k}$ , which may be defined as

$$D_t^{g,k \rightarrow \dot{k}} = \max[0, \alpha^{k \rightarrow \dot{k}} \log(d_t^{g,k} / d_t^{g,\dot{k}})] \quad (8)$$

Note that the dispersal of a gender  $g$  from sub-area  $k$  into sub-area  $\dot{k}$  is zero whenever the depletion ratio of that gender in sub-area  $\dot{k}$  is larger than or equal to the depletion ratio of that gender in sub-area  $k$ . The only extra parameters to be defined relative to the case with independent dynamics in each sub-area are the West Greenland equilibrium fraction of females  $\vartheta$ , and the dispersal parameters  $\alpha^{k \rightarrow \dot{k}}$ .

## Population dynamic model

Unlike the cases for West Greenland humpback (AWMP13) and bowhead whales (AWMP14), as well as for North Atlantic fin whales (AWMP12), I found no studies that would inform us on the current application of the density regulated model to the population dynamics of North Atlantic minke whales.

## MSYR and biological parameters

No attempts were made so far to look into the most likely parameter space for the msyr and biological parameter like age of maturity, birth rate, and survival.

## Need envelopes

The need envelopes to be considered for West Greenland minke whales should probably not be smaller than flat 200, and they should include also a medium and high option. A final settlement for this will have to reflect and agreed approach by the AWMP group relating to an overall need envelope on edible products across all species of large whales and, dependent upon this agreement, a discussion with the Greenlandic delegation relating to an expected and a maximal possible envelope.

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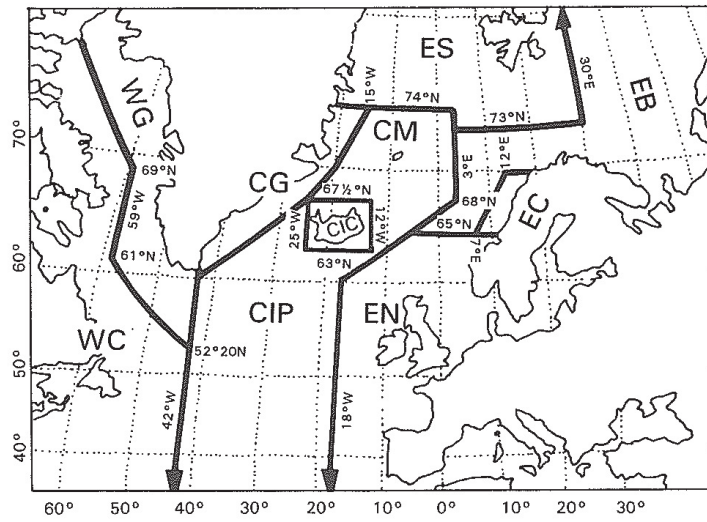


Figure 1: Map of the North Atlantic showing the sub-areas (small areas) defined for the North Atlantic minke whales in 1993. From IWC (1993).

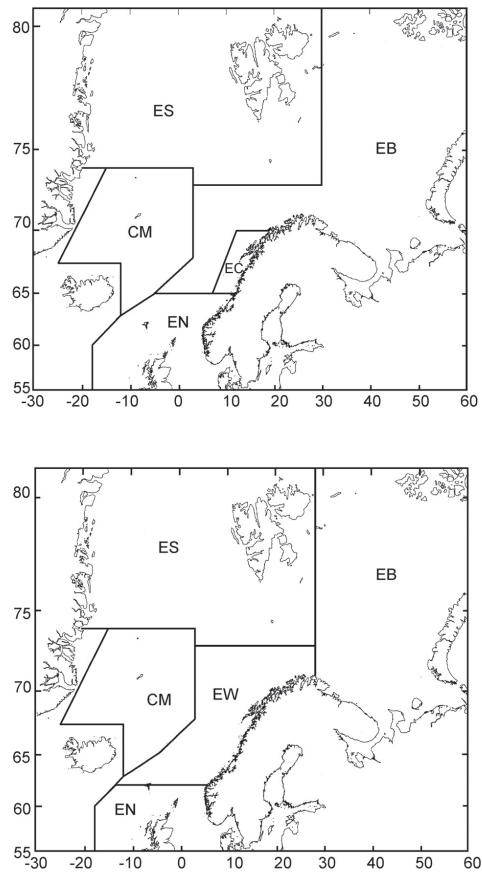


Figure 2: Map of the central and eastern North Atlantic showing the proposed redefined small areas for North Atlantic minke whales in 2004. Top figure: old areas. Bottom figure: new areas. From IWC (2004).