

# Time trend in Discovery mark returns from North Atlantic fin whales in the EG small-area in relation to IST stock structure hypothesis IV.

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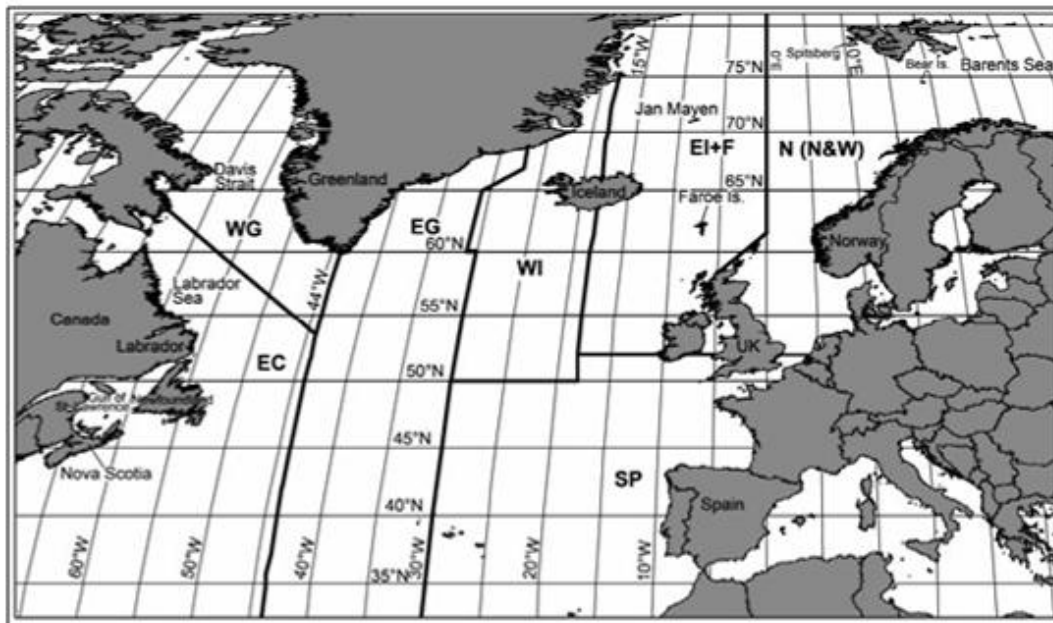
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## ABSTRACT

The best fit of a model to Discovery mark returns according to stock structure hypothesis IV for NA fin whales is obtained when the estimate of the abundance in the EG area is only a fraction of the WI area abundance (0.15). When the ratio of the EG to WI abundance is bound within the range observed in sighting surveys (1.43, std. 0.10) the 5% mixing of the breeding stocks assumed in these areas under the hypothesis is significantly too low and even when the abundance ratio is as low as 0.64. The estimated mixing is 16.5% or higher when the abundance ratio in the areas is set to 1 or higher. A model with dispersion fits the data significantly better than the 5% mixing hypothesis, and better than estimated mixing for any abundance ratio in the areas of 0.54 or higher. The low estimate of natural survival obtained, further implies that dispersion is not just between these two areas but also to other areas. The absolute abundance estimates from sighting surveys refer to larger areas than the marking areas, which explains the poor fit obtained in IST trials.

## INTRODUCTION

At the last meeting a mixing model was fitted to Discovery mark-recapture data (Gunnlaugsson *et al.* 2010, Appendix 3). A significantly better fit was obtained when the annual natural survival was allowed to differ in the two areas with markings, off West Iceland (WI) and East Greenland (EG). This difference in  $S$  as estimated by area was interpreted as an indication that the assumption of constant mixing in the North Atlantic Implementation Simulation Trials (IST) stock structure hypothesis IV is wrong. The SC requested further analysis of the data in this respect. Here this analysis is refined and compared to a model with dispersion.



**Figure 1.** Map of the North Atlantic showing the fin whale Small Areas.

### Basic features of hypothesis IV

Hypothesis IV differs from the others hypotheses in that it assumes that there is no interchange between the three sub-stocks in the central North Atlantic at the breeding areas. The hypothesis assumes that the fin whales feeding west of Iceland (WI small-area) are 90% of an isolated breeding sub-stock (C2) and 5% of each of separate breeding sub-stocks (C1 and C3) that feed mainly on each side of the WI area in the East Greenland (EG) and East Iceland Faroes (EIF) small-areas. Similarly 5% of the C2 breeding sub-stock goes to these areas on each side of the WI area to feed. According to the hypothesis the visiting whales have no memory next year of where they were the year before and do not change their foraging behaviour in response to changes in density of whales and/or prey in any one feeding area but will go back to their native feeding area 95% of the time next year.

Neither of these assumptions is based on any data. There is a lack of genetic structure in the North Atlantic (Pampoulie *et al.* 2008). Breeding sites are unknown, but the whales must be breeding in the deep waters in the open ocean with no geographic barriers. The history of the stock indicates that it recovered quickly in depleted areas. There are no references or data to support the permanently fixed proportional site fidelity of hypothesis IV in whale foraging behaviour. If the C2 breeding component would get exterminated then hypothesis IV predicts that 5% of breeding stocks C1 and C3 would continue to visit the area, but there would be no density response within the area such that it would ever come close to the original density. Such behaviour would have grave consequences for the species in case of anticipated environmental changes.

### MATERIAL

One Discovery mark placed at Canada in 1979 (total about 400, 1965-1979) was recovered at West Iceland (Sigurjónsson *et al.* 1991). This WI recovery from Canada was 9 years after marking and fits well in with gradual dispersal between neighbouring areas. No interchange, direct or indirect, is assumed between these areas under Hypothesis IV so this recovery can not be included.

Two instances have been observed of within season movement between WI and EG areas. One is a radio tagging experiment in 1980 (Watkins *et al.* 1984) where a whale was followed from west off Iceland to East Greenland in the course of a week. Only two such experiments were conducted lasting 2-3 weeks each. The second observation is the reverse where one Discovery mark placed at coastal East Greenland (of a total of 65 there) was found in the catch in Iceland a week later in 1968 (Sigurjónsson and Gunnlaugsson 1985). As same season recoveries are generally not included in mark-recapture analysis, neither of these observations have been included in the IST model test data, but would support higher rates of mixing.

The observations mentioned above are also not used here and same season recoveries are excluded. The data used is given in table 1, recoveries by year after marking for up to 10 years (longest recovery) from Discovery markings in WI (I) and EG (G) small-areas (Gunnlaugsson and Víkingsson 2008). All catches (recoveries) are from the whaling grounds in the WI area. A few markings north-east of Iceland and at the Faroe Islands in the IEF small-area with no recovery were left out. There are no other observations of mixing between these areas and the mixing postulated by hypothesis IV between WI and EIF is ignored here. An estimate of the abundance in the WI area under hypothesis IV when ignoring the assumed 5% EIF mixing would be around 5% too high.

The roughly 200 markings in the WI small-area were all well within the reach of the operation (farthest south 62°20') and all (except 3 that were further east along the south coast with no recovery) concentrated in the general area of the operation. The roughly 100 markings in the EG small-area either took place just west of the boundary between the WI and EG small-areas or along the ice edge and shelf edge off Greenland where density was believed to be highest and marking cruises were thus conducted. In sighting surveys that started after the marking episode the observed distribution is however rather even also over the deep waters. Although densities decline to the South (south of 60°N), the area there is also large so a large part of the total abundance comes from there.

### METHODS

A Binomial Logit model with weight  $n$  (number of observations) was presented last year (Gunnlaugsson *et al.* 2010 appendix 3) using the R-package. This analysis was repeated using ADMB and adopting a Poisson approximation for the recoveries which are very few compared to the number of observations. Here  $d$  is the years since marking and  $a$  indexes the areas. The number of recoveries  $d$  years after marking in each area is  $r_{d,a}$ . The number of observations  $d$  years after marking  $n_{d,a}$  is the sum of catch times remaining marks  $\sum(c \cdot m)$  over all marking experiments  $d$  years after marking.  $S$  is annual natural survival ( $1-M$ ) not including fishing mortality, since that is accounted for by updating the remaining marks with recoveries.  $N_a$  is the abundance in each area at the time of marking.

**Mixing model**

$$r_{d,W}/n_{d,W} \sim S^d Q/N_1$$

$$r_{d,G}/n_{d,G} \sim S^d (1-Q)/N_G$$

where  $Q$  is the proportion of the animals in the catch (all taken in the WI area) that were around then and in the WI area, so  $1-Q$  is the proportion from other areas, that is the EG area. The mixing is assumed random each year, but constant over time, and therefore the  $Q$  can not be separated from the abundance  $N_a$  in each area. The model was therefore not initially presented as such. Either the mixing has to be specified or for instance the ratio of the abundance in the areas. When the mixing is  $b$  the abundance in the areas can be related to the size of the breeding stocks  $B_1=C_2/$  and  $B_G=C_1/$  by  $N_1=(1-b) \cdot B_1 + b \cdot B_G$  and  $N_G=(1-b) \cdot B_G + b \cdot B_1$  and  $Q=((1-b)^2 \cdot B_1 + b^2 \cdot B_G)/N_1$

**Dispersion model**

$$r_{d,W}/n_{d,W} \sim S^d Q_d/N_1$$

$$r_{d,G}/n_{d,G} \sim S^d (1-Q_d)/N_G$$

where  $Q_d$  is the probability that an animal marked in the WI area is found there  $d$  years later so  $Q_1=1-b$  and  $b$  is the annual dispersion rate from the WI area. This must be balanced by animals dispersing into the area from the EG area and then some dispersing back so  $Q_{d+1}=(1-b)Q_d+(1-Q_d)b \cdot N_1/N_G$

**RESULTS**

Table 1 gives the AICc for the mixing and dispersal models. The IACc differs by 2 for these models. Also shown are the results for the mixing model with survival ( $S$ ) estimated by areas, but survival had a lower limit of 0.04. Allowing different survival by area in the dispersal model made little difference and is not included. The estimates of abundance refer to year 0 after marking and as the markings and catches in the WI area are in almost the same limited area concentrated on the whaling grounds and temporary site fidelity has been shown even within these markings (Gunnlaugsson and Víkingsson 2006), the estimate of abundance there may be considered to refer only to a part of the animals in the WI area and is therefore not unreasonable when compared to estimates from sighting surveys (table 4) and the estimate obtained from relatedness (Skaug *et al.* 2006; Skaug *et al.* 2008; Gunnlaugsson *et al.* 2010; Pampoulie *et al.* 2011 this meeting SC/63/RMP1). Although the markings in the EG area are also limited to the northern part of the area, these recaptures are not in the same area as the markings so this argument is not as valid there, but the EG abundance estimate from the mixing model with the postulated mixing in hypothesis IV of 0.05 is very low and much lower than the WI estimate, whereas the reverse is observed in sighting surveys. Estimates from sighting surveys may be biased, but that bias should be the same in both areas. Table 2 shows the results for the mixing model when instead of fixing the mixing ( $b$ ), the abundance ratio ( $N_G/N_1$ ) is fixed at the value estimated in the dispersal model and the average value from sightings surveys (table 4). In both cases the mixing is significantly higher than 0.05. This is true for any ratio over 0.64 (Chi-square test on LL change).

Expected recoveries by year after marking for both the models unconstrained are shown in table 3.

**DISCUSSION**

Analyses of Discovery markings have been considered unreliable due to problematic factors. These are possible misjudgement of mark success, mark mortality, initial mark loss, mark shedding and lack of returns, all of which should lead to fewer mark-recoveries. It is therefore noticeable that the recoveries from the Discovery markings are initially higher, as seen by a lower simple mark-recapture estimate of around 3,000 based on 1-3 year returns (Gunnlaugsson and Sigurjónsson 1989), than those observed from the relatedness samples in the same period (Gunnlaugsson *et al.* 2010). The problematic factors should not affect differently the recovery rate from the areas, except when updating the remaining marks by subtracting the recoveries, where there could be increasingly too many marks assumed left in the external area, where recoveries were few. We tested for the sensitivity to this by preparing another input file where markings were reduced initially by 20% but found this to have a negligible effect on the results.

The markings in the EG area are quite limited spatially to the northern boundary of the area. With the assumption of gradual dispersion between the small-areas one would not expect immediate mixing within these areas either, but rather gradual dispersion everywhere over the larger area. In fact the recoveries with the longest delay (9 and 10 years) are precisely those recoveries that come from farthest west in the EG area. Short term site fidelity was also detected from markings within the WI area (Gunnlaugsson and Víkingsson 2008). With the limited data available other areas can not be modelled as the dispersion into other areas would not be separated from the natural mortality. The low estimate of survival could be explained to some extent by mark shedding,

but double markings (Sigurjónsson *et al.* 1991) and late recoveries from external areas do not support that this is substantial. More likely this indicates that dispersion to the southern parts of the areas, or to other areas is substantial. The late recovery west off Iceland of a whale marked in Canadian waters (not included here) is in full agreement with the dispersion model, but can not be accounted for in the mixing model.

The markings and recoveries are only from the northern parts of the small areas. As seen from the first lines in table 1 the fit to the abundance estimates from sighting surveys for the whole areas is very poor. This explains why results obtained in the IST runs, where these abundances are fitted, are insignificant.

The high degree of mixing obtained with a reasonable ratio of the abundance in the areas is further supported by other data that are not included here such as the same season recovery of a whale marked at East Greenland, and that out of just two tagging experiments at West Iceland one moved over to East Greenland.

## CONCLUSION

With reasonable assumptions on the abundance ratio in the areas, the mixing model only fits the marking data if the mixing is significantly higher than 5%, but a dispersion model fits this data considerably better. This is in agreement with other aspects of this data and the additional data not fitted in these models.

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Table 1. AICc for models with mixing or dispersal (*b*), mixing according to Hypothesis IV (HIV=0.05), abundance from surveys and survival (*S*) estimated by area. Log likelihood (LL) not including constant term. Fixed parameters in mixing model are starred\*. Estimates at lower bound marked with #. *k*: number of estimated parameters. (n=20)

AICc	k	LL	<i>b</i>	$N_G/N_I$	$N_I$	$\ln(S_I)$	$\ln(S_G)$	Model
-4.742	1	3.482	0.05*	1.43*	6,432*	-0.04#		HIV mixing, survey abundances
-6.120	2	5.413	0.107	1.43*	6,432*	-0.04#		Est mixing, survey abundances
-21.880	2	13.293	0.05*	0.09	6,432*	-0.04#		HIV mixing, WI survey abundance
-22.742	2	13.724	0.05*	1.43*	2,250	-0.139		HIV mixing, survey ratio
-29.750	3	18.625	0.05*	0.15	2,700	-0.148		HIV mixing
-30.779	4	20.723	-	-	-	-0.250	-.04#	Est mixing, S by area
-31.753	4	21.210	0.06	0.84	2,311	-0.145		Dispersion

Table 2. Mixing fixed (\*) or estimated with assumptions (\*) about the abundance ratio as estimated with dispersion and as observed in sighting surveys. (LL=18.625, k=3, n=20)

<i>b</i>	s.d. <i>b</i>	$N_G / N_I$	$N_I$
0.05*	-	0.15	2,700
0.160	0.057	0.84*	2,130
0.177	0.057	1.43*	1,850

Table 3. Discovery mark returns (*r*) and the catch times marks remaining (*c·m*) summed over all marking experiments and given by year after marking (*d*) and by small-areas. Also given are expected recoveries according to unconstrained mixing (mix, k=3) and dispersion (disp, k=4) models.

Area:		WI				EG			
<i>D</i>		<i>c·m</i>	<i>r</i>	<i>mix</i>	<i>disp</i>	<i>c·m</i>	<i>r</i>	<i>mix</i>	<i>disp</i>
1		35243	12	10.66	12.37	18337	1	2.12	0.64
2		30316	9	7.90	8.51	14426	1	1.44	0.88
3		26221	6	5.89	5.83	13853	0	1.19	1.11
4		20741	6	4.02	3.62	12797	2	0.95	1.20
5		16862	0	2.81	2.27	11273	1	0.72	1.16
6		15401	1	2.22	1.57	9340	0	0.51	1.01
7		12171	2	1.51	0.92	8408	0	0.40	0.93
8		9496	1	1.01	0.51	8514	1	0.35	0.95
9		5792	0	0.54	0.21	5186	1	0.18	0.57
10		5128	0	0.41	0.11	4688	1	0.14	0.50

Table 4. Total abundance and C.V. for the WI and EG areas from sighting surveys. The C.V. of the ratio is uncorrected for correlation within survey so expectedly too large.

Year	WI	C.V.	EG	C.V.	EG/WI	C.V.
1988	4,243	0.229	5,269	0.221	1.24	0.32
1995	6,800	0.218	8,412	0.288	1.24	0.36
2001	6,565	0.194	11,706	0.194	1.78	0.27
2007	8,118	0.26	12,214	0.20	1.50	0.33
Mean	6,432	0.113	9,400	0.114	1.46	0.16
Arithmetic mean and observed C.V.					1.43	0.10

