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Information of relevance on Evaluation Trials for West Greenland fin whales

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ABSTRACT
The development of a Strike Limit Algorithm (SLA) for fin 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 fin whales (IWC 2010). These trials consider a set of seven stock structure hypotheses, and Punt (2012) showed how the RMP trials could be modified for the evaluation of a SLA for West Greenland fin whales. In this paper I summaries what is known on the stock structure in North Atlantic fin whales, and I look into the population dynamics of North Atlantic fin whales and the dynamics assumed in the RMP trials, in order to provide information and discussions for the construction of Evaluation Trials for an SLA for the harvest of fin whales in West Greenland.

STOCK STRUCTURE

The selection of abstract below summarise what is known about the stock structure in North Atlantic fin whales. In general there is some differentiation on an ocean basis, indicating some degree of separation between fin whales summering in the western, central and eastern North Atlantic, although the actual level of genetic divergence is very low. Current migration rates may be a relevant and meaningful measure, with point estimates revealing that 20 percent or more of individuals in a single area are immigrants. It seems that the differentiation of allozymes is higher than the differentiation in neutral genetic markers, indicating that some degree of differential selection may operate.

Berube et al. 1998: Population genetic structure of North Atlantic, Mediterranean sea and sea of Cortez fin whales *Balaenoptera physalus* (Linnaeus 1758): analysis of mitochondrial and nuclear loci

Abstract: Samples were collected from 407 fin whales, *Balaenoptera physalus*, at four Atlantic and one Mediterranean Sea summer feeding area as well as the Sea of Cortez in the Pacific Ocean. For each sample, the sex, the sequence of the first 288 nucleotides of the mitochondrial (mt) control region and the genotype at six microsatellite loci were determined. A significant degree of divergence was detected at all nuclear and mt loci between North Atlantic/Mediterranean Sea and the Sea of Cortez. However, the divergence time estimated from the mt sequence was substantially lower than the time elapsed since the rise of the Panama Isthmus, suggesting occasional gene flow between the North Pacific and North Atlantic ocean after the separation of the two oceans. Within the North Atlantic and Mediterranean Sea, significant levels of heterogeneity were observed in the mtDNA between the Mediterranean Sea, the eastern (Spain) and the western (the Gulf of Maine and the Gulf of St Lawrence) North Atlantic. Samples collected off West Greenland and Iceland could not be unequivocally assigned to either of the two areas. The homogeneity tests performed using the nuclear data revealed significant levels of divergence only between the Mediterranean Sea and the Gulf of St Lawrence or West Greenland. In conclusion, our results suggest the existence of several recently diverged populations in the North Atlantic and Mediterranean Sea, possibly with some limited gene flow between adjacent populations, a population structure which is consistent with earlier population models proposed by Kellogg, Ingebrigtsen, and Sergeant.

SC/58/PFI8, Danielsdottir et al. 2006: Reanalysis of North Atlantic fin whale allozyme and carbonic anhydrase data

Abstract: The paper presents results of new statistical analyses of three old fin whale allozyme and carbonic anhydrase datasets previously published in Arnason et al. (1992) Danielsdottir et al. (1991b and 1992a). The first dataset is on the genetic variation at 11 variable allozyme loci in 328 fin whales (*Balaenoptera physalus*) sampled in two North Atlantic areas; i.e. off West Iceland and Spain, a total of: 283 (Iceland 1985, 1986, 1987 and 1988) and 46 (Spain 1985) samples, respectively. The data is based on further analysis of genotypes at 11 allozyme loci: *Ada, Ak-1, Gpd, Ldh-A, Mdh-S, Mpi-1, Pep-A, Pgm-1, Pgi and Sod-A*. The new statistical programs applied here include F_{ST}, Confidence Intervals (CI) of F_{ST}, Nm, PCA, MDS, STRUCTURE and graphical illustration of potential populations as in Waples and Gaggiotti (2006). There was significant heterogeneity within each sample and overall samples, all due to heterozygote deficiency. Various genetic analyses on the dataset resulted in significant genetic heterogeneity among the Icelandic and Spanish samples, revealing temporal differences in the Icelandic samples from the years 1981-1988 as well as differences between Icelandic and Spanish samples and few had little overlapping. The level of genetic differentiation was high $(F_{ST}?0.094, 95\%CI0.0400.153, p < 0.0001)$. The CIs of the pairwise F_{ST} varied considerably and were larger in comparisons of larger F_{ST} i.e. between Icelandic and Spanish samples than between Icelandic sample years. This could indicate that the observed level genetic divergence between groups is less than concluded before from the previous results of high F_{ST} and significance between groups, however when considering the lower CI values, all comparisons remained significant. The STRUCTURE analysis indicated 2 groups among the samples. The second dataset (II) is on the allozyme genetic variation of 67 fin whales from three North Atlantic areas; i.e. Newfoundland Canada (n=24), Norway (n=19) and off West Iceland (n=24). There were statistical significant genetic divergences among Newfoundland Canadian, Norwegian and Icelandic samples ($F_{ST} \approx 0.343$, 95% CI was 0.164 - 0.486, $P < 0.0001$). All three F_{ST} pair-wise comparisons varied considerably in their CIs indicating variation in the estimation of significant comparisons from two to all significant comparisons of three made and reducing the earlier level of observed genetic differentiation. The STRUCTURE analysis indicated 3 clusters among the samples. The results from this study based on allozyme loci indicate that the fin whale samples from the feeding grounds off Iceland, Norway, Spain, Greenland and Newfoundland Canada are heterogenous, but genetic divergence is low between groups. The allozyme loci showed heterogeneity within and among the different feeding locations. As previously suggested, there might be variations in herds at feeding locations in the different sample years of Iceland, contributing to the heterogeneity within and among years and feeding locations. The level of genetic differentiation was higher for the allozyme than the microsatellite data (Danielsdottir et al. 2005 and 2006; Berube et al. 1998 and 2006). The third dataset (III) is on the *Ca* locus genotype variation in 1.159 fin whales sampled in two North Atlantic areas; i.e. off Spain (1983 and 1984) and West Iceland (1971,1981-1989), a total of 26 and 1133 samples, respectively. There was heterogeneity in two Icelandic sample years, but no overall significant heterogeneity was observed at this locus within or among samples.

SC/60/PFI11, Pampoulie et al. 2008: Lack of genetic divergence among samples of the North Atlantic Fin Whale collected at feeding grounds: congruence among microsatellite loci and mtDNA in the new Icelandic dataset

Abstract: The main objective of this study was to confirm the level of genetic differentiation observed among samples of fin whale collected at feeding grounds using a new dataset composed of 500 selected individuals genotyped for 15 microsatellite loci and the mtDNA was sequenced. New methods of amplification have been used (especially for the microsatellite loci) to successfully genotyped these selected individuals. Both types of genetic markers employed revealed a lack of genetic differentiation among samples collected and therefore suggest that extensive gene flow might prevail among fin whale population and/or that a recent population expansion of the species occurred. The signal of population expansion detected with the mtDNA might suggest that population of fin whale are not at equilibrium and that further analyses based on this information should be carried out (calculation of potential time of expansion and divergence). However, the comparison of these results to the allozyme data that have been recently submitted revealed that the observed F_{ST} values at the allozyme loci are likely to be due to diversifying selection at different breeding sites that accentuates differences not readily apparent at neutral loci. At neutral markers such as microsatellite loci, in the absence of gene flow, genetic differentiation among populations due to drift and/or mutation will rise given enough time, while selection on non-neutral markers (allozyme) in the absence of gene flow will accentuate differences among populations in a shorter time period, depending on the strength of the selective processes.

SC/58/PFI6, Berube et al. 2006: High rates of gene flow among geographic locations in North Atlantic fin whales (*Balaenoptera physalus*)

Abstract: Our genetic analyses based upon nuclear as well as mitochondrial loci all suggest high levels of gene flow among all North Atlantic sampling areas. While allele or haplotype frequencies may be statistically different among sampling area, the actual level of divergence is *very* low. Therefore the current migration rates [estimated using BayesAss] may be the most relevant and meaningful measure. Our point estimates revealed 20 percent or more of individuals in a single area are immigrants. Such exchange rates are in a range where populations are likely to be demographically correlated, and perhaps should not be viewed as demographically or genetically independent populations. The samples collected off the Faroe Islands proved above average genetically divergent from the remainder of the North Atlantic sample localities. One possible explanation may be some level of pod structure in fin whales, but each pod would have to have large geographic ranges to explain the overall low level of genetic structure across the North Atlantic. The Faroe Island samples differ from the samples collected in other areas by being collected more or less at the same position in and in a very short time (over a few hours). In all other areas only one or two samples may have been collected at the same time and place. Future data analyses and sample collection need take this possibility into consideration.

Our analyses ignored the signal of exponential population expansions detected in the North Atlantic samples by Berube *et al.* (1998). Hence, the high degree of genetic similarity among the North Atlantic sampling areas may be due to recent divergence rather than high gene flow. However, the BayesAss analyses suggest differently. The number of migrants estimated from our F_{ST} estimates is on the order of 30 migrants per generation. While this rate may initially seem much lower, it should be kept in mind that (i) the estimate is an estimate of the effective number of migrants and hence should be related to the effective population size, which may be 6-8 times lower than the census population size.

SC/57/PFI3, Vikingsson and Gunnlaugsson 2005: Stock structure of fin whales (*Balaenoptera physalus*) in the North Atlantic indications from non-genetic data

Abstract: According to the IWC Schedule North Atlantic fin whales are divided into seven management stocks. This division originates in the 1970's and was mainly based on various types of indirect evidence such as distribution of catches, occurrence and length distributions of the catch. In this paper an attempt is made, to summarise the available data on stock structure of North Atlantic fin whales based on nongenetic methods. This includes a wide range of studies based on discovery marking, morphometry, earplug morphology, photo-identification, acoustics and biological parameters. Although each method is rather inconclusive by itself, collectively they indicate a separation between fin whales summering in the western, central and eastern North Atlantic. There also appears to be a more or less isolated stock in the Mediterranean Sea.

SC/58/PFI9, Skaug et al. 2006: Relateness of North Atlantic fin whales

Abstract: A dataset consisting of 15 micro-satellite loci from 226 fin whales from the North Atlantic were screened for related individuals. Five pairs of individuals meet our criterion for being classified as related. For these five pairs we try to infer more precisely the type of relationship from auxiliary information (mtDNA, age, sex, etc.). The results are preliminary. The theoretical basis for the method is outlined.

Heide-Jørgensen et al. 2003: Inshore-offshore movements of two fin whales (*Balaenoptera physalus*) tracked by satellite off West Greenland

Abstract: Two fin whales (*Balaenoptera physalus*) were tagged with satellite linked radio transmitters in a coastal area near Aasiaat in West Greenland and tracked for 76 and 32 days in 2000 and 2001 respectively. In 2000, one whale was tagged on 30 September; it stayed in the tagging area until at least 13 October. On 16 and 17 October it was further south off the coast of West Greenland. On 20 October it had moved approximately 250km southeast to another inshore area. It moved another 100km south along the coast and up to 50km off the coast until 2 November, then appeared back in the area is was located on 20 October until contact was lost on 20 December. In 2001, one whale was tagged on 24 August, it stayed in the coastal area until mid September, where it travelled south along the coast to an area approximately 100km off the coast. From here it continued south to the same inshore area occupied by the whale in 2000. It remained in this area until the last position was received on 25 September. The tracking data suggest a connection between inshore and offshore (> 22km) fin whales and indicates the potential range of fin whales in west Greenland.

Simon et al. 2010: Singing behaviour of fin whales in the Davis Strait with implications for mating, migration and foraging

Abstract: Most baleen whales undertake migrations between low-latitude breeding grounds and high-latitude feeding grounds. Though little is known about the timing of their migration from the Arctic, fin whales are assumed to undertake a similar migratory pattern. To address questions about habitat use and migrations, the acoustic activity of fin whales in Davis Strait, between Greenland and Canada, was monitored continuously for two years using three bottom-moored acoustic recorders. The acoustic power in the fin whale call frequencies peaked in NovemberDecember, showing that fin whales are present in Davis Strait much later in the year than previously expected. The closely timed peaks in song activity and conception time imply that not all fin whales migrate south to mate, but rather start mating at high latitudes rather than or before migrating. Singing activity was strongly linked to daylight hours, suggesting that fin whales might feed during the few daylight hours of the late fall and early Arctic winter. A negative correlation between the advancing sea ice front and power in fin whale frequencies indicates that future changes in sea ice conditions from global warming might change the distribution and migratory patterns of fin whales near the poles.

ASSESSMENT

The latest assessment paper for fin whales off West Greenland is Witting (2008). Assuming an isolated stock it used recent abundance estimates, historical catches starting from 1920, and an age-aggregated and sex-structured population model to examine if the population dynamics of West Greenland fin whales is best described by density regulated growth or by selection-delayed dynamics (earlier referred to as inertia dynamics). Having only three reliable abundance estimates, the abundance data may not reveal the dynamics, although there was strong statistical strong support for the acceptance of selection delayed dynamics and the rejection of density regulated growth. The equilibrium population abundance was estimated to 2,000 (90% CI:$1,400-3,700$) whales, the 2008 depletion ratio to 1.5 (90% CI:$0.67-3.5$), and the exponential growth rate to 0.07 (90% CI:$0.03 - 0.12$).

In order to examine annual growth rates and life-histories in North Atlantic fin whales, I fitted an age- and sex-structured population model with exponential growth to the recent abundance

Year	N_{WG}	N_{EG}	N_{WI}	N_{EIF}
1987	–	–	–	5260 (28)
1988	1100 (35)	5270 (22)	4240 (23)	–
1995	–	10200 (29)	7360 (22)	7170 (29)
2001	–	14200 (19)	7430 (19)	9550 (26)
2005	3230 (44)	–	–	–
2007	4360 (45)	15800 (20)	8900 (26)	–

Table 1: **Abundance** estimates with CV in parenthesis (given in %). WG estimates from IWC (1992), Heide-Jørgensen et al. (2008), and Heide-Jørgensen et al. (2010), and pro-rated estimates for EG, WI and EIF from IWC (2010). The 2007 estimate for EIF is treated as an outlier that is not included in the analysis.

estimates (Table 1) for the West Greenland (WG), East Greenland (EG), West Iceland (WI) and East Iceland/Faroese (EIF) summer aggregations. Applying the best catch series from IWC (2010) and assuming an even sex ratio at birth, I used a Bayesian framework with uniform priors on initial abundance (log scale), first year survival [0.5 to 0.95 of adult survival], the annual birth rate [0.3 to 0.6, from Lockyer and Sigurjonsson 1992], the age of the first reproductive event [5 to 15 years of age, from Lockyer and Sigurjonsson 1992], and the exponential growth rate [typically from -0.05 to 0.1]. All models were initialised in 1978 with a stable age structure. The realised prior and posterior distributions are shown in Figures 1 to 4, and the estimates trajectories in Figure 5. Posterior estimates are given in Table 2.

M		N_0	r	p	p_0	b	a_m	N_t	r_t
WG	$x_{.5}$	.63	.065	.98	.8	.5	7.7	3.7	.065
	$x_{.025}$	.28	.016	.93	.53	.32	5.1	1.9	.016
	$x_{.975}$	1.8	.1	.99	.94	.59	14	7	.1
EG	$x_{.5}$	3.3	.059	.97	.77	.49	8.5	18	.059
	$x_{.025}$	1.9	.031	.93	.52	.32	5.2	13	.031
	$x_{.975}$	5.9	.084	.99	.94	.6	14	24	.084
WI	$x_{.5}$	5.1	.034	.95	.74	.48	9.2	9.4	.034
	$x_{.025}$	3.2	.0043	.91	.51	.31	5.3	6.7	.0043
	$x_{.975}$	8.4	.067	.99	.94	.59	15	14	.067
EI	$x_{.5}$	3.6	.042	.96	.77	.47	9.1	12	.042
	$x_{.025}$	1.5	-0.01	.91	.52	.31	5.2	6	-0.01
	$x_{.975}$	9	.091	.99	.94	.59	15	25	.091

Table 2: **Parameter estimates** for the different models (M). Estimates are given by the median ($x_{.5}$) and the 95% credibility interval ($x_{.025}$ - $x_{.975}$) of the posterior distributions. Abundance is given in thousands, and estimates of N_t and r_t are for 2007.

The point estimate of the annual 1+ growth rate ranged from 3.4% to 6.5% in the four summering aggregations, with an average estimate of 5.0% (95% CI:1.0% – 8.6%). And the point estimate for adult survival ranged from 0.95 to 0.98 with an average estimate of 0.97 (95%

CI: 0.92 – 0.99).

ABUNDANCE DATA

Agreed abundance estimates for West Greenland fin whales are listed in Table 1. Other abundance information include a 2007 estimate of 1,716 (CV:0.40) fin whales in Canadian waters (NAMMCO 2010, 2011).

TRIAL STRUCTURE

Stock structure

The current stock structure hypotheses of the RMP Implementation Simulation Trials (IST) are shown in Figure 7. These trials deal with seven summer feeding aggregations (Figure 6) and seven underlying sets of stock structure hypothesis that are intended to describe how the whales of the summer aggregations are arranged into more or less isolated breeding stock during the winter. The inclusion of both summer and winter aggregations in the model seems unnecessarily complex given that *i*) wintering aggregations of fin whales generally are unknown, that *ii*) there is a lack of knowledge on how the summer and the hypothetical wintering aggregations relate to one another, that *ii*) there is a lack of knowledge on the degree to which different hypothetical wintering aggregations are isolated from one another, and that *iv*) wintering aggregations have no direct relation to our scientific studies, which are all (including surveys and catches) carried out on summer aggregations. It is unclear why it has been considered a necessity that we impose our limited and most likely simplified and maybe erroneous understanding of stock structure in fin whales upon our models of population dynamics.

A simpler structure that only deals with the seven summer aggregations and (permanent) dispersal of whales between them would seem more representative to our study of North Atlantic fin whales. It would deal with the actual system under study without having to postulate hypothetical and arbitrary hypotheses about fin whales during winter, and it would make the population dynamic units of the model equivalent to the units under study. We should note that the summer aggregations of fin whales are also most likely the relevant units that determine the population dynamics of the number of whales in the summer aggregations, simply because the main energetic intake for fin whales, as well as all catches of fin whales, occurs on the summer grounds.

Relating to West Greenland fin whales, six of the stock structure hypotheses of the RMP ISTs assume that West Greenland and East Canada fin whales belong to the same winter breeding stock, with some or none exchange with fin whales in East Greenland and West Iceland. Hypothesis seven assumes instead fin whales in Canada, West Greenland and East Greenland belong to the same sub-stock with some connection to fin whales in West Iceland. Given the lack of evidence on the possible presence of discrete stock boundaries in North Atlantic fin 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 chosen hypotheses. It would instead be possible to make more insightful comments on a model based on summer aggregations only, because this is the scale at which we have data.

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 seven different isolated stocks. It is, however, recommended that the stock term is not associated with these units to reflect the absence of 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 seven 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, at least between some areas like EG and WI, in order to make the model realistic and fitting the data.

Permanent age-structured dispersal in year t relating to unit $\dot{k}$ to and from all other units $k \neq \dot{k}$ would be described as

$$N^{g,\dot{k}}_{t+1,a} = \left(1 - \sum_{k\neq\dot{k}} D_t^{g,\dot{k}\to k}\right)\left(N^{g,\dot{k}}_{t,a-1} - C^{g,\dot{k}}_{t,a-1}\right) s^{\dot{k}}_{a-1} + \sum_{k\neq\dot{k}} D_t^{g,k\to\dot{k}}\left(N^{g,k}_{t,a-1} - C^{g,k}_{t,a-1}\right) s^{k}_{a-1} \qquad (1)$$

where g is gender, C catch, N abundance, and s survival. The dispersal rate could be density and sex dependent like

$$D_t^{g,k\to\dot{k}} = \max[0, \alpha^{k\to\dot{k}} \log(d_t^{g,k}/d_t^{g,\dot{k}})] \qquad (2)$$

where α defines the strength of dispersal, $D_t^{g,k\to\dot{k}}$ describes sex specific dispersal from sub-area k into $\dot{k}$, and $d_t^{g,k}$ is the gender specific depletion ratio is sub-area k at time t.

Relating to West Greenland, it may not be necessary to include permanent dispersal. If associated with a catch and survey mixing matrix of unity, this would essentially make the Evaluation Trials for West Greenland independent of the assumptions on the Implementation Simulation Trials of the RMP.

Population dynamic model

The RMP ISTs apply a density regulated model that is projected from pre-whaling stocks assumed to be in population dynamic equilibrium. This assumption of population dynamics has been found to be unable to explain the long-term dynamics of ENP gray whales, and it seems also not to be the best choice for West Greenland humpback, bowhead and fin whales (see AWMP13, AWMP14, and the assessment section above). The general problem with the density regulated model when applied to the long time-span from pre-whaling up till today is that it is unable to explain the current rate of increase in abundance (it underestimates the rate). Selection-delayed dynamics (Witting 2000, 2002) suggest that this is because exploited populations experience density-dependent natural selection for an increase in the intrinsic growth rate and, thus, also for an increase in carrying capacity. By inspection of Figures 8 and 9 from IWC (2010), it is evident that the RMP ISTs encounter the problem of underestimating the growth in West Greenland, East Greenland, and West Iceland even when the growth rate is at the maximum allowed in the trials (mature msyr of 4%).

An application of the density regulated model on a shorter time scale, as it has been done for ENP gray whales, seems to be a better approach also for North Atlantic fin whales. For West Greenland fin whales, this would require that the current carrying capacity of the density regulated model would have to be set somewhat arbitrary, and the approach used in the trials for interim advice (Figure 10, where current depletion was set to 0.2, 0.5 and 0.8) could be adopted.

MSYR and biological parameters

The RMP ISTs apply a msyr for the mature population component of 2.5% as the base case, and 1% and 4% as the lower and upper limit. These rates are not in good agreement with the average estimate of an annual growth rate of 5.0% (95% CI:1.0% – 8.6%) for the one plus component across the four summer aggregations WG, EG, WI and EIF. For ENP gray whales, the base case assumption on the msyr of the Evaluation Trials was set to the point estimate of 3.5% for a Bayesian assessment. Although the exponential models applied in this paper do not estimate the current depletion ratios for North Atlantic fin whales, the point estimate of an annual one plus growth rate of 5% certainly suggests that a base case assumption of 2.5% mature is too low. A one plus msyr between 3.5% and 4.5% would be more representative.

The conditioning of the RMP ISTs initially assumes an annual natural adult mortality rate of 0.08. This value is not in well agreement with the posterior estimate of an average survival rate of 0.97 (95% CI: $0.92 - 0.99$) across the four summer aggregations of fin whales in the North Atlantic. A readjustment of the mortality rate in the simulation trials would seem appropriate.

Need envelopes

The need envelopes to be considered for West Greenland fin whales should not be smaller than flat twenty, 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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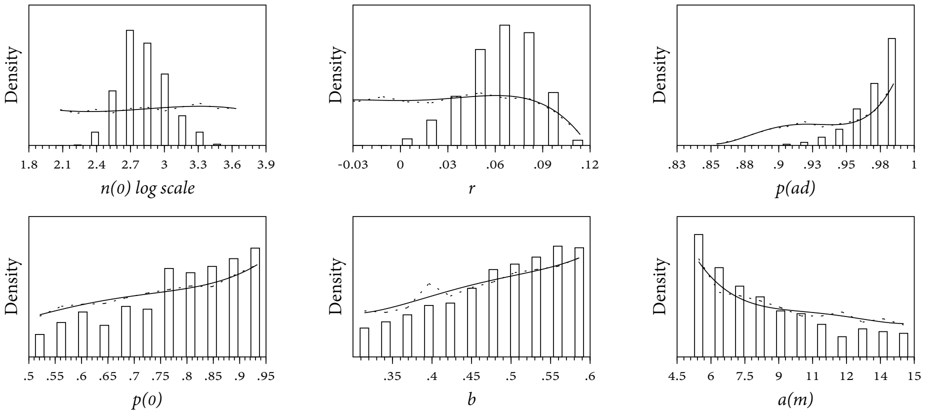


Figure 1: Realised prior and posterior distributions for the age- and sex-structured exponential model for West Greenland fin whales.

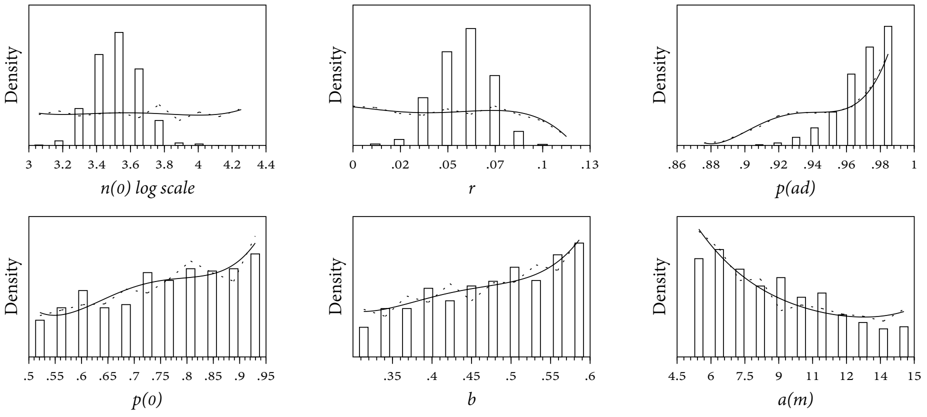


Figure 2: Realised prior and posterior distributions for the age- and sex-structured exponential model for East Greenland fin whales.

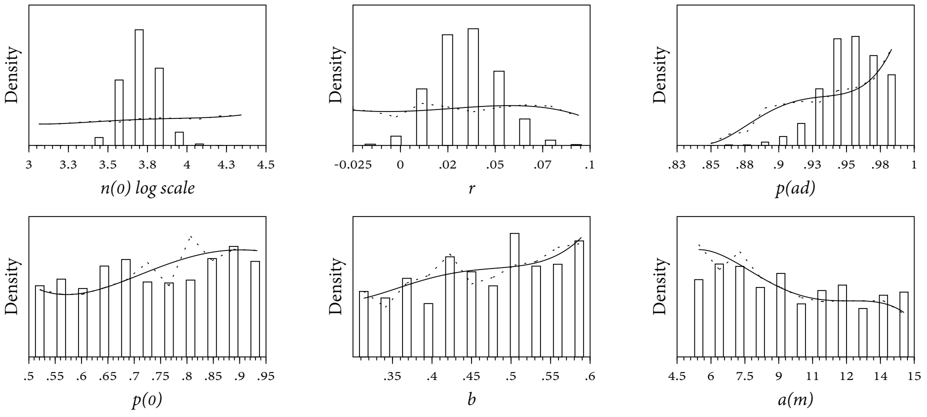


Figure 3: Realised prior and posterior distributions for the age- and sex-structured exponential model for West Iceland fin whales.

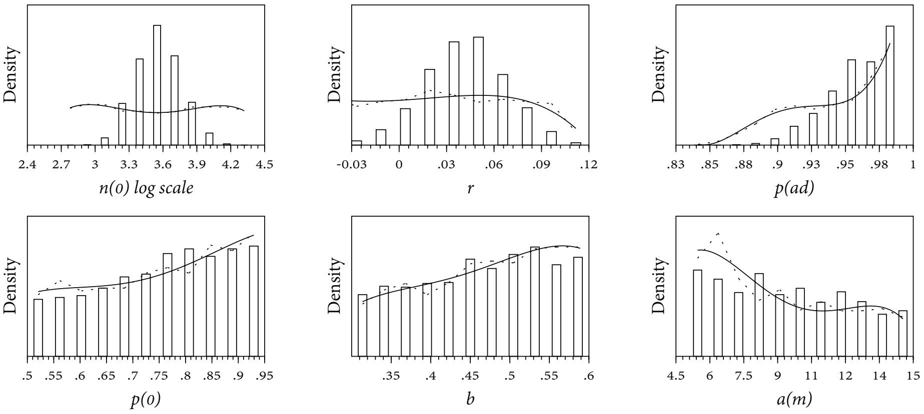


Figure 4: Realised prior and posterior distributions for the age- and sex-structured exponential model for East Iceland/Faroese fin whales.

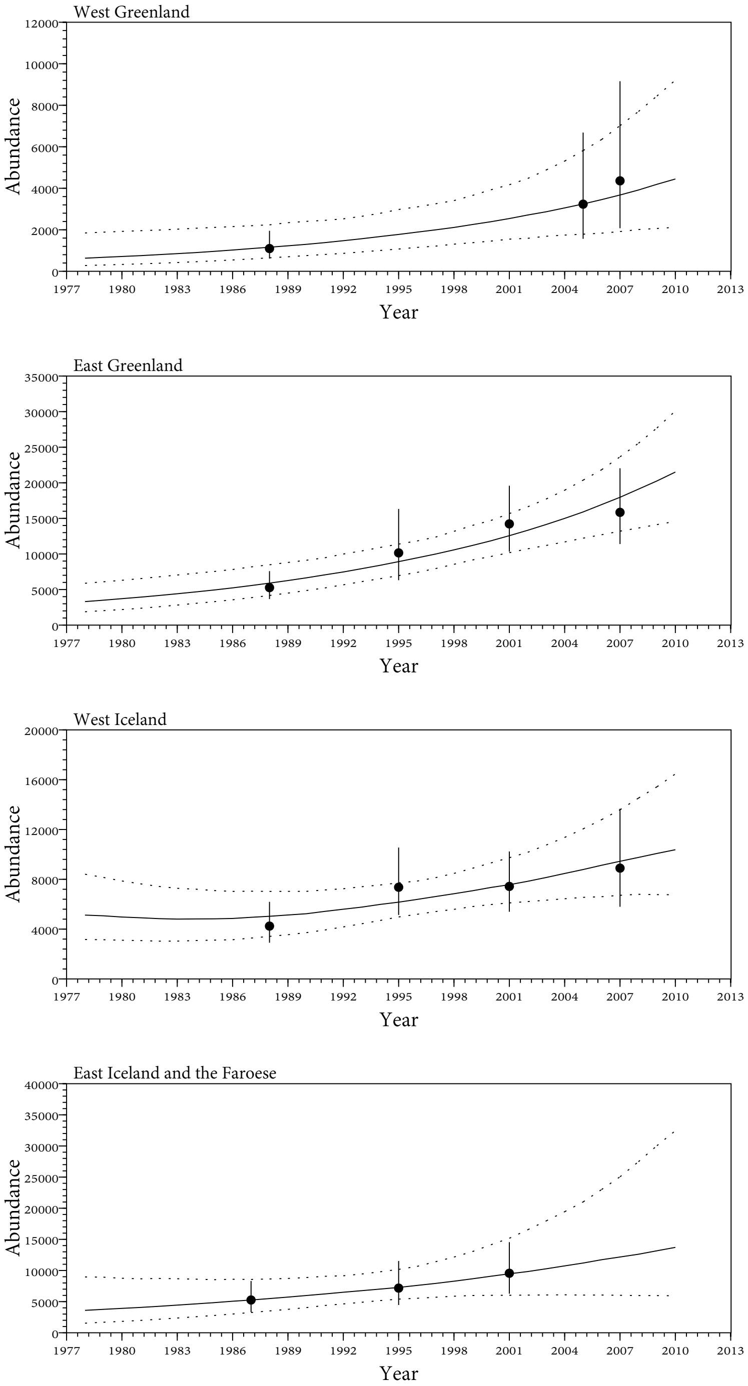


Figure 5: The estimated trajectories and abundance estimates for the summering aggregations of fin whales in West Greenland, East Greenland, West Iceland, and East Iceland and the Faroese.

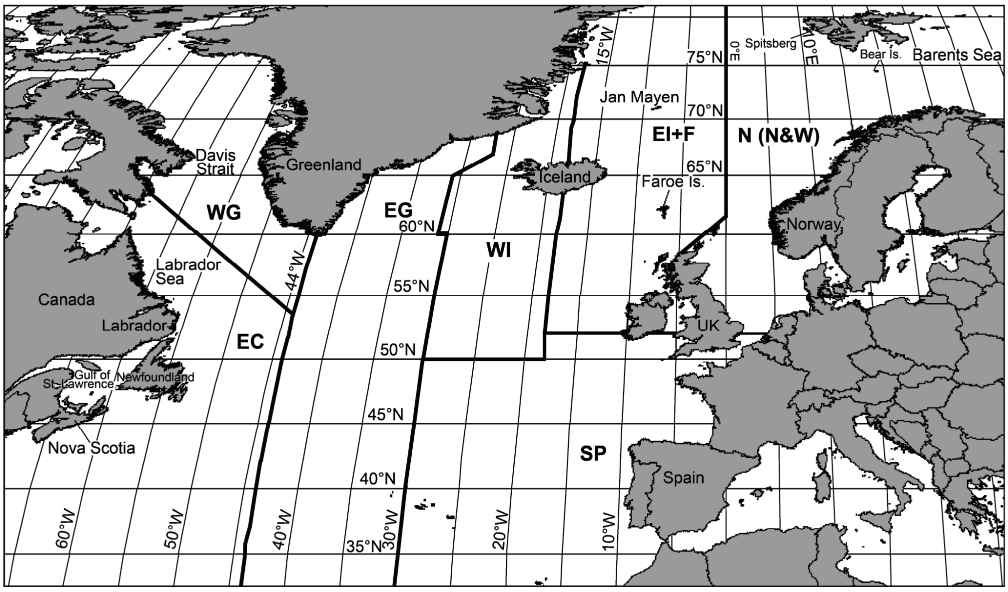
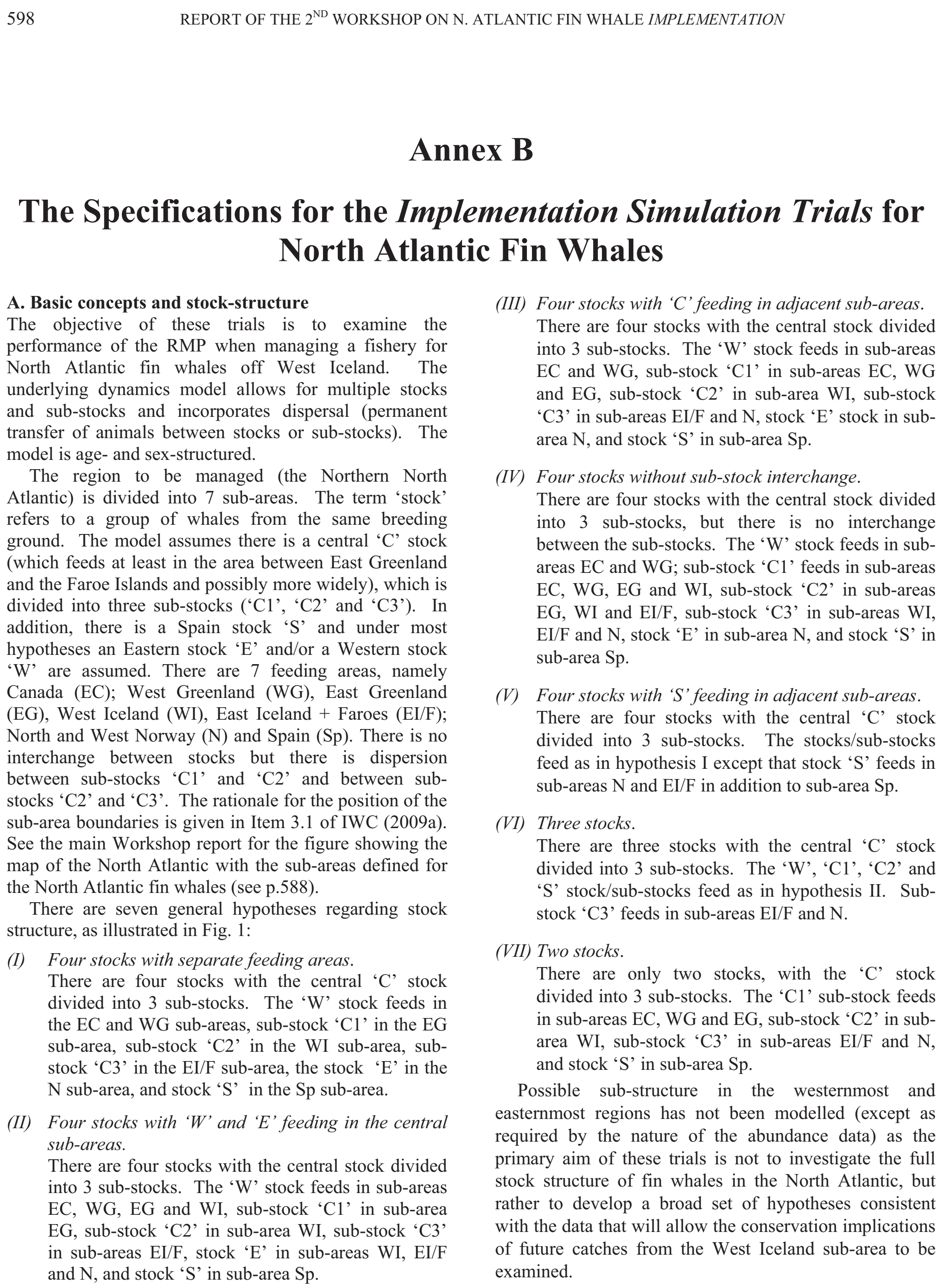


Figure 6: Map of the North Atlantic showing the sub-areas defined for the North Atlantic fin whales. From IWC (2010).



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Annex B

The Specifications for the *Implementation Simulation Trials* for North Atlantic Fin Whales

A. Basic concepts and stock-structure

The objective of these trials is to examine the performance of the RMP when managing a fishery for North Atlantic fin whales off West Iceland. The underlying dynamics model allows for multiple stocks and sub-stocks and incorporates dispersal (permanent transfer of animals between stocks or sub-stocks). The model is age- and sex-structured.

The region to be managed (the Northern North Atlantic) is divided into 7 sub-areas. The term 'stock' refers to a group of whales from the same breeding ground. The model assumes there is a central 'C' stock (which feeds at least in the area between East Greenland and the Faroe Islands and possibly more widely), which is divided into three sub-stocks ('C1', 'C2' and 'C3'). In addition, there is a Spain stock 'S' and under most hypotheses an Eastern stock 'E' and/or a Western stock 'W' are assumed. There are 7 feeding areas, namely Canada (EC); West Greenland (WG), East Greenland (EG), West Iceland (WI), East Iceland + Faroes (EI/F); North and West Norway (N) and Spain (Sp). There is no interchange between stocks but there is dispersion between sub-stocks 'C1' and 'C2' and between sub-stocks 'C2' and 'C3'. The rationale for the position of the sub-area boundaries is given in Item 3.1 of IWC (2009a). See the main Workshop report for the figure showing the map of the North Atlantic with the sub-areas defined for the North Atlantic fin whales (see p.588).

There are seven general hypotheses regarding stock structure, as illustrated in Fig. 1:

(I) Four stocks with separate feeding areas.
There are four stocks with the central 'C' stock divided into 3 sub-stocks. The 'W' stock feeds in the EC and WG sub-areas, sub-stock 'C1' in the EG sub-area, sub-stock 'C2' in the WI sub-area, sub-stock 'C3' in the EI/F sub-area, the stock 'E' in the N sub-area, and stock 'S' in the Sp sub-area.

(II) Four stocks with 'W' and 'E' feeding in the central sub-areas.
There are four stocks with the central stock divided into 3 sub-stocks. The 'W' stock feeds in sub-areas EC, WG, EG and WI, sub-stock 'C1' in sub-area EG, sub-stock 'C2' in sub-area WI, sub-stock 'C3' in sub-areas EI/F, stock 'E' in sub-areas WI, EI/F and N, and stock 'S' in sub-area Sp.

(III) Four stocks with 'C' feeding in adjacent sub-areas.
There are four stocks with the central stock divided into 3 sub-stocks. The 'W' stock feeds in sub-areas EC and WG, sub-stock 'C1' in sub-areas EC, WG and EG, sub-stock 'C2' in sub-area WI, sub-stock 'C3' in sub-areas EI/F and N, stock 'E' stock in sub-area N, and stock 'S' in sub-area Sp.

(IV) Four stocks without sub-stock interchange.
There are four stocks with the central stock divided into 3 sub-stocks, but there is no interchange between the sub-stocks. The 'W' stock feeds in sub-areas EC and WG; sub-stock 'C1' feeds in sub-areas EC, WG, EG and WI, sub-stock 'C2' in sub-areas EG, WI and EI/F, sub-stock 'C3' in sub-areas WI, EI/F and N, stock 'E' in sub-area N, and stock 'S' in sub-area Sp.

(V) Four stocks with 'S' feeding in adjacent sub-areas.
There are four stocks with the central 'C' stock divided into 3 sub-stocks. The stocks/sub-stocks feed as in hypothesis I except that stock 'S' feeds in sub-areas N and EI/F in addition to sub-area Sp.

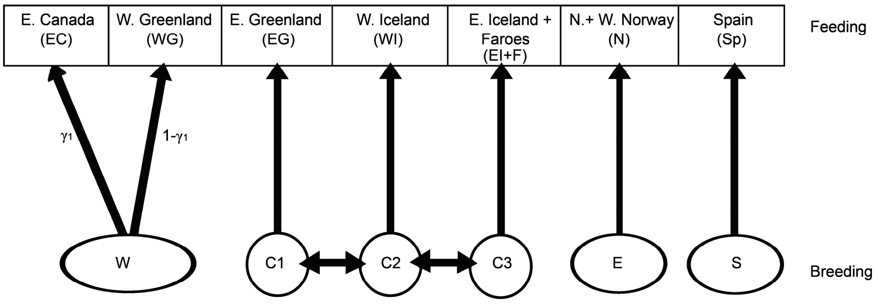
(VI) Three stocks.
There are three stocks with the central 'C' stock divided into 3 sub-stocks. The 'W', 'C1', 'C2' and 'S' stock/sub-stocks feed as in hypothesis II. Sub-stock 'C3' feeds in sub-areas EI/F and N.

(VII) Two stocks.
There are only two stocks, with the 'C' stock divided into 3 sub-stocks. The 'C1' sub-stock feeds in sub-areas EC, WG and EG, sub-stock 'C2' in sub-area WI, sub-stock 'C3' in sub-areas EI/F and N, and stock 'S' in sub-area Sp.

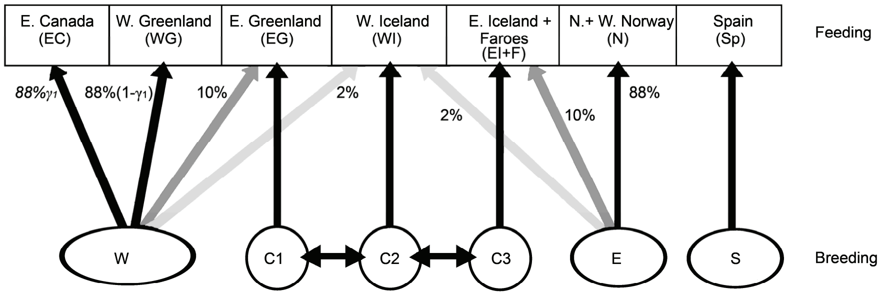
Possible sub-structure in the westernmost and easternmost regions has not been modelled (except as required by the nature of the abundance data) as the primary aim of these trials is not to investigate the full stock structure of fin whales in the North Atlantic, but rather to develop a broad set of hypotheses consistent with the data that will allow the conservation implications of future catches from the West Iceland sub-area to be examined.

Figure 7: IWC stock-structure hypotheses for North Atlantic fin whales. From IWC (2010).

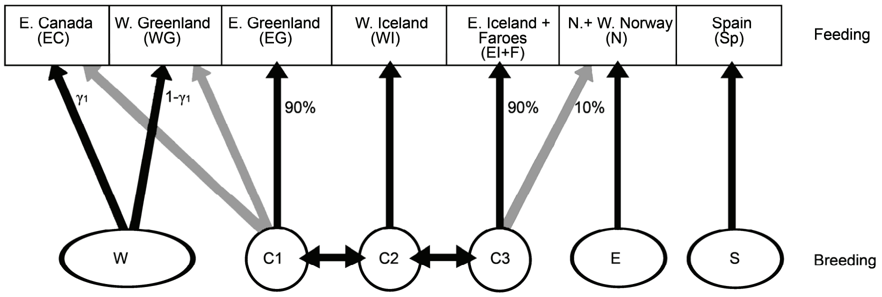
Hypothesis (I). Base case: 4 breeding stocks with separate feeding sub-areas



Hypothesis (II). 4 breeding stocks with the W and E stocks also feeding in the central sub-area



Hypothesis (III). 4 breeding stocks with the C stock feeding in adjacent sub-areas



Hypothesis (IV). 4 breeding stocks but without interchange between the C sub-stocks

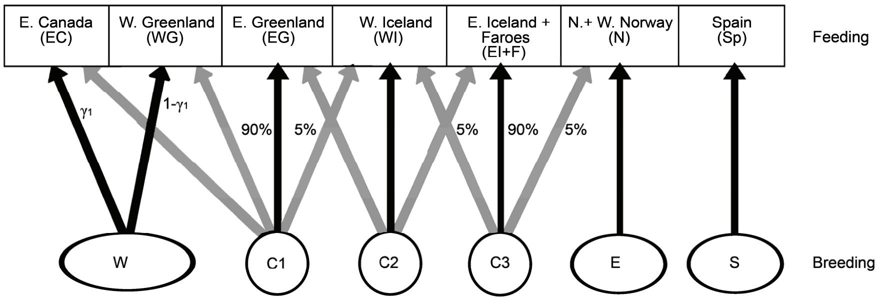
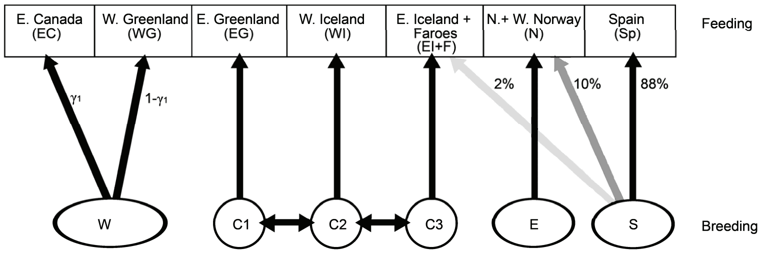
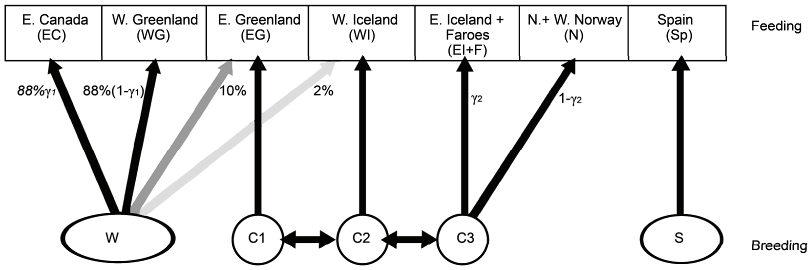


Fig. 1. Stock structure hypotheses for North Atlantic fin whales.

Hypothesis (V). 4 breeding stocks with the S stock feeding in the two adjacent sub-areas



Hypothesis (VI). 3 breeding stocks



Hypothesis (VII). 2 breeding stocks

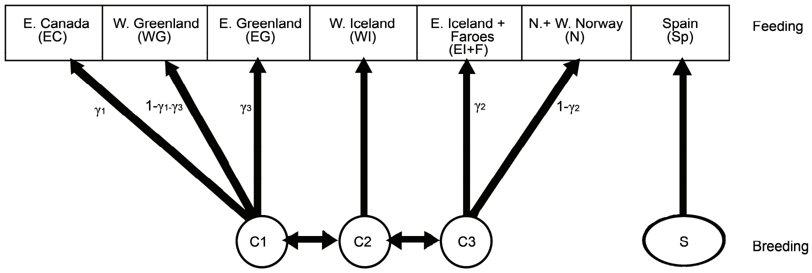
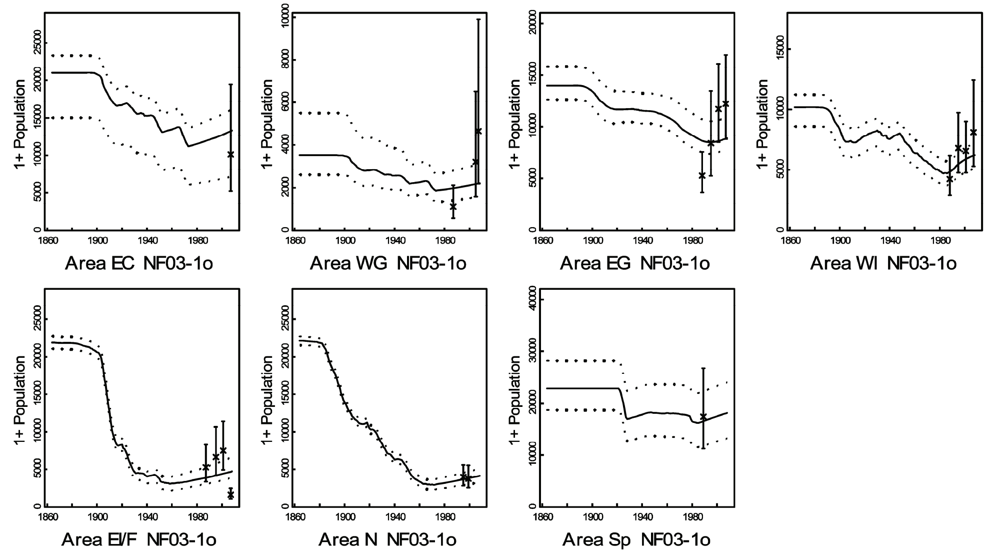


Fig. 1. (cont.) Stock structure hypotheses for North Atlantic fin whales.


NF03-1 previous version with sampling variances; Median & 90%ile 1+ populations by sub-area

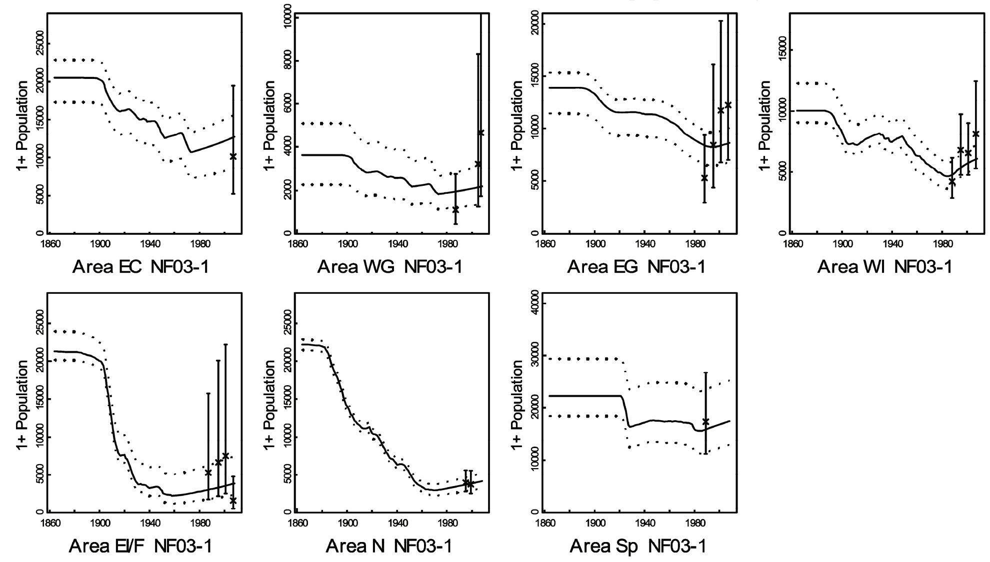

NF03-1 with additional variances; Median & 90%ile 1+ populations by sub-area

Figure 8: Conditioning plots for Trial NF03-1 before and after additional variance was included in the data. From IWC (2010).

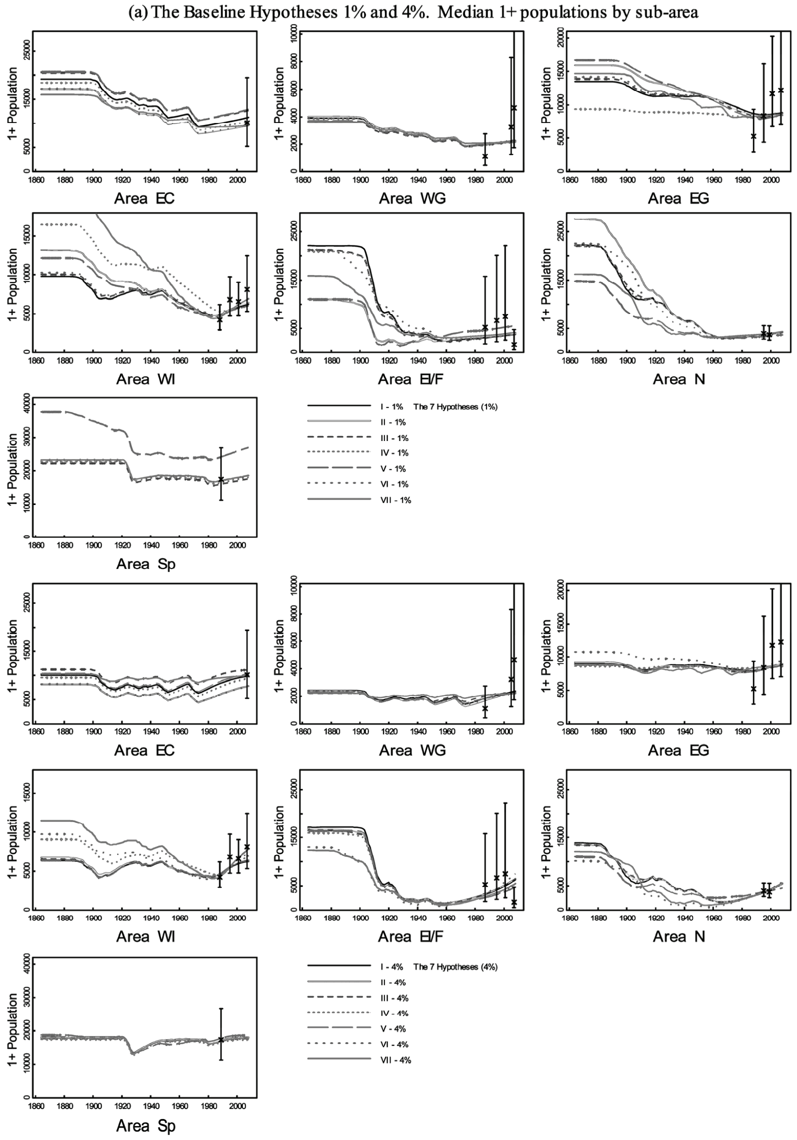


Figure 9: RMP Implementation Simulation Trials of the base case hypothesis. From IWC (2010).

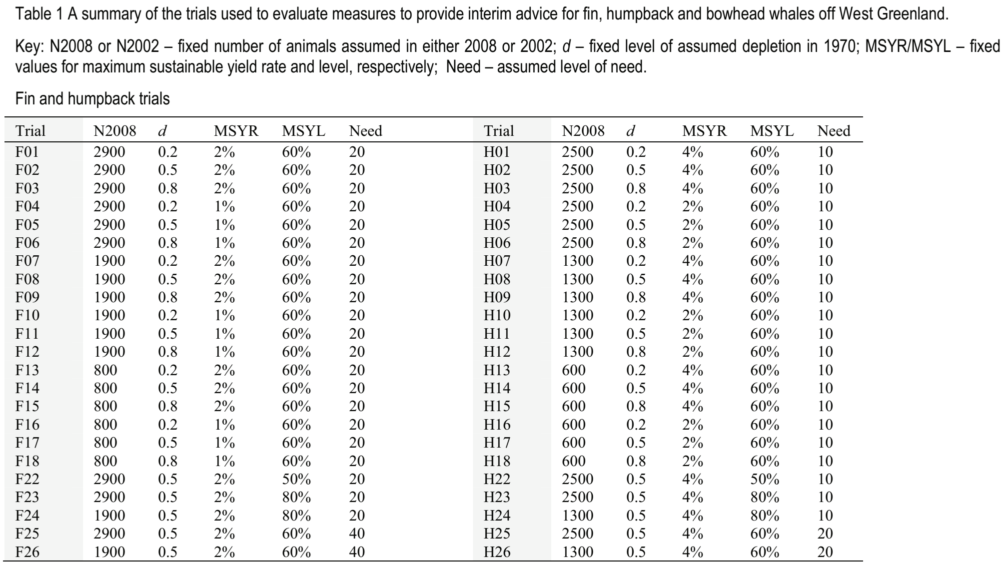


Table 1 A summary of the trials used to evaluate measures to provide interim advice for fin, humpback and bowhead whales off West Greenland.

Key: N2008 or N2002 – fixed number of animals assumed in either 2008 or 2002; *d* – fixed level of assumed depletion in 1970; MSYR/MSYL – fixed values for maximum sustainable yield rate and level, respectively; Need – assumed level of need.

Fin and humpback trials

Trial	N2008	*d*	MSYR	MSYL	Need	Trial	N2008	*d*	MSYR	MSYL	Need
F01	2900	0.2	2%	60%	20	H01	2500	0.2	4%	60%	10
F02	2900	0.5	2%	60%	20	H02	2500	0.5	4%	60%	10
F03	2900	0.8	2%	60%	20	H03	2500	0.8	4%	60%	10
F04	2900	0.2	1%	60%	20	H04	2500	0.2	2%	60%	10
F05	2900	0.5	1%	60%	20	H05	2500	0.5	2%	60%	10
F06	2900	0.8	1%	60%	20	H06	2500	0.8	2%	60%	10
F07	1900	0.2	2%	60%	20	H07	1300	0.2	4%	60%	10
F08	1900	0.5	2%	60%	20	H08	1300	0.5	4%	60%	10
F09	1900	0.8	2%	60%	20	H09	1300	0.8	4%	60%	10
F10	1900	0.2	1%	60%	20	H10	1300	0.2	2%	60%	10
F11	1900	0.5	1%	60%	20	H11	1300	0.5	2%	60%	10
F12	1900	0.8	1%	60%	20	H12	1300	0.8	2%	60%	10
F13	800	0.2	2%	60%	20	H13	600	0.2	4%	60%	10
F14	800	0.5	2%	60%	20	H14	600	0.5	4%	60%	10
F15	800	0.8	2%	60%	20	H15	600	0.8	4%	60%	10
F16	800	0.2	1%	60%	20	H16	600	0.2	2%	60%	10
F17	800	0.5	1%	60%	20	H17	600	0.5	2%	60%	10
F18	800	0.8	1%	60%	20	H18	600	0.8	2%	60%	10
F22	2900	0.5	2%	50%	20	H22	2500	0.5	4%	50%	10
F23	2900	0.5	2%	80%	20	H23	2500	0.5	4%	80%	10
F24	1900	0.5	2%	80%	20	H24	1300	0.5	4%	80%	10
F25	2900	0.5	2%	60%	40	H25	2500	0.5	4%	60%	20
F26	1900	0.5	2%	60%	40	H26	1300	0.5	4%	60%	20

Figure 10: Trials used for providing interim advice for West Greenland fin whales. From IWC (2009).