

Annex D

Report of the Sub-Committee on the Revised Management Procedure (RMP)

Members: Bannister (Convenor), Acquarone, Allison, An, Apostolaki, Baba, Bjørge, Bøthun, Rudolf, Borodin, Bradford, Brandao, Breiwick, Brownell, Butterworth, Cañadas, Castro, Childerhouse, Chilvers, Cipriano, Cooke, Donovan, Duran, Fortuna, Gallego, Goodman, Goto, Grønvik, Gunnlaugsson, Hammond, Hatanaka, Henriette Payet, Holloway, Hurbungs, Ilyashenko, Ipatova, Ishizuka, Jackson, Kanda, Kato, Kitakado, Koski, Koya, Leaper, Lens, Lockyer, Lopez-Mirones, Lovell, Lusseau, Lyrholm, Miller, Miller, Miyashita, Morishita, Mundnich, Øien, Okada, Olamura, Ólafsdóttir, Olavarria, Palka, Pampoulie, Panigada, Pastene, Perrin, Polacheck, Punt, Rademeyer, Ramirez, Robbins, Scordino, Shimada, Skaug, Slooten, Štrbenac, Víkingsson, Wade, Walløe, Waples, Williams, Winship, Yamakage, Yasokawa, Young.

1. INTRODUCTORY ITEMS

1.1 Convenor's opening remarks

As Convenor, Bannister welcomed the participants.

1.2 Election of Chair and appointment of rapporteurs

Bannister was elected Chair. Bannister, Butterworth, Cooke, Hammond, Polacheck, and Punt acted as rapporteurs.

1.3 Adoption of Agenda

The adopted Agenda is shown in Appendix 1.

1.4 Available documents

The documents considered by the sub-committee were SC/60/RMP1, SC/60/PFI1-13, SC/60/Rep3, SC/60/Rep5, and relevant extracts from past reports of the Committee.

2. REVISED MANAGEMENT PROCEDURE (RMP) – GENERAL ISSUES

2.1 Matters related to MSYR and MSYL

2.1.1 Review MSYR Workshop report, if appropriate suggest changes to the plausible range

Donovan presented a Chair's summary of the Report of the Workshop (SC/60/Rep5).

The sub-committee expressed appreciation to Workshop participants and particularly to Donovan for his chairmanship. It noted that it had not been possible to fully explore some issues at the Workshop. In particular, the limitations of existing methods described under SC/60/Rep5 Items 4.1.1 – 4.1.5 and the reconciliation of past trajectories with models including MSYR under SC/60/Rep5 Item 4.1.2 had not been fully dealt with. The sub-committee agreed that it was important to make progress on these issues at this meeting and established an *ad-hoc* Working Group under Butterworth to complete as much work as possible in the time available (see Item 2.4). In addition to the above, a specific point raised to be considered by the *ad-hoc* Working Group was how to determine MSYR/MSYL when stochasticity is introduced. The sub-committee did not think that the issue of whether or not environmental covariates should be included once the meta-analysis (SC/60/Rep5, Item 5.1) was complete should be discussed by the *ad-hoc* Working Group. Similarly, the issue of how MSYR is integrated into models of population dynamics in mixed-stock models (density dependence on the feeding grounds vs the breeding grounds) was beyond the scope of the Working Group. The sub-committee agreed that this latter issue should be taken up in the context of specific *Implementations*, for example for North Atlantic fin whales.

2.1.2 Modelling MSY-related parameters under stochastic dynamics

Cooke referred to recently completed analyses that developed further the work presented in SC/59/RMP10 relating to the implications of environmentally-induced variability in population dynamics on the plausible range of sustainable yield rates for baleen whales. The simulation studies presented last year had been extended to keep track of cases where stocks of whales increased faster than expected under an assessment model that ignored environmentally-induced variability. Cooke reported that the results showed that ignoring environmental variability can result in overestimation of median MSYR. There was no time to discuss these results at this meeting. Instead, the sub-committee agreed to postpone discussion of this item, to which SC/60/RMP1 also pertained, on the understanding that these issues would be taken up at the intersessional meeting proposed under Item 2.4.

2.2 Finalise the process for reviewing proposals to amend the RMP

The sub-committee was pleased to see the progress made at the MSYR intersessional workshop but recognised that considerable additional work was needed before the process for reviewing proposals to amend the RMP could be finalised. Most of this work related to the plausible range of MSYR considered in the RMP, discussed under Item 2.1, but there was also a need to integrate this into a final process for reviewing the results from simulation trials as previously specified in JCRM 9 (suppl.): 89-91.

The sub-committee recalled that last year it had agreed that it would be in a better position to review a need for additional trials to model any further environmental variation once the review of MSY rates had been completed (JCRM 10 (suppl.): 91). The sub-committee agreed that, depending on the results of the review of MSY rates, intersessional work might be needed to accomplish this and that sufficient time should be allocated for this item at next year's meeting so that the process for reviewing proposals to amend the RMP could be finalised.

2.3 Consideration of the Norwegian proposal to amend the RMP

The sub-committee recalled that SC/59/RMP4 presented to the meeting last year contained results for all single stock trials for a proposed alternative to the CLA. The sub-committee reiterated its agreement last year that detailed consideration of these results should await completion of the work to reconsider the plausible range for MSYR (Item 2.1). This work and the process for reviewing proposals to amend the RMP (Item 2.2) would be finalised at

next year's meeting and the sub-committee agreed that the Norwegian proposal should be considered then. If additional trials were required, advance notice would need to be given to allow full consideration of the proposal.

2.4 Work plan

Based on the results of the *ad-hoc* Working Group (See Item 2.1.1). The sub-committee considered the items identified for further work under section 5 of the Report of the MSYR Workshop (SC/60/Rep5).

Meta-analysis

The sub-committee confirmed that this exercise should consider estimates of population trend for various populations (see Table 1 of SC/60/Rep5). In addition to considering species or species-group as a covariate, consideration should be given to population depletion. Branch was identified as an appropriate scientist to carry out the work under guidance from an intersessional group (see below). The work should commence relatively soon and be based on the estimates already available, being extended later if estimates for other populations (see below) are developed and advised.

Models of the effect of environmental variability on yield curves

The sub-committee endorsed the recommendations of the MSYR Workshop that the following aspects of the model and results of SC/N07/MSYR1 (Cooke) should be further evaluated:

- (1) The impact on estimates of MSYR of taking account of the past catches that had induced the initial depletion of 0.25 assumed for the simulations.
- (2) Calculation of median bias of MSYR estimates as a function of σ and p on a finer grid of values than reported at present.
- (3) Sensitivity of this median bias to alternative distributional assumptions to the lognormal for the impact of environmental variability.
- (4) Differentiating the impacts of environmental variability on recruitment and survival while remaining within the simpler framework of an age-aggregated population mode.

In further discussion, it was agreed that any estimation procedures tested in such evaluations should fix MSYL rather than treat it as an estimable parameter; further, in taking account of past catches, both the options of assuming pre-exploitation abundance to be at K and treating this as an estimable parameter merited consideration.

To facilitate further work on this topic, Cooke prepared Appendix 2 summarising the population model, data generation and estimation procedures used for the computations reported in SC/N07/MSYR1, and agreed to make his computer code available to others.

Cooke tabled an extension of his earlier analyses in SC/N07/MSYR1, which included a review of the extent to which available information on the trajectories of baleen whale populations was consistent with deterministic models based on the density-dependent response mechanism conventionally assumed. The sub-committee agreed that this was an important topic which needed further consideration in the MSYR review process.

Improving current estimates

The sub-committee agreed that abundance estimates for East Greenland-Iceland fin whales and from catch-at-age analyses for Antarctic minke whales in Table 1 of SC/60/Rep5 were unlikely to be appreciably improved in the short term.

Stocks for which estimates could potentially be obtained

The following possibilities were identified, with the scientists responsible for following up and advising further indicated in parenthesis:

- (1) Western North Pacific blue, fin, Bryde's and sei (Kitakado)
- (2) Western North Atlantic blue (Donovan)
- (3) Western North Atlantic right (Wade)
- (4) Eastern and Central North Pacific humpback (Wade)
- (5) Southern Hemisphere humpback (Butterworth)

To progress these matters further so as to enable decisions regarding MSYR for use in RMP trials to be made at the next Committee meeting, an intersessional steering group comprised of Butterworth (Convenor), Cooke, Donovan, Gunnlaugsson, Kitakado, Punt, Skaug and Walløe was appointed. For the environmental variability models, and possibly also the meta-analysis identified above, the sub-committee considered that a two-day intersessional meeting was necessary, and recommended that consideration be given to linking this to the Second Fin Whale Intersessional Workshop (see Item 3.2.10) to be able to make common use of invitees. Funding of £3,000 would be necessary for this purpose.

3. RMP – PREPARATIONS FOR IMPLEMENTATION

3.1 Western North Pacific Bryde's whales

3.1.1 Finalise abundance estimates for western North Pacific Bryde's whales

SC/60/PFI2 presented abundance estimates by survey block and mode (e.g. normal closing or abeam closing) for western North Pacific Bryde's whales. Two sets of abundance estimates from the more recent sighting surveys (1998-2002) and the past ones (1988-1996) were presented based on conventional line transect methods under the assumption that $g(0)=1$. The recent surveys were conducted following the RMP Guidelines for sighting surveys and under oversight by the Committee, while the earlier ones were done prior to these guidelines being in place. The survey blocks were redefined to exclude portions in which little or no survey effort was possible (i.e. areas north of 39° in *sub-area* 1E and *sub-area* 2) based on the recommendations and suggestions made the last year. The effective search half width (esw) was estimated using the hazard-rate model with or without covariates. For both the periods, the esw and the mean school size stratified by *sub-area* were selected as the best estimates based on the fact that they had the minimum AIC and on Bonferroni's multiple t-tests respectively. The paper also presented abundance estimates for the past surveys (1988-1996) using similar methodology and data stratifications. These estimates were given to permit estimation of the additional variance for the recent estimates.

Kitakado presented SC/60/PFI3 in which abundance estimates for western North Pacific Bryde's whales were provided. These estimates are intended for use in the CLA. The estimation procedure consisted of three stages: 1) obtain abundance estimates by survey block for 1988-1996 and 1998-2002 from SC/60/PFI2; 2) estimate the process error (additional variance) based on these abundance estimates using a mixed-effect model and restricted maximum

likelihood methodology; and 3) provide point and variance estimates for abundances in 1998-2002 for the RMP-defined areas by integrating the information from two different survey modes in the 1998-2002 surveys, taking into account the extent of process error. It was noted that abundance estimates from the 1988-1996 surveys, which were not subject to oversight by the Committee because no oversight procedures existed at that time, did not affect the point estimates of abundance intended for use in the CLA but were used only for the estimation of process error. Computations were made for nine different run sets to assess the impact of model assumptions and the data utilised in the estimation of the process error and abundances. For the base case run set (Run #1), the effective strip widths and mean school sizes were estimated by *sub-area* and survey period and a log-normal mixed-effect model was employed for the estimation of process error. The best fit mixed model based on AIC was model 4 in which the abundances are assumed to differ between the two survey periods and there is an interaction between survey period and latitude band. For this model and run set #1, the estimated value of the additional CV was 0.447 (CV=43.1%). The resulting abundance estimates and their CVs taking into account the additional variance component are 4,957 (CV=39.8%), 11,213 (CV=49.8%) and 4,331 (CV=55.3%) for *sub-areas* 1W, 1E and 2 were respectively. The estimated abundance for the whole area was 20,501 (CV=33.7%). The authors concluded that these abundance estimates and their associated CVs meet the requirements for abundance estimates for use in the CLA based on the RMP guidelines and recommended that the sub-committee accept them for this purpose. SC/60/PFI3 also provided estimates for a count-based model (Run #9) so survey blocks with zero counts could be included in the analyses. The results were similar to those in the base scenario with a slightly higher estimate for the additional variance component.

The sub-committee considered that these two papers represented a substantial improvement both in the analyses and documentation for the western North Pacific Bryde's whale abundance surveys. It appreciated the large amount of effort that had gone into addressing the issues raised at last year's meeting and agreed that all of the substantive issues raised last year had been addressed satisfactorily.

There was discussion on whether the results based on Run #1 or Run #9 provided the most appropriate estimate of additional variance for use in the RMP. The method used in Run #1 has been reviewed previously by the sub-committee and the estimation approach has been accepted for use with other surveys to estimate additional variance abundance estimates for RMP. However, the method cannot account for survey blocks in which a zero estimate was obtained. The zero estimates are, therefore, left out of the calculation of additional variance. The situation of zero estimates for survey blocks had not arisen previously for surveys for which additional variance was estimated for use in the RMP. The approach used in Run #9 represented a new approach for estimating additional variance based on a negative binomial distribution, which could handle zero estimates. In this regard, the approach was preferable. However, as the method was still considered under development and not fully tested, the sub-committee agreed that estimates based on Run #1 were preferable at present. It also noted that the estimates of the CV for the total abundance using the two approaches varied by ~3% and that the choice of method did not affect the point estimates.

There was also discussion about whether model 4 with Run #1 was the most appropriate. While model 4 had the best fit to the data in terms of AIC, the sub-committee noted the lack of fit to the more recent survey estimates and the reasonableness of attempting to estimate area by time period changes in abundance based on only two surveys in which there was large CV associated with all of the estimates. Nevertheless, the sub-committee decided to use AIC as the basis for model selection. In conclusion, the sub-committee agreed that the estimates based on Run 1 and Model 4 were acceptable for use in the CLA (Table 1).

3.1.2 Review of proposed research plan

The Committee agreed last year (JCRM 10 (suppl.) 9) that three of the four RMP variants (1, 3 and 4) considered during the *Implementation* for the western North Pacific Bryde's whales performed acceptably from a conservation perspective and recommended that those variants could be implemented without a research program. It also agreed that variant 2 (i.e. *sub-area* 2 is taken to be a *Small Area* and the complete *sub-area* 1 is treated as a *Small Area*) was not acceptable without research because conservation performance was 'unacceptable' on three 'medium' plausibility trials in which there were two stocks of Bryde's whales in the western North Pacific, one of which consists of two sub-stocks (stock structure hypothesis 4).

SC/60/PFI9 was a research proposal which aimed to determine whether or not sub-stocks occur in *sub-area* 1. It was written using the pro-forma agreed last year and considered most of the specific suggestions provided by the Committee on last year's draft. The ultimate objective of the research program is to be able to provide information to the Committee so that it can modify (or confirm) its decisions regarding the appropriate plausibility for the trials on which variant 2 performed 'unacceptably'.

The sub-committee welcomed the revised research proposal and noted that it more closely followed the format recommended at last year's meeting (JCRM 10 (suppl.): 96-97). Discussion focused on the age-composition data. Several members noted that a key part of the original basis for considering a hypothesis in which there are two stocks, one of which consists of two sub-stocks, was the difference in total mortality in *sub-areas* 1W and 1E. Those members stated that the data for each new age-reading should be recorded, earplugs should be read in random order, and an evaluation of age-reading error should be conducted. Furthermore, they noted that given that the original basis for stock structure hypothesis 4, was the historical earplug data, these data should be re-examined. Other members pointed out that the old commercial data included some biases, and therefore re-reading of old earplugs might not resolve whether the differences in age-composition between *sub-areas* 1W and 1E reflect sub-stocks or not. They considered that a more comprehensive study including collection of new age data should be conducted.

The research proposal aims to examine earplug data for future whaling operations in *sub-areas* 1W and 1E. However, it was not clear whether the effect would be as large today as during the period of commercial whaling. It was noted that this could be examined using the *Implementation Simulation Trials* based on stock structure hypothesis 4 and the sub-committee recommended that this work be done.

Some members noted that there were no plans to present results of power analyses for the genetic work before 2010 even though the genetic work was seen as the primary source of information for evaluating the plausibility of stock structure hypothesis 4. They noted that it was difficult to assess whether the genetic data, in itself, would be sufficient to be able to show that stock structure 4 was implausible, particularly given the past difficulties in the Committee regarding the interpretation of non-significant statistical tests based on genetics data. Pastene noted that results of power analyses have been presented to previous meetings (e.g. Kitakado et al. 2005). The sub-committee therefore recommended that the results from previous (and any new) power analyses for the western North Pacific Bryde's whales be presented and discussed at the next meeting.

Other members highlighted the value of tag-based techniques to evaluate stock structure hypotheses. In response to a question, Pastene stated that the research program would not start until the RMP is implemented for western North Pacific Bryde's whales.

After much discussion, and noting that Japan intended to take catches in both *sub-areas* 1W and 1E (rather than just *sub-area* 1W as expected under variant 2), the sub-committee agreed that it was not necessary to make a final decision regarding the research proposal at this year's meeting. It therefore agreed to discuss the proposal further next year.

3.1.3 Work plan

The sub-committee agreed that its work plan for the 2009 Annual meeting would be:

- (1) Review the research proposal as submitted to the 2009 meeting.
- (2) Use *Implementation Simulation Trials* to evaluate the effect (and power) for current and historical age-composition data.
- (3) Review previous (and any new) genetic power analyses for western North Pacific Bryde's whales.

3.2 North Atlantic fin whales

3.2.1 Report of the First Intersessional Workshop

Donovan presented a Chair's summary of the Report of the Workshop (SC/60/Rep3).

The sub-committee thanked Donovan and the participants of the First Intersessional Workshop, noting that successful completion of this Workshop and the associated work arising from the deliberations at the Workshop was essential for the Committee to be able to complete the *Implementation* for the North Atlantic fin whales within the two-year timeframe identified in the *Requirements and Guidelines for Implementations*.

3.2.2 Objectives of the First Annual Meeting

The primary purpose of the first Annual Meeting is to review the results of the conditioning and to finalise the *Implementation Simulation Trials*. The specific objectives for this meeting (JCRM (Suppl. 5): 86-87) were:

- (1) final consideration of the plausibility of the various hypotheses and hence the weight assigned to each of the trials (the overall balance of the *Implementation Simulation Trials* will be accounted for when weights are assigned);
- (2) discussion of what data/research may reduce the number of hypotheses and possible time-frames for this research/data collection;
- (3) updates/improvements to standard data sets (i.e. abundance, catches, bycatches) for use by the *CLA* in final trials and when evaluating the plausibility of hypotheses and hence assigning weights to trials (new data would not be used when conditioning the trials);
- (4) specification of operational features (geographical and temporal) and management variants;
- (5) development of a timetable for the remaining work (including circulation of trial results and format); and
- (6) initial discussion of the inputs for actual application of the *CLA* (catches, bycatches, estimates of abundance and projected future anthropogenic removals).

3.2.3 Review results of conditioning

The manner in which the trials were to be conditioned was specified at the First Intersessional Workshop. The work was guided by an intersessional steering group, which led to some changes to the specifications developed during the Workshop. Specifically, a tag-reporting rate was estimated for Discovery tags released in Canada for the bulk of the trials, and trials were conducted for $MSYR_{mat}=2.5\%$ as well as for $MSYR_{mat}=1\%$ and $MSYR_{mat}=4\%$. The sub-committee thanked Allison and Rademeyer for their considerable work during the intersessional period.

'Conditioning' a set of simulation trials involves fitting the operating models to the available data. The conditioned trials should be able to mimic the available data adequately. The *Implementation Simulation Trials* for North Atlantic fin whales are based on abundance and tagging data (all trials) and CPUE data (a subset of the trials). A small group (Allison, Butterworth, Gunnlaugsson, Polacheck, Punt, Rademeyer, Wade) was established to examine the results of the conditioning which had been conducted by Allison and Rademeyer during the intersessional period. This small group identified several diagnostic tables and plots (see Appendix 3 for a summary). The full set of diagnostic tables and plots will be archived by the Secretariat and be available to the Committee.

In general, the operating model is able to mimic the data used for conditioning. The sub-committee noted that the fits to abundance estimates for *sub-area* WG were occasionally poor, but that this was not a concern given the focus on future RMP catches off West Iceland. More importantly, the trials are unable to reflect the increase in abundance off East Greenland. This may be caused by changes in distribution. The sub-committee therefore established four new trials to specifically examine this issue. They were based on stock structure hypothesis I) in which the rate of mixing of WI animals in *sub-area* EG increased from 1985 to 2005 and then (a) either remained at this level, or (b) declined to the 1985 level by 2030. It was also noted that some of the fits to the tagging data were relatively poor. For example, there appears to be a trade-off between fitting the tags recovered in *sub-area* C from tagging in that *sub-area* and tags recovered in *sub-area* WI from tagging conducted there. The sub-committee therefore agreed to add two new trials (based on stock-structure hypothesis I) in which the weight assigned to the tagging data was multiplied by 10.

The sub-committee noted that the operating model fitted the 'recent' CPUE indices and the historical CPUE data for *sub-area* EI/F adequately and the historical CPUE for *sub-area* WI poorly, irrespective of whether or not the CPUE data were included in the likelihood function. Only when the historical catches are set to their 'high' values (50% struck and lost rate; all catches that were unspecified to species assumed to be fin whales) was it possible to observe an appreciable decline in the abundance in *sub-area* WI.

In summary, the sub-committee agreed that the conditioning had been achieved satisfactorily for the purposes of conducting *Implementation Simulation Trials*.

3.2.4 Updates to standard datasets

SC/60/PF113 presented abundance estimates for fin whales from the Icelandic and Faroese survey areas (see Fig. 1 of SC/60/PF113). Combined single platform estimates were provided using three degrees of certainty in species identification, and with and without a bias correction for distance estimation. In addition an estimate of $g(0)$ using mark-recapture (or sight-resight) methods was provided. Density and abundance were estimated using stratified line transect methods (Buckland *et al.* 2001) using the DISTANCE 5.0 (Thomas *et al.* 2005) software package. Total abundance for the combined platform estimate using the identification certainty classification considered most comparable to that used in previous analyses and with no correction for bias in distance estimation was 21,628 (0.15) (95% C.I. 15,731-27,739). The double platform analysis resulted in a mean value for $g(0)$ for the primary platform of 0.77 (CV 0.10), which is similar to that estimated for 2001. The magnitude of other sources of bias in the data was also analysed, but the uncorrected estimate for the combined platforms was considered most comparable to earlier survey estimates. This estimate is lower (but not significantly so) than the total estimate for 2001 of 24,887 (95% C.I. 18,186-30,214) (Vikingsson *et al.* in press).

3.2.5 Final consideration of plausibility (including weighting of trials in terms of overall balance)

The sub-committee reviewed the *Implementation Simulation Trials*, including the trials selected following the review of the conditioning (see Item 3.2.3). It assigned plausibility ranks of "High", "Medium", "Low" to each hypothesis (factor) and hence to each trial, as specified in the *Requirements and Guidelines for Implementations* (JCRM 7 (Suppl): 86-7). Given a plausibility rank for each hypothesis, the ranks for each trial were constructed as follows: (a) if a factor was assigned a "low" rank, all the trials based on that factor were assigned a "low" rank, (b) if the main factor determining the difference between a trial and the associated base trial (trials NF01-NF14) was ranked "medium", that trial was also ranked "medium", and (c) if all the factors on which a trial was based were ranked "high", that trial was also ranked "high".

Of the final set of 57 trials (see Table 2), 25 were assigned "high" weight, 25 were assigned "medium" weight, and 7 "low" weight. The sub-committee agreed that the seven trials assigned "low" weight (NF13, 29-22, 1x-2x) would not be considered further.

3.2.5.1 STOCK STRUCTURE HYPOTHESES

There are seven stock structure hypotheses (hypotheses I – VII; see Item 2.1.2 of SC/60/Rep3). The information available to assign plausibility ranks to these hypotheses includes genetic data, mark-recapture information, catch and sightings distributions and the results of model fits (e.g. conditioning of trials). In relation to using the results of model fits, previous discussions in the Committee have noted that the stock hypotheses should be considered as archetypes rather than as specific testable hypotheses so care should be taken in not over-interpreting the results of model fits. In any case, the sub-committee has already agreed that all trials were conditioned satisfactorily (see Item 3.2.3).

The genetic data for North Atlantic fin whales are equivocal regarding the number of stocks. Specifically, significant differences, indicating at least three genetic stocks, have been found based on allozyme studies between samples from Newfoundland, Canada, Norway, and Iceland (Danielsdóttir *et al.* 1991, 1992). In contrast, DNA-based analyses suggest low levels of divergence among fin whales in North Atlantic feeding grounds. Given an inability to select between genetic methods (but see Item 3.2.10), the genetics data provide no strong basis to select among the hypotheses. However, the sub-committee noted that stock structure hypothesis VII was inconsistent with the allozyme data and some non-genetic evidence (SC/M06/FW7), and therefore ranked this hypothesis as "medium". The Intersessional Workshop agreed that the mark-recapture data provided insights into local movements of fin whales, but that the data were too few to inform hypotheses of structure at the ocean basin level. Similarly, the trials are comparable with the catch and sightings distributions.

The sub-committee considered whether stock structure hypothesis IV should be assigned "high" or "medium" plausibility. After much discussion, all but one member agreed that this hypothesis should be assigned "high" plausibility. Appendix 4 provides a minority statement from that member and counter-comments from other members who participated in the discussion. The sub-committee noted that the plausibility assigned to stock structure hypothesis IV could be modified given additional information/analyses at the next *Implementation Review*. Furthermore, if an RMP variant performs adequately for all trials except those for stock structure hypothesis IV, it could be recommended "with research" if a program of research could be established which could show that this hypothesis is implausible within ten years.

The sub-committee noted that the sensitivity tests in which there is time-dependence of mixing of WI animals in *sub-area* EG (trials NF43-46) fit the data for *sub-area* EG better than the baseline version of stock structure hypothesis I and were consequently assigned "high" plausibility. Trials not based on this assumption are also of "high" plausibility (except for stock structure hypothesis VII) because the mechanism of time-dependent mixing is largely speculative at present.

In summary, there is little basis to select among any of the stock structure hypotheses and the sub-committee agreed to assign hypotheses I-VI "high" plausibility and hypothesis VII "medium" plausibility. There is a baseline stock structure hypothesis (I), but that hypothesis was selected primarily because it represents a case where achieving conservation objectives is likely to be more difficult rather than because it was considered more biologically plausible.

3.2.5.2 OTHER

MSYR: The sub-committee had previously had extensive discussions regarding the plausibility of different $MSYR_{mat}$ values during the *Implementation* for the western North Pacific minke whales (JCRM 6 (Suppl.): 83). For that *Implementation* (and the *Implementation* for western North Pacific Bryde's whales (JCRM 9 (Suppl): 95)), $MSYR_{mat}=1\%$ was assigned "medium" plausibility while $MSYR_{mat}=4\%$ was assigned "high" plausibility. In the absence of the completion of the MSYR Review (see Item 2.1), the sub-committee agreed that $MSYR_{mat}=2.5\%$ and $MSYR_{mat}=4\%$ would be assigned "high" plausibility and $MSYR_{mat}=1\%$ would be assigned "medium" plausibility.

Catch series: The best (qualitative) fit to the CPUE data for *sub-area* WI occurs for the "high" catch series. This catch series and the "best" catch series were assigned "high" plausibility. Given that the "high" catch series is qualitatively more consistent with the data, the sub-committee assigned "low" plausibility to the "low" catch series. Projections under RMP variants will consequently not be conducted for trials NF19-NF22. The sub-committee agreed to add two further trials based on stock structure hypothesis IV ($MSYR_{mat}$ values of 2.5% and 4%) and the "high" catch series and to assign these trials

"high" plausibility, noting that including the "high" catch series resulted in time-trajectories of abundance that were more consistent with the qualitative information on the operation of the early fishery of West Iceland.

Alternative boundary between WI and EI/F: The default boundary between *sub-areas* WI and EI/F is set to 18°W. Trials NF23 and NF24 examine moving this boundary to 14°W. There is no reason not to assign this factor "high" plausibility.

Alternative abundance estimates/CPUE data: Sensitivity tests NF29 and NF30 involve pro-rating abundance estimates for *sub-areas* EG, WI and EI/F to unsurveyed areas to the south. The sub-committee considered this factor to be of "medium" plausibility. Given the concerns expressed in the past with CPUE data in general (IWC, 1988) and the CPUE series for North Atlantic fin whales in particular (IWC, 2007), including CPUE data in the likelihood function was assigned "medium" plausibility.

Alternative mark loss rates: The default assumption is that no marks are lost, based on analyses of (limited) data by Gunnlaugsson and Sigurjónsson (1989). The alternative assumptions regarding mark-loss rates (trial NF33-38) were assigned "high" plausibility owing primarily to lack of definitive information on tag loss rates.

Higher weight on the tagging data: These sensitivity tests (NF41 and NF42) inflate the contribution of the tagging data to the objective function by multiplying the tagging likelihood component by 10. This level of weight is not consistent with the actual number of tags, and effectively captures the assumption that the surveys are less reliable than indicated by their CVs. This factor was assigned "medium" plausibility.

Selectivity decreasing: The possibility of declining selectivity with age was introduced to allow the trials to be based on a previous estimate of M of 0.04yr⁻¹. The value of M (0.08yr⁻¹) used in the bulk of the trials is based on catch curve analyses (see Annex J of SC/60/Rep3). However, a lower value for M is more consistent with the demography of fin whales and, given information on calving intervals, with the $MSYR_{mat}$ values included in the *Implementation Simulation Trials* for North Atlantic fin whales. This factor was assigned "high" plausibility.

Reporting rate for tags placed in Canada: The Intersessional Workshop recommended setting the reporting rate to 1 for all tagged animals. However, better fits were possible when the reporting rate for tags placed in Canadian waters was treated as an estimable parameter. The trials based on a Canadian reporting rate of 1 (NF01x, NF02x) are of general interest, but this factor was assigned "low" plausibility.

The Icelandic fishery was suspended in 1915 in *subareas* WI and WI/F and restarted later. The sub-committee noted that the time-trajectory of 1+ abundance for *sub-area* WI for stock hypothesis VII declines sharply and continuously over time when $MSYR_{mat}$ is assumed to be 1%. In contrast, the time-trajectory of 1+ abundance for *sub-area* EI/F increases from its minimum level. The behaviour for *sub-area* WI seems therefore inconsistent with the qualitative operational information for a fishery which was suspended due to low abundance and restarted when abundance increased (or at least didn't decline much further but catching efficiency increased). This, and the size of the decline in abundance over time under hypotheses VII, led the sub-committee to agree to assign trial NF13 "low" plausibility.

The sub-committee did not have time to review the conditioning for the new trials specified under this item and Item 3.2.3. It established a small group (Allison, Butterworth, Donovan, Gunnlaugsson, Punt, and Wade) to review the conditioning and provide a short report to plenary. They reported that the conditioning of the new trials was satisfactory and the results are included in Appendix 3.

3.2.6 Data/research to reduce hypotheses

Genetic data are somewhat difficult to interpret for fin whales. Specifically, DNA-based analyses revealed low levels of genetic divergence among geographic fin whale samples which may be interpreted in two different ways: (i) the degree of gene flow between sampling partitions is high; or (ii) the rate of gene flow in fact is low, and the low degree of genetic divergence is due to a recent divergence of current North Atlantic fin whale populations. The sub-committee therefore identified that the spatial distribution of dyads of close relatives (identified by the degree of genetic similarity at microsatellite loci) could be used to resolve whether hypothesis (i) or (ii) is correct.

In addition, divergent selection has been invoked as an explanation for the discrepancy between the DNA- and allozyme-based results (and has implications for the number of breeding stocks). Data analyses aimed specifically at detecting signatures of selection could be undertaken (e.g. by analysis of those DNA sequences encoding for the allozymes at which high levels of genetic divergence was detected) to resolve this uncertainty. A proposal to conduct this work is given as Appendix 5.

3.2.7 Specification of operational features and management variants

All of the future catches will be assumed to be taken from the West Iceland sub-area, given advice to the sub-committee regarding the expected whaling operations.

The management variants will be based on three *Small Area* definitions:

- (a) West Iceland
- (b) West Iceland + East Greenland
- (c) West Iceland + East Greenland+ East Iceland/Faroes

The management variants to be considered in trials will be:

- (1) Catch limits set by *Small Areas* (although the entire catch will be taken from West Iceland sub-area).
- (2) Catch cascading over the following two groups of sub-areas: (1) West Iceland+East Greenland, and (2) West Iceland+East Greenland+East Iceland/Faroes. The catch limits for the East Greenland and East Iceland/Faroes *Small Areas* will be ignored and only the catch limit for West Iceland will be removed from the modelled breeding populations.
- (3) Catch limits set for the West Iceland *Small Area* based on the survey estimates for the area of the West Iceland sub-area north of 60°N.

3.2.8 Specification and classification of final trials

The full list of specified trials, including the weights of each trial, is found in Appendix 6.

3.2.9 Inputs for actual application of the CLA

The sub-committee noted that documents would be needed to select the catches and abundance estimates for use in the CLA. It agreed that this matter should be discussed at the Second Intersessional Workshop (see Item 3.2.10) and finalised at the 2009 Annual Meeting.

3.2.10 Work plan

The sub-committee agreed that the tasks that have to be completed during the First Annual Meeting had been completed successfully and that the *Implementation* for North Atlantic fin whales remained on track for completion at the 2009 Annual Meeting.

In accordance with the 'Requirements and Guidelines for *Implementations*' (JCRM 7 (suppl.): 84-92) plans were developed for the Second Intersessional Workshop for the North Atlantic Fin Whale *Implementation*. The objectives for this Workshop are to:

- (1) review the results of the final trials and develop recommendations for consideration by the full Committee on:
 - a. management areas;
 - b. RMP variants (e.g. Catch-cascading, Catch-capping);
 - c. associated operational constraints (e.g. temporal restrictions);
 - d. suggestions for future research (either within or outside whaling operations) to narrow the range of plausible hypotheses/eliminate some hypotheses; and
 - e. 'less conservative' variant(s) with their associated required research programs and associated duration.
- (2) continue to discuss the inputs to the actual application of the CLA will continue.

The sub-committee re-established a Steering Group under Donovan (Allison, Butterworth, Cooke, Cunningham, Gunnlaugsson, Hammond, Palsbøll, Punt, Rademeyer, Skaug, and Víkingsson) to guide the work for this Workshop. The Second Intersessional Workshop will be held in Spring 2009, in a location to be decided, for a period of five days. There are costs associated with travel and subsistence, estimated as £10,000. The tasks to be completed before this Workshop are:

- (1) run the *Implementation Simulation Trials* and develop initial plots and tables;
- (2) develop and run the single-stock trials needed to apply the criteria for evaluating conservation performance; and
- (3) prepare documents for any abundance estimates which might be used in the CLA (given the decisions under item 3.2.7, only abundance estimates for sub-areas EG, WI, and EI/F will be needed to be reviewed because the remaining sub-areas are *Residual Areas* for this *Implementation*).

The sub-committee anticipates completing the *Implementation* at the 2009 Annual Meeting. The objectives for the Second Annual Meeting (JCRM 7 (suppl.): 89) are to:

- (1) review the results of the Second Intersessional Workshop (including any additional trials); and
- (2) agree recommendations for *Implementation* including the specifications of the inputs to the CLA.

3.3 North Atlantic common minke whales

3.3.1 Implementation Review

The last *Implementation Review* for North Atlantic minke whales was conducted in 2003 (JCRM 6, 171-183) and a new one had been scheduled last year for 2008 (JCRM 10, 99-100).

A working group met immediately prior to the Scientific Committee meeting to conduct the Review. Its report is contained in Appendix 7. The main conclusions and further subcommittee discussion are summarised here.

3.3.1.1 HISTORY

Implementation Simulation Trials were developed for North Atlantic minke whales between 1990 and 1993. They arose from the model for multi-stock robustness trials of mixed coastal and pelagic whaling. The full specifications of the trials are given in RIWC 43: 189-195 (Annex I, Appendix 4). The results are given in RIWC 43: 167-185 (Annex I, Appendix 2, Table 2) and described in RIWC 44: 48-49. *Medium Areas* were based on the management areas listed in the ICRW Schedule: Eastern (Northeast Atlantic management area), Central (Central North Atlantic management area) and Western (West Greenland and Canadian East Coast management areas). These were divided into *Small Areas* (EN, EB, EC and ES in the Eastern *Medium Area*; CIC, CIP, CG and CM in the Central *Medium Area*; and WG in the western *Medium Area*). Catch-cascading over the Central and Eastern *Medium Areas* was the recommended implementation option.

The Committee conducted an *Implementation Review* in 2003 (JCRM (suppl) 6: 12-13; 88-89; 171-183), at which it reviewed new information on stock structure and estimates of abundance. It recommended a southward shift in the boundary of the EN *Small Area*, abolition of the EC *Small Area*, and a boundary at 28°E through the EB *Small Area* to create a new EW *Small Area* (for maps see JCRM 6, p.171). Limited additional *Implementation Simulation Trials* were conducted to check that the additional variance arising from the non-synoptic nature of recent surveys was within the bounds modelled in the previous trials.

3.3.1.2 STOCK STRUCTURE

A new analysis of 16 microsatellite loci and the mtDNA control region from six areas of the North Atlantic found very little genetic variation (SC/60/PFI10). This may be consistent with a panmictic population. However, the results were also consistent with recent divergence from a small founding population, such that current stock structure is not reflected in the genetics.

An analysis of the genetic data from the Norwegian catches taken during 2003-06 found no significant genetic divergence between Small Areas, whether in microsatellites or in mtDNA (SC/60/PFI1). This was in contrast to the results from the 1997-2002 catches which had been considered during the 2003 *Implementation Review*.

There had been a change in laboratory in 2003, and it was suspected that the apparent heterogeneity found in the 1997-2002 data had been caused by laboratory errors. The subcommittee recommended that the 1997-2002 data be analysed in more detail with a view to determining whether the apparent heterogeneity could be laboratory artefact.

3.3.1.3 ABUNDANCE ESTIMATES

The abundance estimates for all areas considered by the subcommittee and their current status are listed in Table 2 of Appendix 7.

Northeast Atlantic (Norwegian and Barents Seas) and CM *Small Area* (Jan Mayen): New abundance estimates were received for the Northeast Atlantic area from Norwegian surveys conducted during 2002-07 (SC/60/PFI4). These used the same methodology as the estimates from 1996-2001 that had been accepted at the 2003 *Implementation Review*. The new estimates were not yet final, and in particular the additional variance component arising from their multi-year, non-synoptic nature had not yet been calculated. The subcommittee agreed that these estimates could be used for conditioning *Implementation Simulation Trials* (ISTs), but not for use in the RMP until they are finalised.

North Sea (EN *Small Area*): The sub-committee agreed that the estimate of 13,281 (CV 0.36) from the SCANS 2005 shipboard survey (LIFE04NAT 2008) for the EN *Small Area* was acceptable for use both in conditioning *Implementation Simulation Trials* and in the RMP. Estimates from aerial surveys were not considered suitable. Results from 2007 surveys were not considered, pending finalisation of the analysis.

Icelandic coastal: Revised estimates were available from a reanalysis of the 1987 and 2001 aerial surveys of 24,532 (CV 0.32) and 43,633 (CV 0.19) respectively (Borchers *et al.* 2008). The subcommittee agreed that these estimates were acceptable for use in conditioning ISTs and in the RMP.

SC/60/PFI12 presented estimates of abundance from an aerial survey in 2007. The abundance estimate using data from both primary observers was 10,680 (95% CI 5,873-17,121) (CV 0.29). The primary observer who made most of the harbour porpoise sightings made much fewer minke whale sightings in particular within 200m of the plane and no duplicates with the control observer that would enable estimation of distance error and $g(0)$. The other primary observer had experience from partial surveys conducted under the Icelandic Research Program during 2003-2005 to detect seasonal abundance changes and on a survey off West Greenland in September 2005. This observer duplicated all sightings within short radial distances and had low distance estimation error. The distance estimates by this observer tended to be greater than those made by the control observer. The abundance estimate for minke whales using this observer alone and standard cue counting methods was 15,055 (95% CI 6,357, 27,278) (CV 0.36). This observer may have overestimated distances to some degree and the $g(0)$ for this observer may have been lower than 1 although that is not apparent from the limited duplicate sighting data.

The change in survey altitude would have resulted in a 44% reduction in the effective area searched if observers searched within the same declination angle as in 2001, but the effective search area was estimated to be just 15% smaller in 2007 than in 2001, indicating that the observers compensated for lower altitude by changing their searching behaviour. The decrease in the estimate compared to 2001 is unlikely to be an artefact of changes in survey methods alone. There is some evidence that minke whale density was increasing over the course of the survey, suggesting that the peak in seasonal abundance might have been missed.

The sub-committee noted that the reason advanced for excluding data from one of the observers was that this observer did not detect any minke whales within 200m of the trackline and duplicated none of the minke whales detected by the control observer precluding estimation of distance error or $g(0)$. Gunnlaugsson pointed out that the counts from the two primary observers were significantly different at the 5% level and the duplicate counts were significantly different at the 1% level. Other members responded that the significance of differences in counts may also be overestimated due to clumping of whales.

The sub-committee noted that this observer did make observations of other species (particularly harbour porpoise) close to the trackline. There was no reason to suspect problems in species identification, nor any other obvious reason why this observer should have had a reduced ability to detect minke whales close to the trackline. Despite the difference in detections and the inability to estimate distance error or $g(0)$ for this observer, the sub-committee agreed that there was no *a priori* reason to exclude these data.

The sub-committee agreed that the abundance estimate of 10,680 (CV=0.29) based on data from both observers meets the requirements for use in conditioning trials and for use in the RMP. Gunnlaugsson believed that the estimate of 15,055 (CV=0.36) based on data from the observer for whom it was possible to estimate $g(0)$ also meets these requirements, noting that the lower estimate is incompletely corrected for $g(0)$.

West Greenland: The sub-committee noted that the AWMP Standing Working Group had accepted an estimate of 10,800 (CV 0.71) whales in 2005 (JCRM 10 p. 126). The subcommittee agreed that this estimate was suitable both for conditioning trials and also, should it be required, for use in the RMP.

Western North Atlantic: The sub-committee accepted an estimate of 3,312 (CV 0.74) for the Gulf of Maine, Bay of Fundy and western Scotian shelf (Waring *et al.* 2007) for use in conditioning trials, but noted that its use in the RMP was unlikely to be called for.

3.3.1.4 IMPLEMENTATION SIMULATION TRIALS

The sub-committee agreed that no new *Implementation Simulation Trials* were needed at this time, because the review of new information on stock structure and abundance did not reveal any new hypotheses which are not captured qualitatively by the existing set of 16 trials.

The sub-committee noted that the North Atlantic *Implementation Simulation Trials* were developed before the *Requirements and Guidelines for Implementations* (JCRM 7(Suppl.): 84-92) were adopted, but considered that they follow the intent of the *Requirements and Guidelines*. The sub-committee therefore agreed that it was not necessary to modify the existing trials for the current *Implementation Review*, but that the next *Implementation Review* in 2013 should be based on following the *Guidelines and Requirements*.

The sub-committee identified a number of research topics relating to stock structure, results from which could enhance the 2013 *Implementation Review*, as listed in Appendix 7.

3.3.1.5 MANAGEMENT AREAS

The sub-committee recommended that the *Medium Areas* remain unchanged, there being no new evidence to support population differentiation in the North Atlantic, while the earlier evidence on which the *Medium Areas* were based should be regarded as still valid until shown otherwise.

Walløe proposed that the boundary between EW and EB *Small Areas* that had been introduced in 2003 should be removed, on the grounds that the original evidence on which it had been based was weak and that the new information (see Item 3.3.1.2) did not support it. To evaluate this proposal, the sub-committee considered three analyses in addition to those discussed in Appendix 7:

- (1) a closer examination of the 1997-2002 genetic data (see Appendix 8) on which the 2003 boundary decision had been based showed that haplotypic diversity across the 28°E line was small in F_{st} terms, but a chi-squared test was significant. The significance disappeared when the 1998 data were omitted, but there were no obvious features that singled out either the 1998 sample or any other subset of the data;
- (2) an analysis of catch positions of pairs of closely related individuals (see Appendix 9) showed no marked tendency for related individuals to be found in the same subarea. Within the eastern *Medium Area*, divided into subareas EN, EW, EB and ES, only 7 out of 24 pairs of close relatives were taken within the same subarea;
- (3) an analysis of catch and sightings positions (see Appendix 10) showed that sightings were distributed across most of the EB *Small Area* up to about 75°N (surveying to the north tends to be limited by ice) but the catches (from which the genetic data derive) were largely confined to the south-western corner, near the EW boundary, where they formed part of a continuous whaling ground along the coasts of Finnmark and Troms. The eastern part of the area was closed to catching by the Russian EEZ.

The sub-committee agreed that a decision on deleting the EW/EB boundary should be postponed to next year, pending an examination of whether there are differences between the 1997-2002 and the 2003-2007 data and whether these could be explained by changes in laboratory procedures (see 3.3.1.2).

There was no proposal to change the boundaries of the ES *Small Area*. Although there was no genetic evidence to support it being separate from the EB and EW *Small Areas*, it was considered desirable to retain the subarea from a precautionary and operational point of view.

3.3.2 Recommendations

The sub-committee recommended that the *Implementation Review* be completed next year, when a recommendation on boundary changes could be made based on the additional work identified above. It is expected that finalised abundance estimates for the eastern and CM areas will also be available then.

3.4 North Pacific common minke whales (RMP/NPM)

Last year (JCRM 10 (suppl.): 10) the Committee agreed that rather than starting an *Implementation Review* this year, i.e. in 2008, it would be better to discuss and synthesize the available new information first (in the spirit of a *pre-Implementation assessment*). An intersessional Steering Group under Kitakado was established and some aspects of the work with respect to J-stock had been progressed through the North Pacific Minke whale working group (NPM) under Kitakado during this meeting.

Japanese scientists reported that they currently have a very heavy workload in preparing data and analyses for the forthcoming JARPNII review. In addition the in-depth assessment of western North Pacific minke whales, with emphasis on J-stock, is currently underway. Both will contribute to the *Implementation* process. In the light of the above, and the experience of the lengthy original *Implementation* which had led to the development of the *Requirements and Guidelines for Implementation*, they believed it was appropriate to delay consideration of this item until the JARPNII review and the in-depth assessment had been completed.

Noting that the agreement last year related to preparing for the *Implementation Review* and not undertaking it, the subcommittee agreed to defer further general consideration of this item to the next meeting.

4. WORK PLAN

(1) RMP – general matters

An intersessional meeting (held in conjunction with the Second Fin Whale Intersessional Workshop) needs to be conducted to further discussions regarding MSYR for use in RMP (including the impact of environmental variability on estimates of MSYR) so that a final decision can be made on this matter, and hence also on the Norwegian proposal to revise the RMP, at the 2009 Annual Meeting. A meta-analysis of existing and revised estimates of trends (see Item 2.4) is needed for this meeting. Costs associated with travel and subsistence for this meeting are estimated as £3,000. An intersessional steering group comprised of Butterworth (Convenor), Cooke, Donovan, Gunnlaugsson, Kitakado, Punt, Skaug and Walløe was appointed to guide this work and organise the meeting.

(2) Implementation for the western North Pacific Bryde's Whales

In order for the Committee to be in a position to finalise this matter, the revised research proposal and previous genetic power analyses need to be reviewed at the 2009 Annual Meeting.

(3) Implementation for North Atlantic fin whales

The ability to complete the programming work needed to implement and then condition the *Implementation Simulation Trials* was substantially enhanced by the extra computational support for the Secretariat that was funded last year. Without a continuation of this support, the Committee will not be in a position to meet the strict timetable agreed in the Requirements and Guidelines for *Implementations*. A proposal for the continued support is given as Appendix 11.

Assuming that the proposal is agreed and funded, the sub-committee should be in a position to complete the *Implementation* at next year's meeting. The Second Interessional Workshop will be held in Spring 2009, at a location to be selected, for a period of five days. There are costs associated with travel and subsistence, estimated as £10,000. The sub-committee re-established a Steering Group under Donovan (Allison, Butterworth, Cooke, Cunningham, Gunnlaugsson, Hammond, Palsbøll, Punt, Rademeyer, Skaug, and Vikingsson) to guide the work for this Workshop. Allison (together with Cunningham and Rademeyer) should run the *Implementation Simulation Trials* and develop initial plots and tables, and also develop and run the single-stock trials needed to apply the criteria for evaluating conservation performance.

(4) Implementation Review for North Atlantic minke whales

The Committee should be in a position to complete the *Implementation Review* at next year's meeting. Papers should be submitted to the meeting based on work identified under Item 3.3.1.4 (boundary between sub-areas EW and EB) and abundance estimates for the eastern and CM areas.

5. ADOPTION OF REPORT

The report was adopted at 18:49 on 10 June 2008. The sub-committee thanked the chair for guiding them through a long agenda. The Chair and Cooke thanked the rapporteurs.

REFERENCES

- Borchers et al. 2008 [To come]
Buckland et al. 2001 [To come]
Danielsdottir, A.K., Duke, E.J., Joyce, P. and Arnason, A. 1991. Preliminary studies on genetic variation at enzyme loci in fin whales (*Balaenoptera physalus*) and sei whales (*Balaenoptera borealis*) from the North Atlantic. *Rep. int. Whal. Comm* (special issue) 13: 115-24.
Danielsdottir, A.K., Sigurjónsson, J., Mitchell, E. and Arnason, A. 1992. Report of the pilot study of genetic variation in North Atlantic fin whales (*Balaenoptera physalus*). Paper SC/44/NAB15 presented to the IWC Scientific Committee, June 1992 (unpublished) 10ppm.
Gunnlaugsson, T. and Sigurjónsson, J. 1989. Analysis of North Atlantic fin whale marking data from 1979-1988 with special reference to Iceland. *Rep. int. Whal. Comm* 39: 383-88.
International Whaling Commission. 1992. Report of the Comprehensive Assessment Workshop on Catch Per Unit Effort (CPUE). *Rep. int. Whal. Comm* 38:157-62.
International Whaling Commission. 2007. Report of the Joint NAMMCO/IWC Scientific Workshop on the Catch History, Stock Structure and Abundance of North Atlantic Fin Whales, 23-26 March 2006, Reykjavík, Iceland. *J. Cetacean Res. Manage.* 9:451-68
Kitakado, T., Kanda, N. and Pastene, L.A. 2005. A prospective evaluation of statistical power for population identification under island models. Paper SC/M05/BR3 presented to the Workshop on the pre-implementation assessment of western North Pacific Bryde's whales, Tokyo, Japan, March 21-24 2005 (unpublished). 14pp. [Paper available from the Office of this Journal].
Thomas et al. 2005 [To come]
Vikingsson, G.A., Pike, D.G., Desportes, G., Øien, N. and Gunnlaugsson, Th. In press. Distribution and abundance of fin whales (*Balaenoptera physalus*) in the Northeast and Central Atlantic as inferred from the North Atlantic Sightings Surveys 1987-2001. *NAMMCO Sci. Publ.* 7

Table 1
Agreed abundance estimates and their CVs (1998-2002) for use in the *CLA* for the western north Pacific Bryde's whales.

Area	Estimate	CV
1W	4,957	39.8
1E	11,213	49.8
2	4,331	55.3
Total Area	20,501	33.7

Table 2. The Implementation Simulation Trials for North Atlantic fin whales.

Trial No.	No. of Stocks	Stock Hypothesis	MSY _{Rmat}	Catch series	Boundaries	Future surveys	Mark loss rate	Other	Trial Weight	Notes
NF01	4	I	1%	Best	Baseline	EG,WI,El+F	0	-	M	Base case: 4 stocks, separate feeding areas
NF02	4	I	4%	Best	Baseline	EG,WI,El+F	0	-	H	Base case: 4 stocks, separate feeding areas
NF03	4	II	1%	Best	Baseline	EG,WI,El+F	0	-	M	4 stocks; 'W' & 'E' feed in central sub-areas
NF04	4	II	4%	Best	Baseline	EG,WI,El+F	0	-	H	4 stocks; 'W' & 'E' feed in central sub-areas
NF05	4	III	1%	Best	Baseline	EG,WI,El+F	0	-	M	4 stocks; 'C' feeds in adjacent sub-areas
NF06	4	III	4%	Best	Baseline	EG,WI,El+F	0	-	H	4 stocks; 'C' feeds in adjacent sub-areas
NF07	4	IV	1%	Best	Baseline	EG,WI,El+F	0	-	M	4 stocks without sub-stock interchange
NF08	4	IV	4%	Best	Baseline	EG,WI,El+F	0	-	H	4 stocks without sub-stock interchange
NF09	4	V	1%	Best	Baseline	EG,WI,El+F	0	-	M	4 stocks as in I but 'S' in adjacent sub-areas
NF10	4	V	4%	Best	Baseline	EG,WI,El+F	0	-	H	4 stocks as in I but 'S' in adjacent sub-areas
NF11	3	VI	1%	Best	Baseline	EG,WI,El+F	0	-	M	3 stocks (no 'E' stock)
NF12	3	VI	4%	Best	Baseline	EG,WI,El+F	0	-	H	3 stocks (no 'E' stock)
NF13	2	VII	1%	Best	Baseline	EG,WI,El+F	0	-	L	2 stocks (no 'W' or 'E' stock)
NF14	2	VII	4%	Best	Baseline	EG,WI,El+F	0	-	M	2 stocks (no 'W' or 'E' stock)
NF15	4	I	1%	High	Baseline	EG,WI,El+F	0	-	M	High historic catch series
NF16	4	I	4%	High	Baseline	EG,WI,El+F	0	-	H	High historic catch series
NF17	4	III	1%	High	Baseline	EG,WI,El+F	0	-	M	High historic catch series
NF18	4	III	4%	High	Baseline	EG,WI,El+F	0	-	H	High historic catch series
NF19	4	I	1%	Low	Baseline	EG,WI,El+F	0	-	L	Low historic catch series
NF20	4	I	4%	Low	Baseline	EG,WI,El+F	0	-	L	Low historic catch series
NF21	4	III	1%	Low	Baseline	EG,WI,El+F	0	-	L	Low historic catch series
NF22	4	III	4%	Low	Baseline	EG,WI,El+F	0	-	L	Low historic catch series
NF23	4	III	1%	Best	NI catch from WI	EG,WI,El+F	0	-	M	N Iceland catch inc. in WI sub-area
NF24	4	III	4%	Best	NI catch from WI	EG,WI,El+F	0	-	H	N Iceland catch inc. in WI sub-area
NF25	4	III	1%	Best	Baseline	WI	0	-	M	Survey WI only with greater precision
NF26	4	III	4%	Best	Baseline	WI	0	-	H	Survey WI only with greater precision
NF27	4	III	1%	Best	Baseline	N 60°N	0	-	M	WI & El+F surveys exc. S 60°N strata
NF28	4	III	4%	Best	Baseline	N 60°N	0	-	H	WI & El+F surveys exc. S 60°N strata
NF29	4	III	1%	Best	Baseline	EG,WI,El+F	0	Pro-rate abund.	M	Pro-rate abundance data for conditioning
NF30	4	III	4%	Best	Baseline	EG,WI,El+F	0	Pro-rate abund.	M	Pro-rate abundance data for conditioning
NF31	4	III	1%	Best	Baseline	EG,WI,El+F	0	Fit to CPUE	M	Inc. CPUE data in the likelihood calculation
NF32	4	III	4%	Best	Baseline	EG,WI,El+F	0	Fit to CPUE	M	Inc. CPUE data in the likelihood calculation
NF33	4	I	1%	Best	Baseline	EG,WI,El+F	0.2 → 0.1	-	M	Mark loss =20% in yr 1; 10%/yr thereafter
NF34	4	I	4%	Best	Baseline	EG,WI,El+F	0.2 → 0.1	-	H	Mark loss =20% in yr 1; 10%/yr thereafter
NF35	4	III	1%	Best	Baseline	EG,WI,El+F	0.2 → 0.1	-	M	Mark loss =20% in yr 1; 10%/yr thereafter
NF36	4	III	4%	Best	Baseline	EG,WI,El+F	0.2 → 0.1	-	H	Mark loss =20% in yr 1; 10%/yr thereafter
NF37	4	IV	1%	Best	Baseline	EG,WI,El+F	0.2 → 0.1	-	M	Mark loss =20% in yr 1; 10%/yr thereafter
NF38	4	IV	4%	Best	Baseline	EG,WI,El+F	0.2 → 0.1	-	H	Mark loss =20% in yr 1; 10%/yr thereafter
NF39	4	I	1%	Best	Baseline	EG,WI,El+F	0	Selectivity decr	M	Selectivity decr. 4%/yr after age 8; M=0.04
NF40	4	I	4%	Best	Baseline	EG,WI,El+F	0	Selectivity decr	H	Selectivity decr. 4%/yr after age 8; M=0.04
NF41	4	I	1%	Best	Baseline	EG,WI,El+F	0	Wt tag likelihd	M	Tag likelihood weight = * 10
NF42	4	I	4%	Best	Baseline	EG,WI,El+F	0	Wt tag likelihd	M	Tag likelihood weight = * 10
NF43	4	I	1%	Best	Baseline	EG,WI,El+F	0	C2->EG	M	C2 substock enters EG beginning yr 1985
NF44	4	I	4%	Best	Baseline	EG,WI,El+F	0	C2->EG	H	C2 substock enters EG beginning yr 1985
NF45	4	III	1%	Best	Baseline	EG,WI,El+F	0	C2->EG	M	C2 substock enters EG beginning yr 1985
NF46	4	III	4%	Best	Baseline	EG,WI,El+F	0	C2->EG	H	C2 substock enters EG beginning yr 1985
NF48	4	IV	4%	High	Baseline	EG,WI,El+F	0	-	H	4 stocks without sub-stock interchange; High catch series
NF01b	4	I	2.5%	Best	Baseline	EG,WI,El+F	0	MSYR 2.5%	H	Base case: 4 stocks, separate feeding areas
NF03b	4	II	2.5%	Best	Baseline	EG,WI,El+F	0	MSYR 2.5%	H	4 stocks; 'W' & 'E' feed in central sub-areas
NF05b	4	III	2.5%	Best	Baseline	EG,WI,El+F	0	MSYR 2.5%	H	4 stocks; 'C' feeds in adjacent sub-areas
NF07b	4	IV	2.5%	Best	Baseline	EG,WI,El+F	0	MSYR 2.5%	H	4 stocks without sub-stock interchange
NF09b	4	V	2.5%	Best	Baseline	EG,WI,El+F	0	MSYR 2.5%	H	4 stocks as in I but 'S' in adjacent sub-areas
NF11b	3	VI	2.5%	Best	Baseline	EG,WI,El+F	0	MSYR 2.5%	H	3 stocks (no 'E' stock)
NF13b	2	VII	2.4%	Best	Baseline	EG,WI,El+F	0	MSYR 2.5%	M	2 stocks (no 'W' or 'E' stock)
NF47	4	IV	2.5%	High	Baseline	EG,WI,El+F	0	MSYR 2.5%	H	4 stocks without sub-stock interchange; high catches
NF01x	4	I	1%	Best	Baseline	EG,WI,El+F	0	Fix C tag rep	L	Fix Canada tag reporting rate = 1
NF02x	4	I	4%	Best	Baseline	EG,WI,El+F	0	Fix C tag rep	L	Fix Canada tag reporting rate = 1

Appendix 1

AGENDA

1. INTRODUCTORY ITEMS

- 1.1 Convenor's opening remarks
- 1.2 Election of Chair and appointment of rapporteurs
- 1.3 Adoption of Agenda
- 1.4 Available documents

2. REVISED MANAGEMENT PROCEDURE (RMP) – GENERAL ISSUES

- 2.1 Matters related to MSYR and MSYL
 - 2.1.1 Review MSYR Workshop report, if appropriate suggest changes to the plausible range
 - 2.1.2 Modelling MSY-related parameters under stochastic dynamics
- 2.2 Finalise the process for reviewing proposals to amend the RMP
- 2.3 Consideration of the Norwegian proposal to amend the RMP
- 2.4 Work plan

3. RMP – PREPARATIONS FOR IMPLEMENTATION

- 3.1 Western North Pacific Bryde's whales
 - 3.1.1 Finalise abundance estimates for western North Pacific Bryde's whales
 - 3.1.2 Review of proposed research plan
 - 3.1.3 Work plan
- 3.2 North Atlantic fin whales
 - 3.2.1 Report of the First Intersessional Workshop
 - 3.2.2 Objectives of the First Annual Meeting
 - 3.2.3 Review results of conditioning
 - 3.2.4 Updates to standard datasets
 - 3.2.5 Final consideration of plausibility (including weighting of trials in terms of overall balance)
 - 3.2.5.1 Stock structure hypotheses
 - 3.2.5.2 Other
 - 3.2.6 Data/research to reduce hypotheses
 - 3.2.7 Specification of operational features and management variants
 - 3.2.8 Specification and classification of final trials
 - 3.2.9 Inputs for actual application of the CLA
 - 3.2.10 Work plan
- 3.3 North Atlantic common minke whales
 - 3.3.1 Implementation Review
 - 3.3.1.1. History
 - 3.3.1.2. Stock structure
 - 3.3.1.3. Abundance estimates
 - 3.3.1.4. Implementation Simulation Trials
 - 3.3.1.5. Management areas
 - 3.3.2. Recommendations
- 3.4 North Pacific common minke whales (RMP/NPM)
 - 3.4.1 Progress on developing an inventory of the new data available
 - 3.4.2. Recommendations

4. WORK PLAN

5. ADOPTION OF REPORT

Appendix 2

ESTIMATION OF *MSYR* IN THE PRESENCE OF ENVIRONMENTALLY-INDUCED VARIABILITY: FURTHER SPECIFICATION OF MODELS USED IN SC/59/RMP10 AND SC/NO1/MSYR1

Justin Cooke

Model for the true population ("operating model")

The true population is simulated using a bulk, non-age structured model:

$$x_{t+1} = x_t \exp(r(x_t, t) - F_t)$$

x_t : stock size in year t

F_t : fishing mortality rate in year t

$r(x, t)$: net recruitment rate, given by:

$$r(x, t) = r_{\max} \left(1 - e^{-(\sigma \eta_t + \frac{1}{2} \sigma^2)} \right) \left(1 - q + q(x/K)^z \right)$$

K : mean carrying capacity (set to 1.0 so that all population sizes are relative to K)

z : density-dependent exponent (set to 2.39)

q : habitat quality ($0 < q \leq 1$) (values used in trials are 0.1, 0.4 and 0.9)

σ : level of environmental variability (values used in trials are 0.0, 0.5 and 1.0)

η_t : standard $N(0, 1)$ random variables, not necessarily uncorrelated

Serial correlation in environmental variability is modelled by invoking a sequence v_t of uncorrelated $N(0, 1)$ random variables, such that:

$$\begin{aligned} \eta_0 &= v_0 \\ \eta_t &= \rho v_t + \sqrt{1 - \rho^2} v_{t-1} \quad (t = 1, 2, \dots) \end{aligned}$$

The serial correlation ρ was set to 0.0, 0.5 or 0.9 in different trials.

$MSYR$ and $MSYL$ depend on both q and z and are found by maximisation of the yield $x r(x, t)$.

In the simulations, the population is subject to T_0 years of exploitation at a constant fishing mortality rate, followed by T_1 years of protection with annual surveys of population size.

During the monitoring period, an annual population estimate is obtained that is log-normally distributed with a given CV:

$$y_t = x_t \exp(\tau \zeta_t) \quad (t = T_0 + 1, \dots, T_0 + T_1)$$

where $\tau^2 = \ln(1 + CV^2)$ and the ζ_t are standard normal uncorrelated random variables. Values used for CV were 0.0, 0.2, and 0.5.

There are two ways of specifying the depletion of the population at the start of the monitoring period:

Method 1 (used in SC/59/RMP10) defines the depletion level as a fraction of K . The population model is started at $t = T_0$ with $x_t = DK$, where D is the specified depletion level. Using this method, the period of exploitation is not explicitly modelled.

Method 2 is to start the population at $t = 0$ with $x_0 = K$. The level of fishing mortality is found which depletes the population to DK after T_0 years. If the population declines to below DK without catches, the simulation is discarded and a new simulation is run.

Model for the fitted population (assessment model)

The assessment model is deterministic:

$$\begin{aligned} x_{t+1} &= (x_t - \tilde{c}_t) \exp(r(x_t)) \\ r(x) &= r_0 \left(1 - (x/K)^z \right) \end{aligned}$$

c_t is the catch in year t . \tilde{c}_t is the capped catch in year t : $\tilde{c}_t = \min(c_t, 0.5x_t)$. The catch-capping is used to prevent the fitted population becoming negative during the search for the minimum. The capping would not normally be active at the solution.

Parameter estimation

r_0 and K are free parameters to be estimated. The assessment model is fitted in each of two ways:

- (i) with the assumption $x_0 = K$;
- (ii) with x_0 (the initial population size) as an additional free parameter to be estimated.

When the true population has been simulated using method 2, then it is necessary to treat x_0 as a free parameter, because the period with catches has not been simulated.

The exponent z is kept fixed at the value 2.39, which corresponds to $MSYL = 0.6$. The estimate of $MSYR$ is given by $r_0 z/(1+z)$.

The model fitting is fitted by minimising the following expression for the deviation between observed and predicted abundance:

$$Q = \sum_{t=T_0+1}^{T_0+T_1} \left(\log(y_t/x_t) / \tau \right)^2$$

The model is fitted by a nested minimisation over K , r_0 and, optionally x_0 . The minimisation over K is performed at the innermost level, the minimisation over x_0 , if applicable, at the outermost level. At each level, the function Q is first evaluated over a grid of points, to check for multiple minima, before the minimum is located.

Significance testing

A tally is kept of trials where the assumption $x_0 = K$ would be rejected in favour of $x_0 < K$ is kept by computing for each trial the difference

$\Delta = Q(x_0 = K) - Q(\hat{x}_0)$. The cases where $\hat{x}_0 < K$ and $\Delta > 1.92$ constitute cases where the assumption $x_0 = K$ would be rejected in favour of a lower value of x_0 at the 2.5% significance level.

Reporting of results

For each trial, the following statistics are saved: best estimates of each of the fitted parameters (r_0 , K and x_0), the goodness-of-fit Q , and the time series of true, observed and fitted population sizes by year during the monitoring period. The desired percentiles of each of the saved statistics are computed, separately for each statistic.

Appendix 3

IMPLEMENTATION SIMULATION TRIAL CONDITIONING FOR NORTH ATLANTIC FIN WHALES

Contents:

Graphs showing the following results:

- Fig 3a Median 1+ population trajectories by sub-area for the 7 basic stock structure hypotheses, with MSYR=1%
- Fig 3b Median 1+ population trajectories by sub-area for the 7 basic stock structure hypotheses, with MSYR=2.5%
- Fig 3c Median 1+ population trajectories by sub-area for the 7 basic stock structure hypotheses, with MSYR=4%
- Fig 4a Median 1+ population trajectories by sub-area for the MSYR=1% hypothesis I trials (1 = baseline; 15=high catch; 19=low catch; 33=mark loss; 39=selectivity decrease; 1x=Fix Canada tag reporting rate to 1, 41=10x tag likelihood)
- Fig 4b Median 1+ population trajectories by sub-area for the MSYR=4% hypothesis I trials (2 = baseline; 16=high catch; 20=low catch; 34=mark loss; 40=selectivity decrease; 2x=Fix Canada tag reporting rate to 1, 42=10x tag likelihood)
- Fig 5a Median 1+ population trajectories by sub-area for the MSYR=1% hypothesis III trials (5 = baseline; 17=high catch; 21=low catch; 35=mark loss; 31=fit CPUE, 29=pro-rate abundance)
- Fig 5b Median 1+ population trajectories by sub-area for the MSYR=4% hypothesis III trials (6 = baseline; 18=high catch; 22=low catch; 36=mark loss; 32=fit CPUE, 30=pro-rate abundance)
- Fig 6a Median 1+ population trajectories by sub-area for the MSYR=1% hypothesis IV trials (7 = baseline; 37=mark loss)
- Fig 6b Median 1+ population trajectories by sub-area for the MSYR=4% hypothesis IV trials (8 = baseline; 38=mark loss)
- Fig 7a. Median, 5% and 95%ile 1+ population trajectories by sub-area for Hypothesis I, MSYR = 1% and 4%.
- Fig 7b. Median, 5% and 95%ile 1+ population trajectories by sub-area for Hypothesis III, MSYR = 1% and 4%.
- Fig 8a Fit to the mark recapture data for Hypotheses I showing MSYR = 1 and 4%.
- Fig 8b Fit to the mark recapture data for Hypotheses III showing MSYR = 1 and 4%.
- In Figs 8, the top row shows tags released in the Canada/West Greenland sub-area and recovered in Canada/West Greenland, East Greenland and West Iceland respectively (from left to right). Similarly the middle and bottom rows show tags released in East Greenland and West Iceland respectively.
- Note that for hypothesis I, there is no mechanism for tags released in Canada/West Greenland to get to West Iceland (and vice versa); so that the top right-most plot and middle left-most plot should be ignored for this hypothesis.

Fig 3a

Median 1+ by sub-area; Baseline Hypotheses w. MSYR = 1%

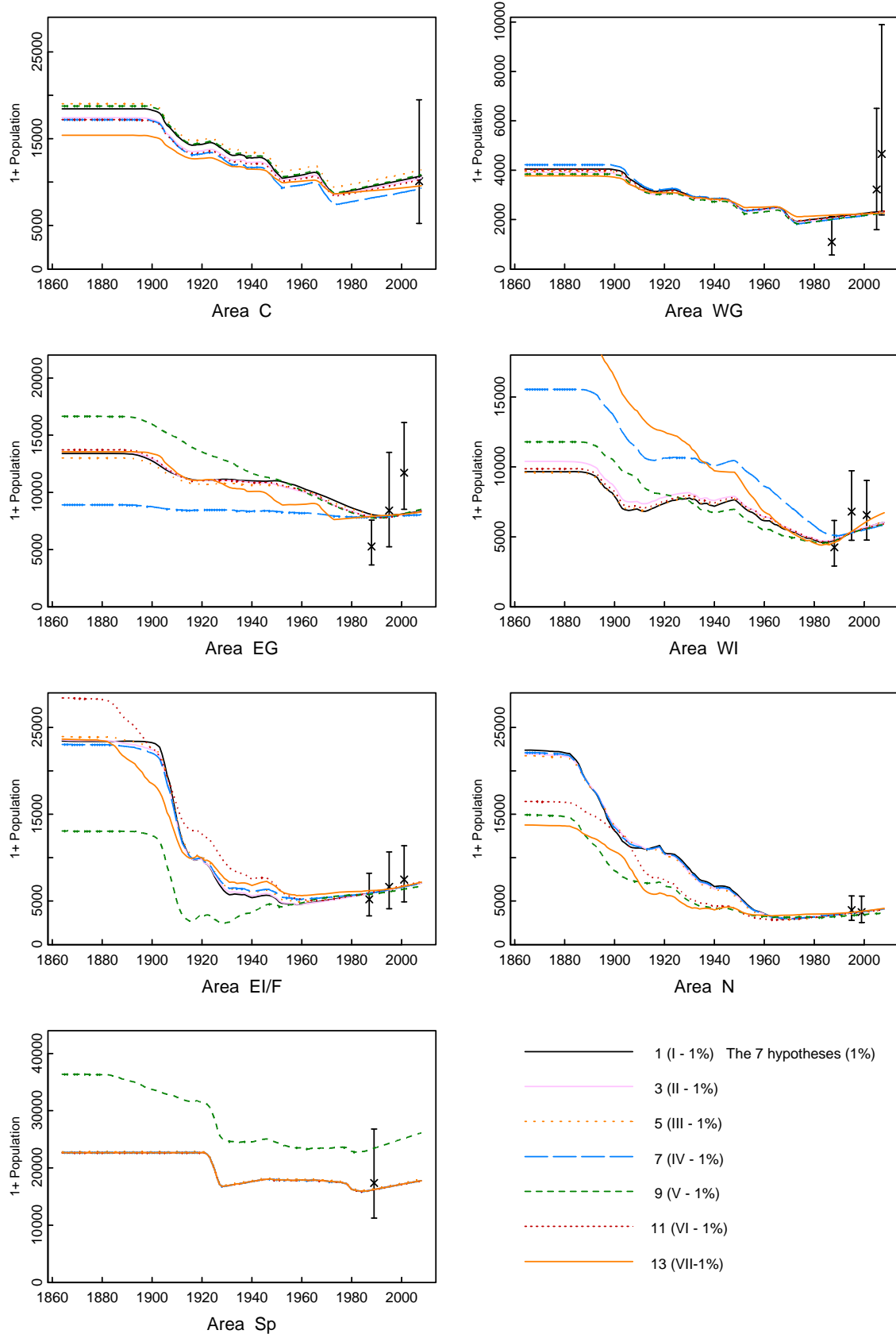


Fig 3b

Median 1+ by sub-area; Baseline Hypotheses w. MSYR = 2.5%)

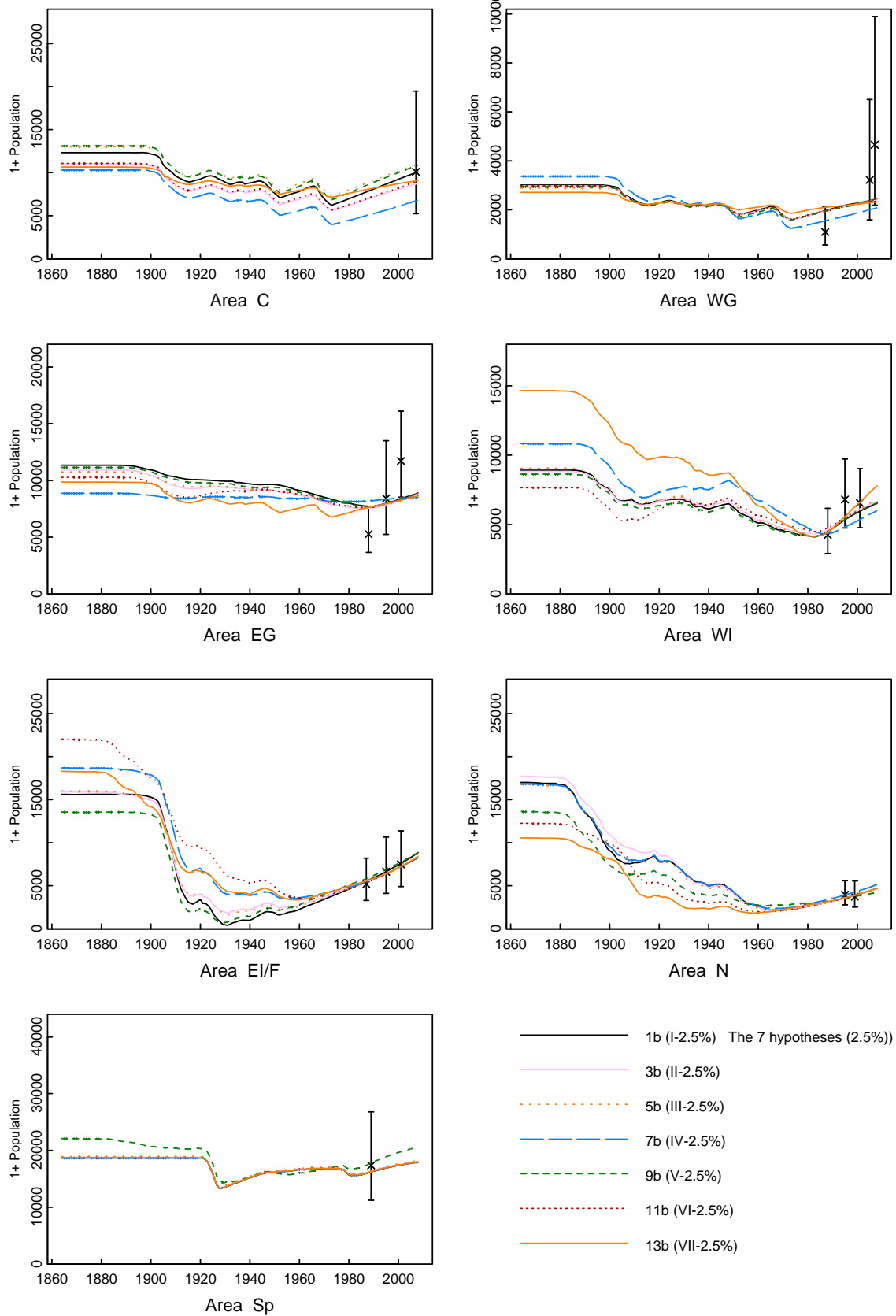


Fig 3c

Median 1+ by sub-area; Baseline Hypotheses w. MSYR = 4%

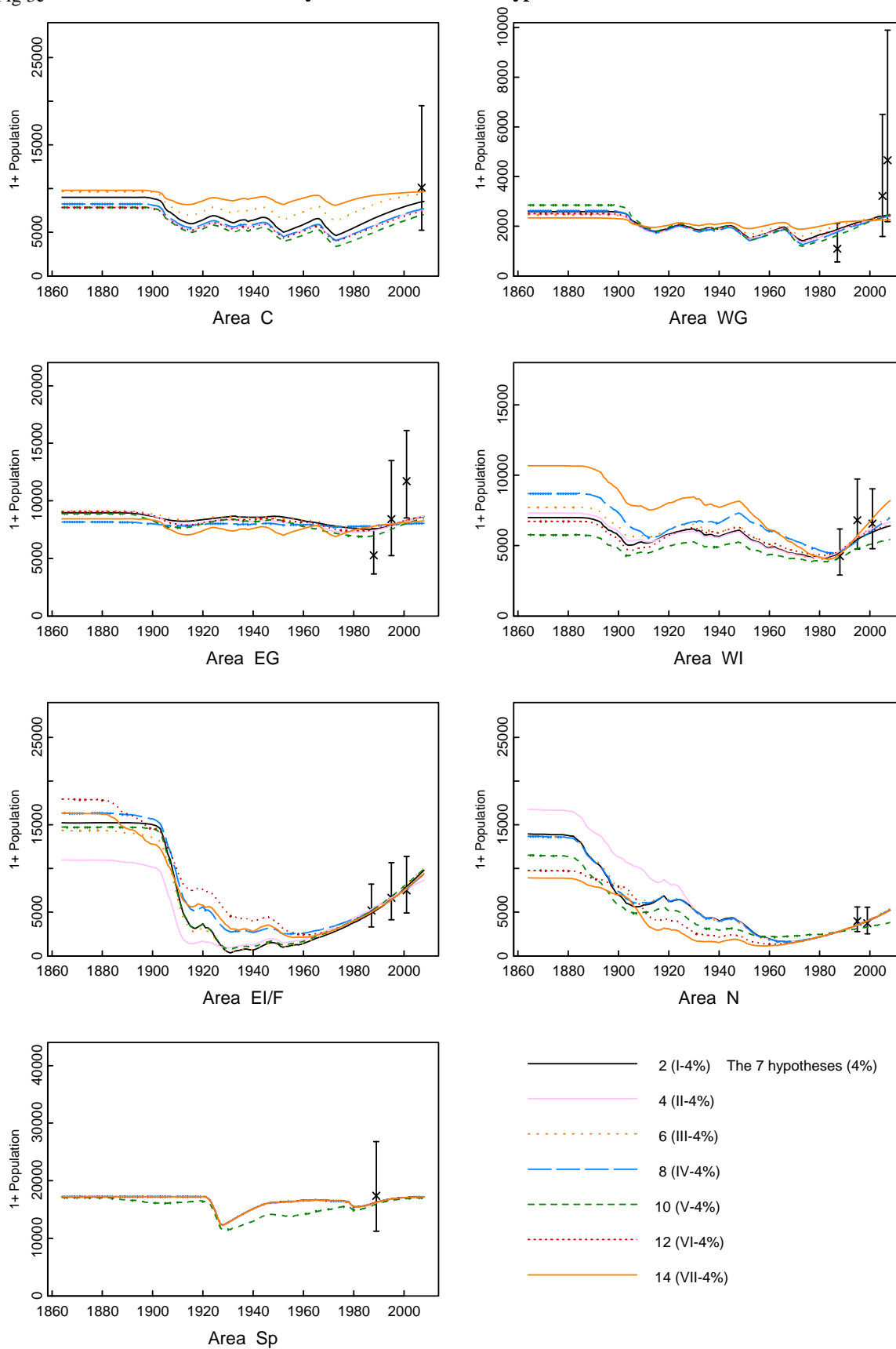


Fig 4a

Median 1+ by sub-area; Hypothesis 1 - 1% variants

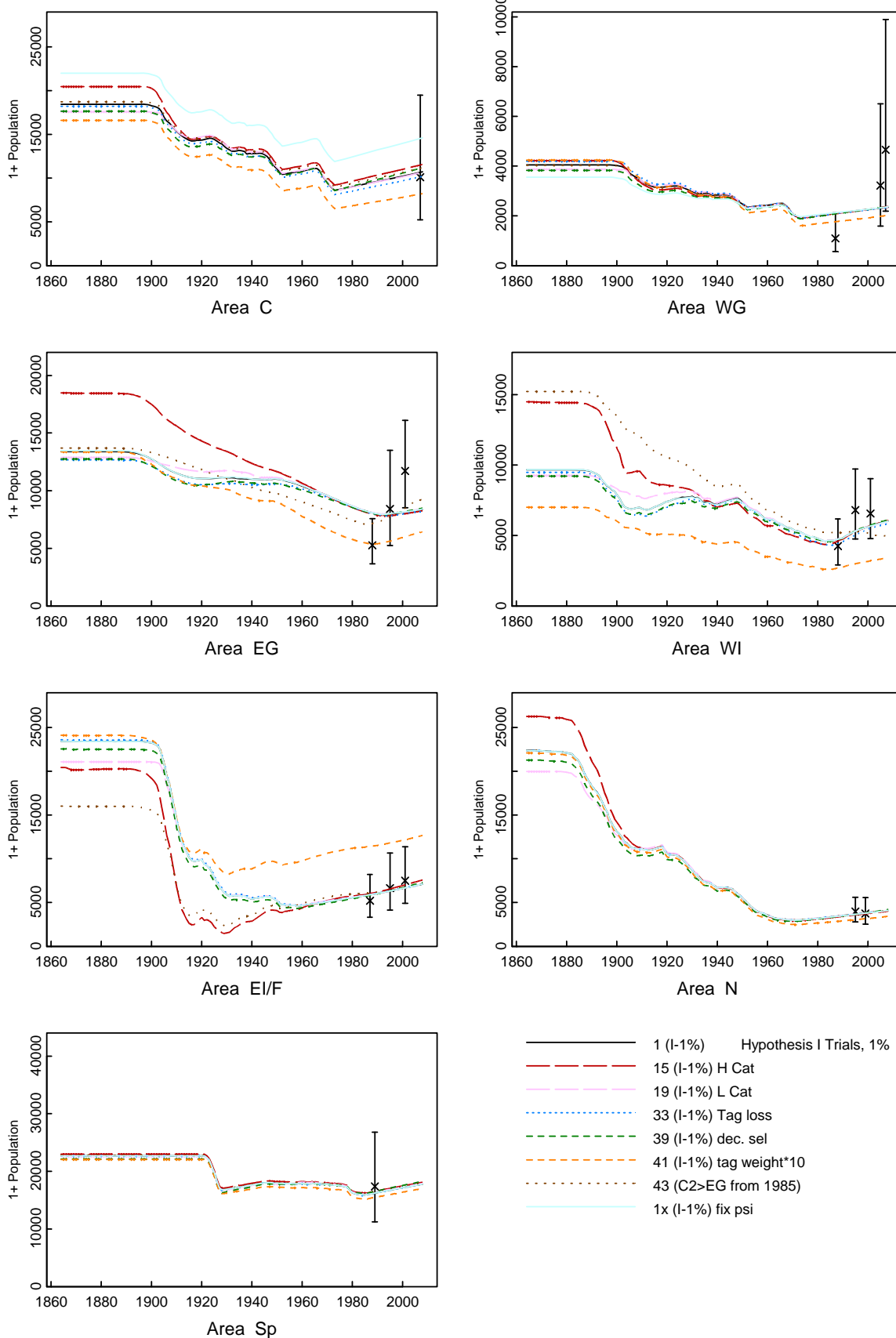


Fig 4b

Median 1+ by sub-area; Hypothesis 1 - 4% variants

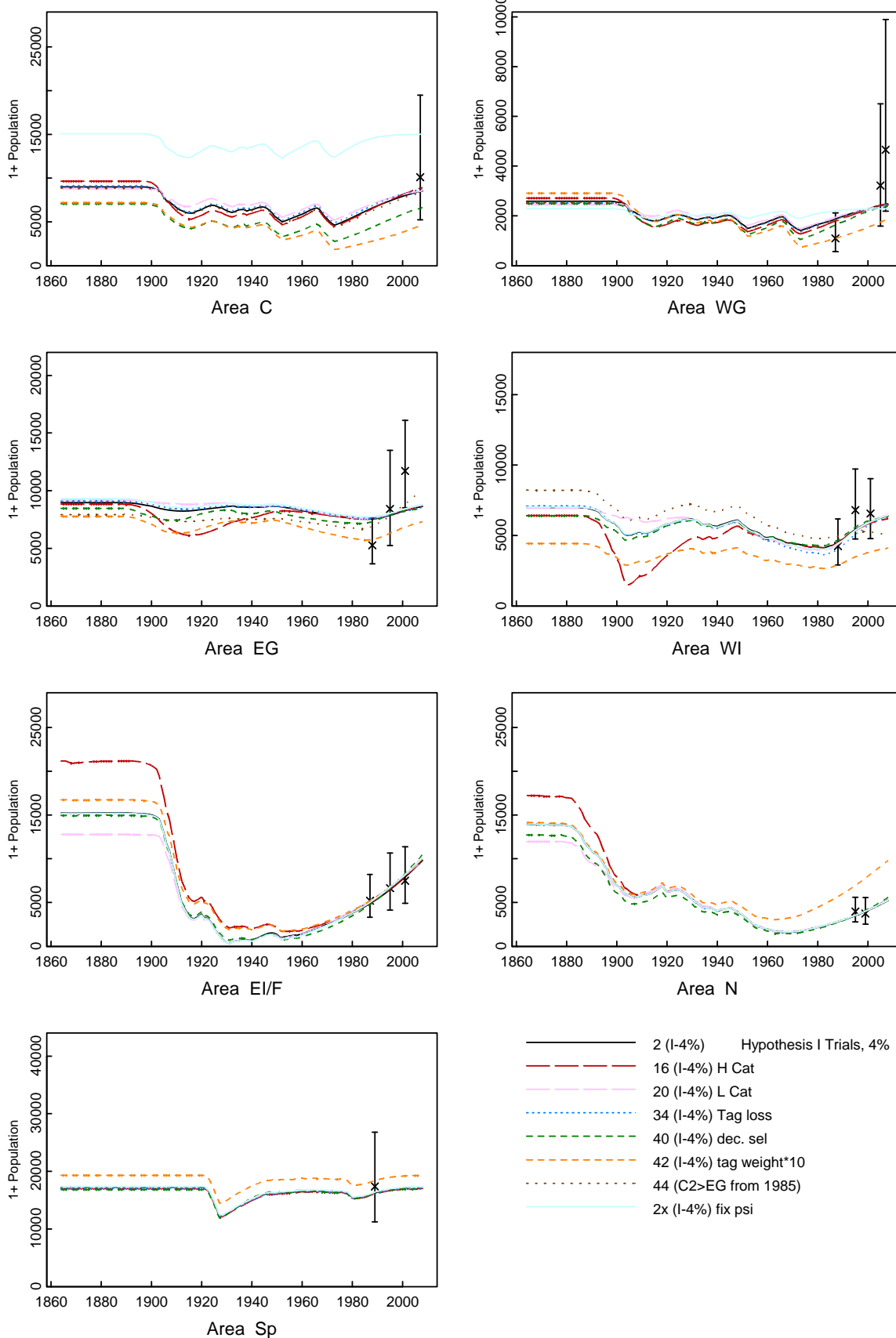


Fig 5a

Median 1+ by sub-area; Hypothesis III 1% variants

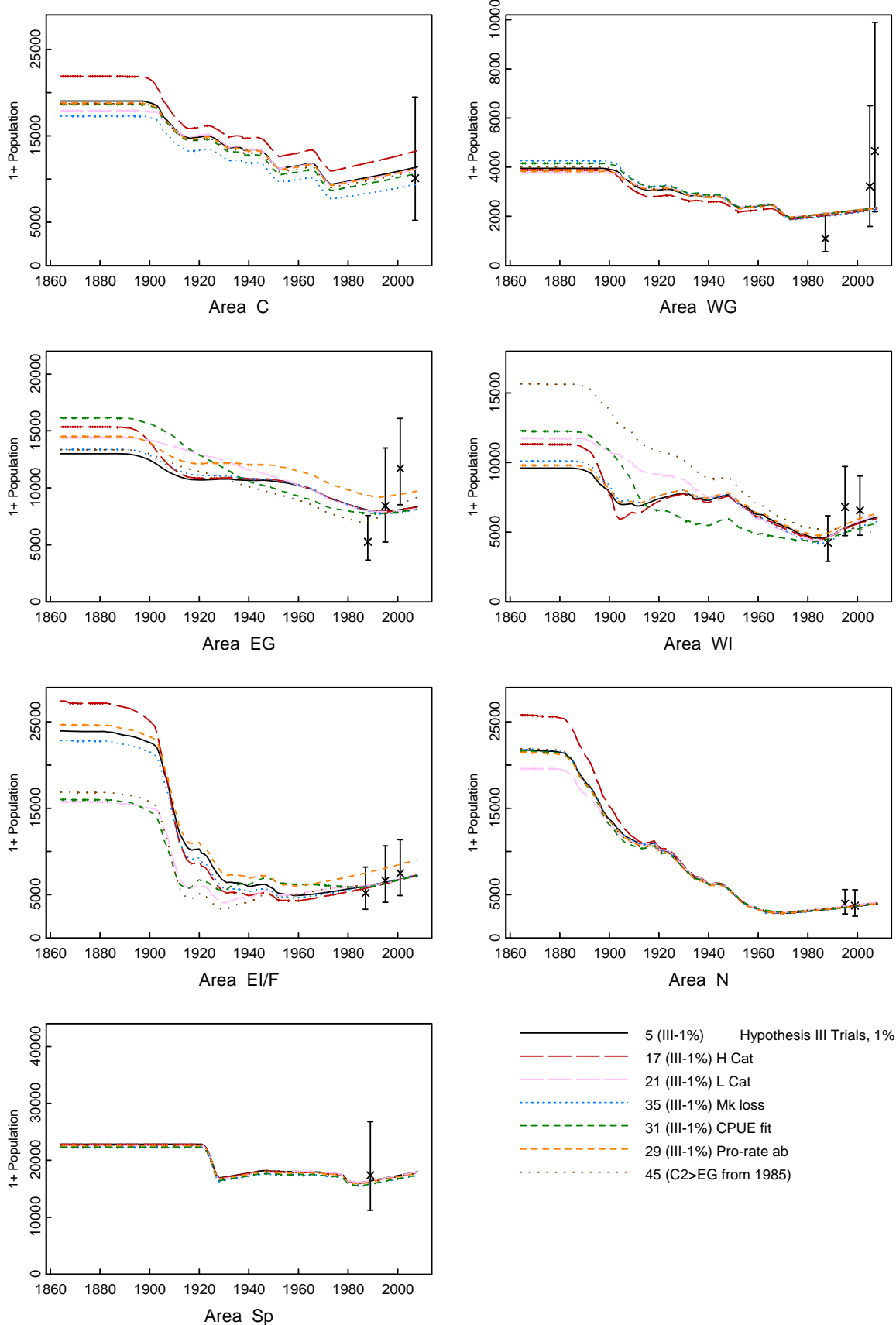


Fig 5b

Median 1+ by sub-area; Hypothesis III 4% variants

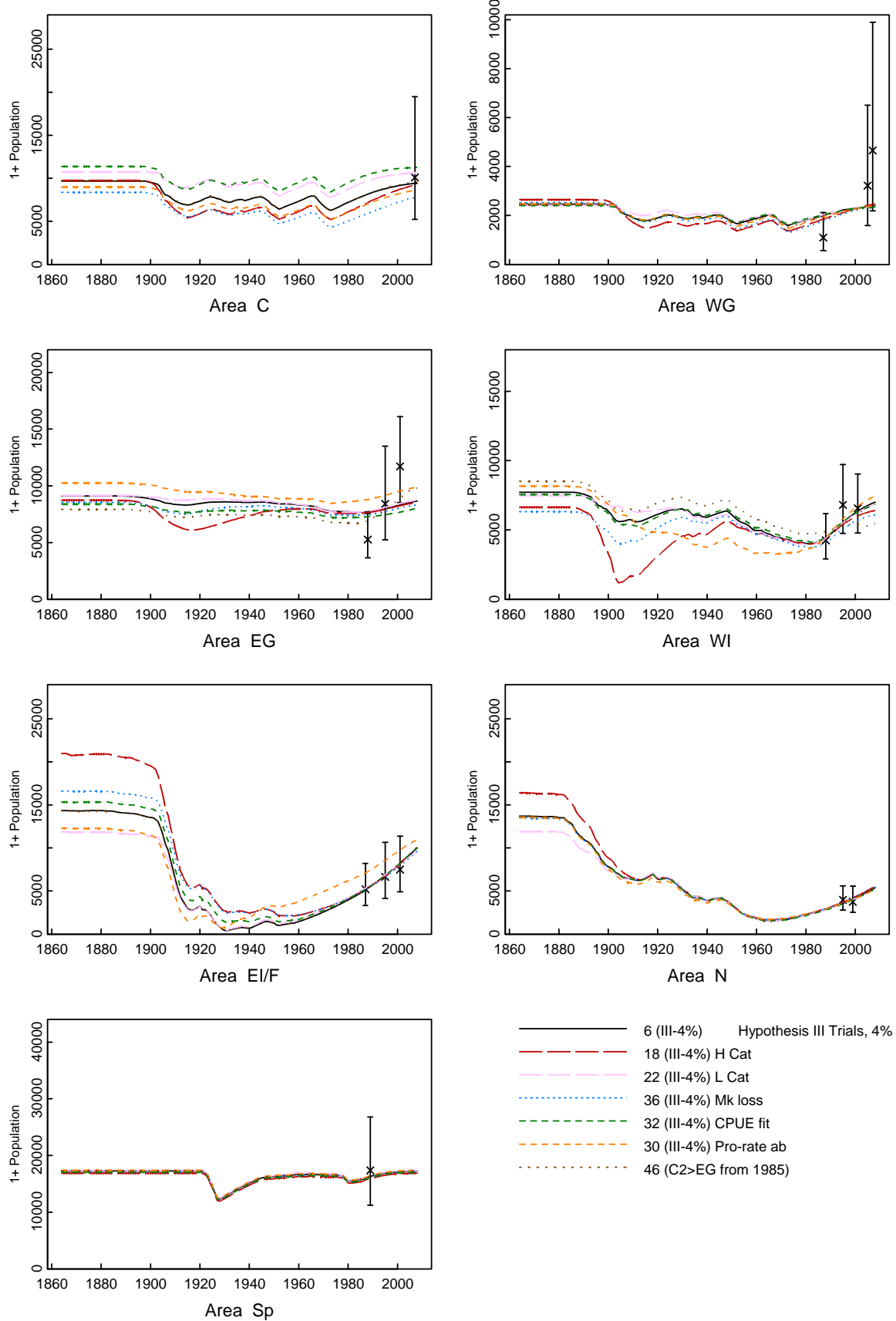


Fig 6a

Median 1+ by sub-area; Hypothesis IV 1% variants

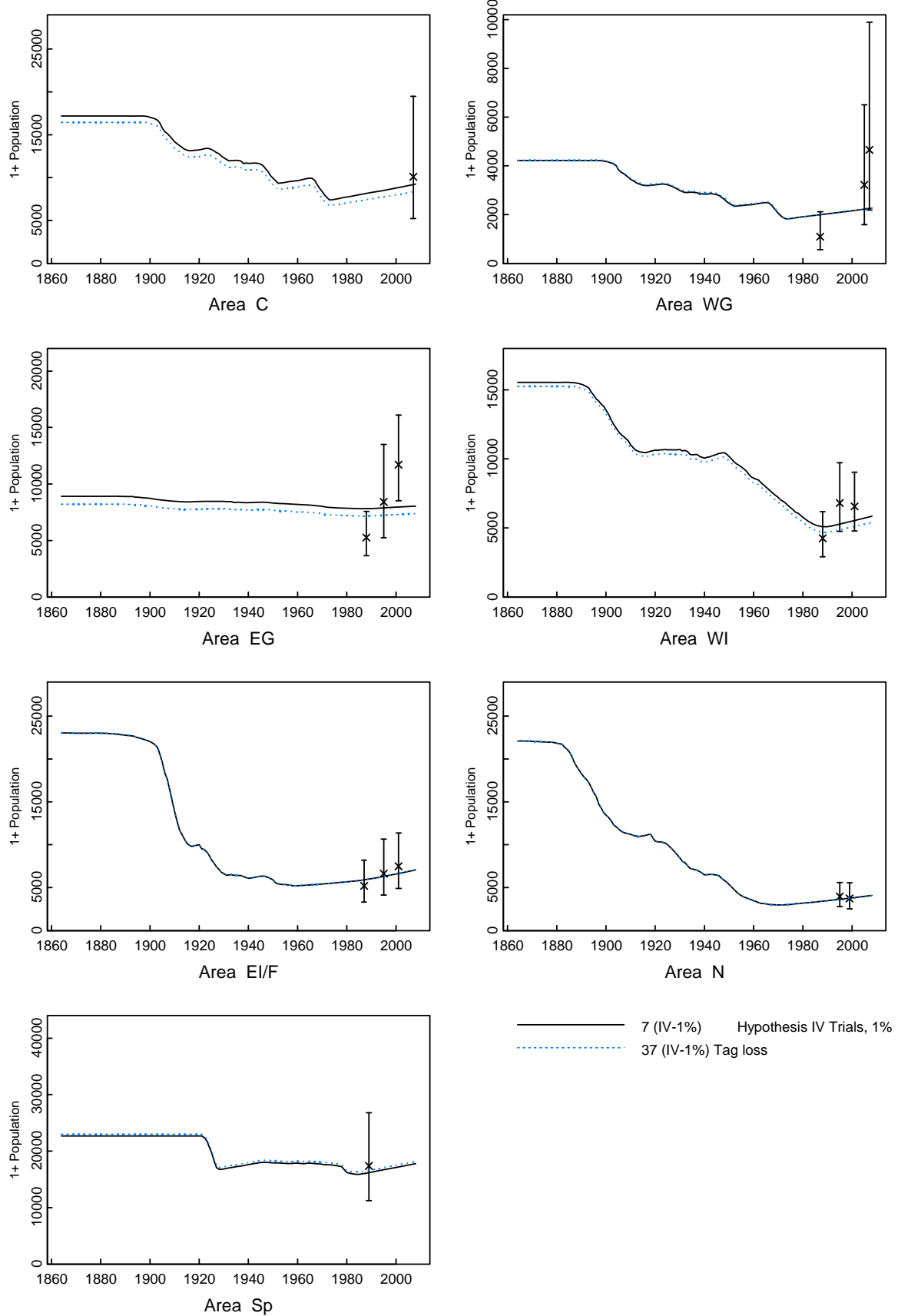


Fig 6b

Median 1+ by sub-area; Hypothesis IV 4% variants

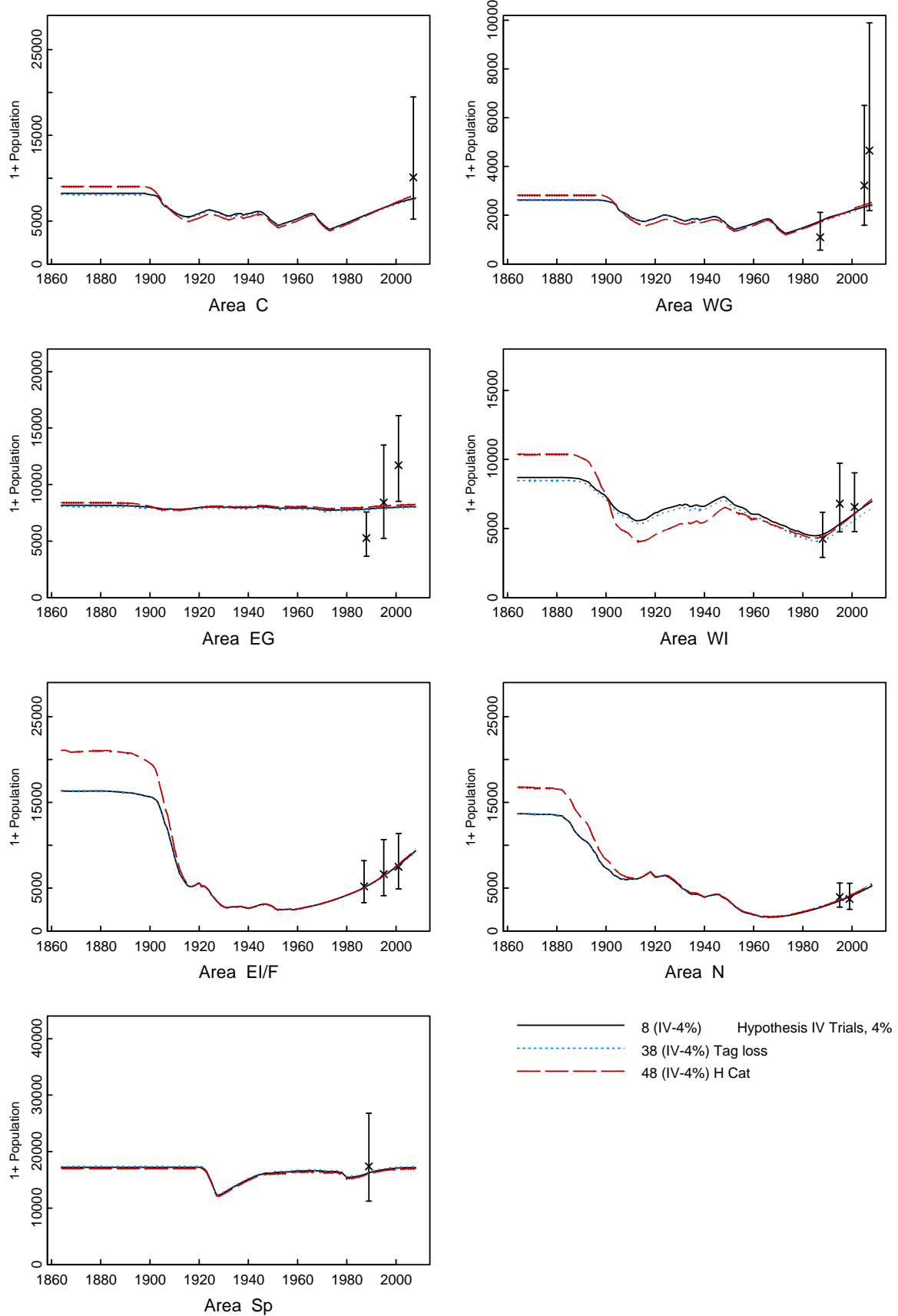


Fig 7a.

Median + 90%ile 1+ trajectories by sub-area; HYPOTHESIS I

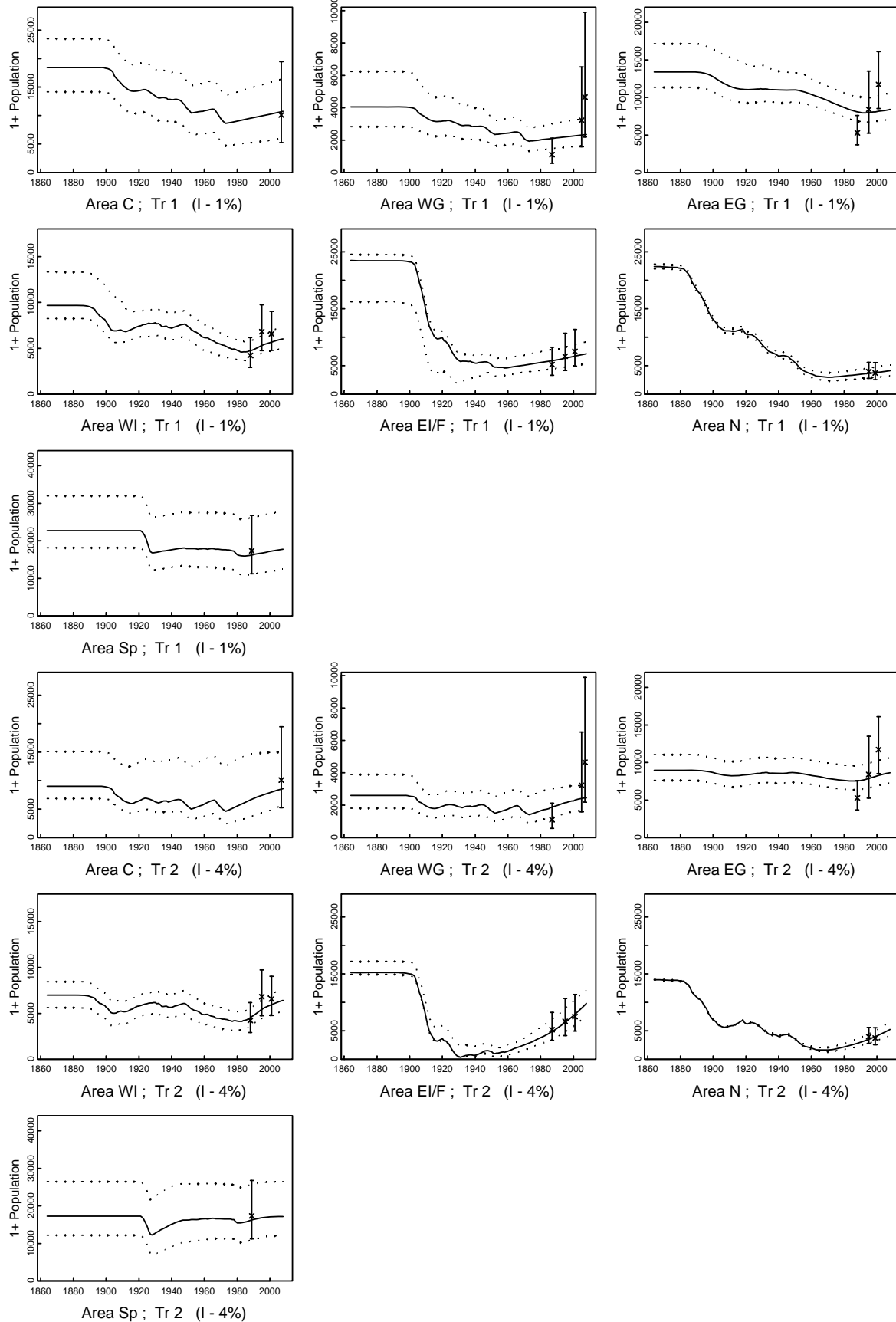


Fig 7b

Median + 90%ile 1+ trajectories by sub-area; HYPOTHESIS III

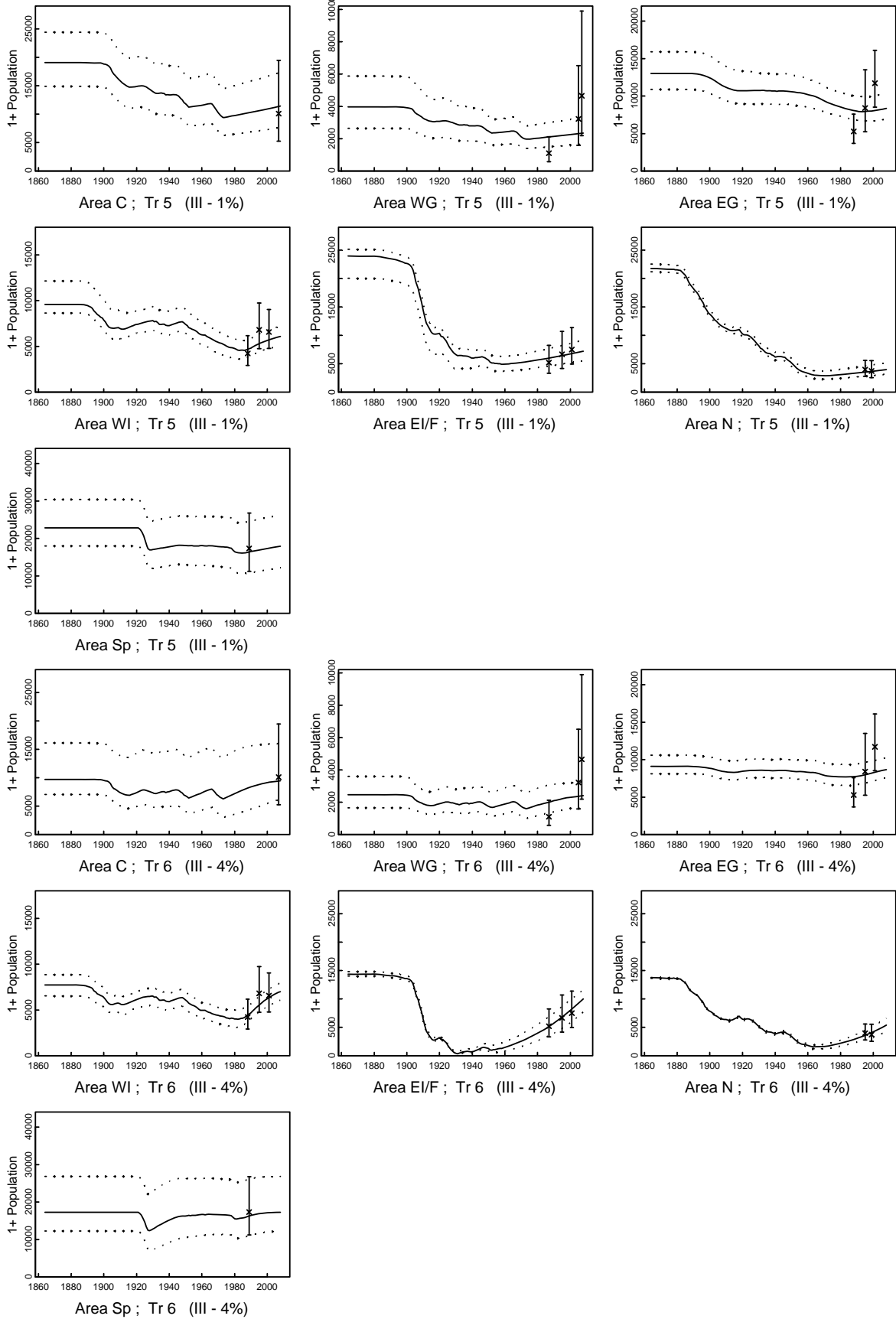


Fig 8a

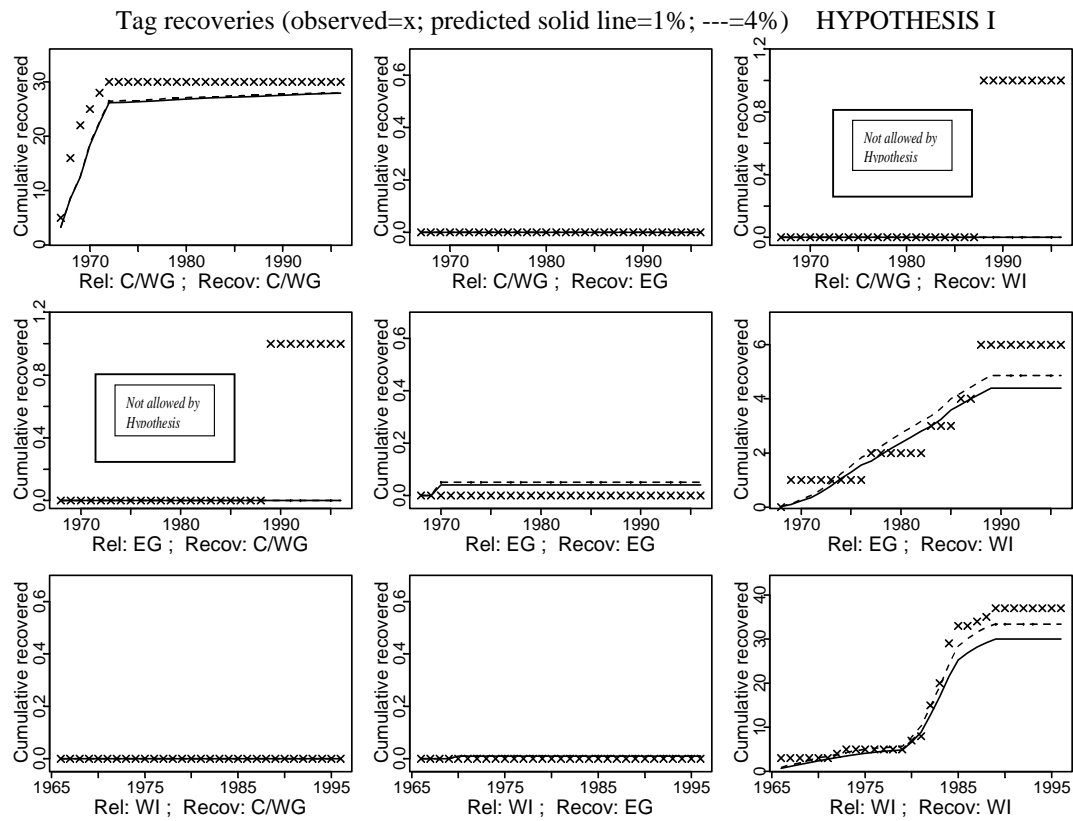


Fig 8b

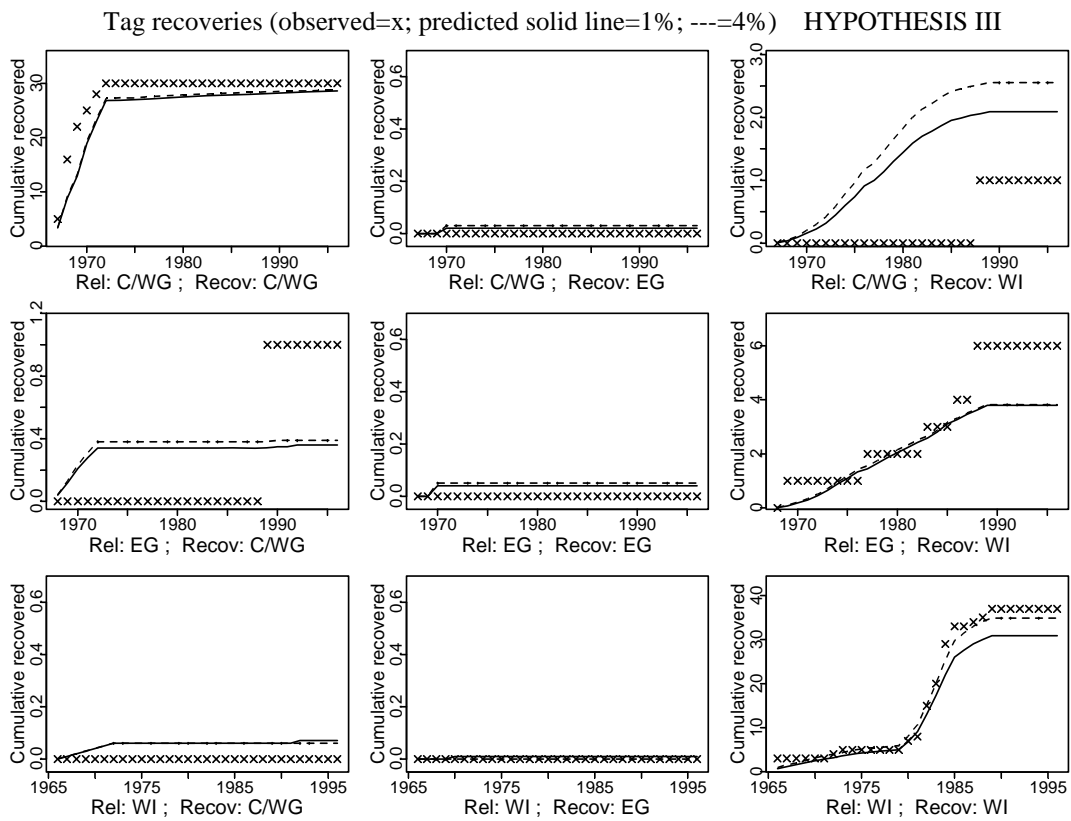


Table 1. Values, based on the fits to the actual data, for the objective function minimized during the conditioning process and the component contributions to this function, the values for the mixing parameters (γ 1-3), the values for the dispersal rates (disp 1, 2), the reporting rate for tags placed in Canada waters (Ψ_C), and the values for stock-specific carrying capacity (K_{mat} 1-6). (The fits to the tagging data have been adjusted to exclude contributions from combinations not allowed by the stock hypothesis model).

Trial	Hyp-MSY	Nstk	Adj Total Fit	Abund fit	AdjTag fit	CPUE fit	γ_1	γ_2	γ_3	Disp 1	Disp 2	Ψ_C	K_{mat} 1	K_{mat} 2	K_{mat} 3	K_{mat} 4	K_{mat} 5	K_{mat} 6	
NAF1	1-1	6	217.2	15.6	201.7		0.81	-	-	0.062	0.000	0.77	7659	4426	3085	7930	7526	8032	Hyp. 1
NAF1b	1-2.5	6	213.0	12.6	200.4		0.79	-	-	0.056	0.017	0.60	5203	3840	2991	5223	5706	6704	
NAF2	1-4	6	212.7	12.6	200.1		0.76	-	-	0.060	0.004	0.47	3793	2995	2144	5592	4679	6226	
NAF1b	1-1x	6	217.8	16.2	201.6		0.84	-	-	0.062	0.000	1.00	8371	4426	3085	7929	7526	8032	Hyp. 1; fix C tag rep
NAF1bx	1-2.5x	6	214.7	14.5	200.2		0.86	-	-	0.056	0.017	1.00	6423	3846	2984	5225	5706	6700	
NAF4x	1-4x	6	214.2	14.8	199.4		0.85	-	-	0.059	0.012	1.00	5670	3117	2356	5089	4679	6225	
NAF3	2-1	6	250.5	15.2	235.3		0.81	-	-	0.064	0.000	0.86	8186	3731	3039	7146	8357	8050	Hyp. 2
NAF	2-2.5	6	246.7	12.4	234.3		0.76	-	-	0.057	0.010	0.60	5192	3156	2707	4759	6687	6724	
NAF4	2-4	6	246.1	12.0	234.1		0.73	-	-	0.059	0.015	0.46	3805	2645	2234	3028	6396	6191	
NAF5	3-1	6	248.7	15.6	233.2		0.82	-	-	0.053	0.000	0.87	7160	4893	3190	8923	6464	8032	Hyp. 3
NAF	3-2.5	6	245.3	12.8	232.5		0.80	-	-	0.047	0.010	0.70	4800	4010	2905	6255	5009	6704	
NAF6	3-4	6	245.1	12.7	232.4		0.78	-	-	0.042	0.013	0.62	3645	3390	2588	5347	4063	6225	
NAF7	4-1	6	260.2	15.9	244.3		0.77	-	-	-	-	0.73	6758	3150	5166	8324	6998	8288	Hyp. 4 no dispersion.
NAF	4-2.5	6	259.4	20.2	239.2		0.73	-	-	-	-	0.45	4185	3386	3372	6814	5303	6924	
NAF8	4-4	6	252.7	13.7	239.0		0.73	-	-	-	-	0.47	3434	2954	2719	5938	4292	6217	
NAF9	5-1	6	222.6	17.1	205.6		0.79	-	-	0.081	0.036	0.70	7340	5517	4029	4235	3675	13798	Hyp. 5 S in adj area
NAF	5-2.5	6	214.5	12.6	201.9		0.80	-	-	0.056	0.017	0.61	5219	3786	2867	4325	3793	8712	
NAF10	5-4	6	222.0	17.2	204.8		0.68	-	-	0.135	0.008	0.40	3469	3013	1930	4818	3207	6499	
NAF11	6-1	5	250.2	15.5	234.6		0.80	0.63	-	0.064	0.001	0.84	8113	3821	3144	15063	8128		Hyp. 6: (5 stpcks)
NAF	6-2.5	5	245.9	12.3	233.6		0.78	0.63	-	0.066	0.000	0.64	5423	2882	2343	11659	6700		
NAF12	6-4	5	245.9	12.6	233.3		0.74	0.64	-	0.064	0.000	0.51	3916	2551	2026	9570	6223		
NAF13	7-1	4	264.1	15.1	249.0		0.46	0.63	0.42	0.011	0.024	1.00	11303	6315	12380	8031			Hyp. 7: (4 stpcks)
NAF	7-2.5	4	260.7	12.7	248.1		0.46	0.63	0.42	0.011	0.024	1.00	8189	4876	9458	6700			
NAF14	7-4	4	261.6	13.8	247.8		0.47	0.64	0.42	0.013	0.007	1.00	7031	3040	8998	6229			
NAF15	1-1	6	217.9	15.7	202.2		0.81	-	-	0.052	0.026	0.78	8201	6283	4784	6998	8849	8012	High catch series
NAF16	1-4	6	211.8	12.0	199.8		0.77	-	-	0.061	0.002	0.47	4153	2964	2136	7111	5774	6227	
NAF17	3-1	6	249.0	15.8	233.2		0.84	-	-	0.053	0.003	1.00	8090	5785	3776	10337	7632	8047	
NAF18	3-4	6	244.6	12.1	232.6		0.78	-	-	0.048	0.001	0.57	3810	3252	2222	7812	4721	6206	
NAF47	4-2.5	6	222.8	13.6	209.3		0.77	-	-	1.000	1.000	0.58	5128	3003	4315	8534	6341	6700	
NAF48	4-4	6	221.0	12.9	208.1		0.74	-	-	1.000	1.000	0.47	3830	2951	3273	7666	5238	6225	
NAF19	1-1	6	217.5	15.7	201.8		0.81	-	-	0.062	0.000	0.77	7295	4214	2931	7130	6718	7963	Low catch series
NAF20	1-4	6	212.5	12.7	199.8		0.77	-	-	0.058	0.013	0.52	3776	3098	2334	4284	4014	6223	
NAF21	3-1	6	249.4	15.8	233.6		0.81	-	-	0.045	0.016	0.87	6752	5371	3787	6159	6008	7963	
NAF22	3-4	6	245.0	12.9	232.0		0.80	-	-	0.048	0.016	0.69	3860	3435	2442	4415	3564	6224	
NAF29	3-1	6	257.1	22.7	234.4		0.81	-	-	0.049	0.001	0.86	6960	5473	3261	9210	6350	8060	Pro-rate abundance
NAF30	3-4	6	253.0	18.3	234.7		0.76	-	-	0.030	0.045	0.56	3326	3820	2734	4598	4103	6222	
NAF31	3-1	6	393.0	20.8	241.8	130.4	0.77	-	-	0.105	0.075	0.71	6485	5762	3815	6631	6451	8288	Fit CPUE data
NAF32	3-4	6	391.8	14.2	232.2	145.3	0.82	-	-	0.044	0.006	0.83	4316	3039	2428	5861	3968	5923	

Trial	Hyp-MSY	Nstk	Adj Total Fit	Abund fit	AdjTag fit	CPUE fit	γ_1	γ_2	γ_3	Disp 1	Disp 2	Ψ_C	$K_{mat\ 1}$	$K_{mat\ 2}$	$K_{mat\ 3}$	$K_{mat\ 4}$	$K_{mat\ 5}$	$K_{mat\ 6}$	
NAF33	1-1	6	221.7	17.0	204.6		0.81	-	-	0.050	0.000	1.00	7589	4333	3083	7930	7526	8022	Tag loss
NAF34	1-4	6	216.1	13.9	202.2		0.77	-	-	0.047	0.012	0.65	3859	3043	2375	5091	4679	6212	
NAF35	3-1	6	254.5	17.5	237.0		0.79	-	-	0.045	0.004	0.98	6482	5158	3388	8379	6524	7664	
NAF36	3-4	6	248.6	14.2	234.5		0.75	-	-	0.042	0.001	0.68	3281	3191	2114	6216	3904	6321	
NAF37	4-1	6	269.6	19.7	249.9		0.76	-	-	-	-	0.88	6626	2765	5039	8315	7000	8268	
NAF38	4-4	6	259.5	14.9	244.6		0.74	-	-	-	-	0.63	3454	2921	2659	5951	4291	6212	
NAF39	1-1	6	216.9	15.0	202.0		0.81	-	-	0.062	0.000	0.74	8788	5138	3587	9320	8740	9481	Decr. Selectivity
NAF40	1-4	6	226.2	12.5	213.8		0.70	-	-	0.305	0.007	0.36	3830	3476	2626	6108	5217	7288	
NAF41	1-1	6	2069.0	87.1	1981.9		0.75	-	-	0.149	0.019	0.52	6496	4379	2327	8000	7356	7561	Weight tag data
NAF42	1-4	6	2104.0	97.4	2006.6		0.71	-	-	0.120	0.004	0.42	3415	2657	1514	5607	4964	7068	
NAF43	1-4	6	220.2	15.0	205.2		0.81	-	-	0.045	0.027	0.77	7659	4772	4937	5450	7526	8032	C2 to EG from 1985
NAF44	1-4	6	213.9	11.9	202.1		0.76	-	-	0.050	0.011	0.48	3806	2654	2749	5082	4679	6224	
NAF45	3-1	6	224.0	15.0	209.0		0.81	-	-	0.039	0.024	0.84	7073	5142	5009	6289	6771	8032	
NAF46	3-4	6	218.6	12.2	206.5		0.78	-	-	0.042	0.012	0.62	3705	2924	2849	5340	4064	6225	

Appendix 4

ARGUMENTS REGARDING THE PLAUSIBILITY OF STOCK STRUCTURE HYPOTHESIS IV

NORTH ATLANTIC FIN WHALES - 1ST HYPOTHESIS IV PLAUSIBILITY - GUNNLAUGSSON

Site fidelity of fin whales has been demonstrated from several photo-id studies (Seipt et al. 1990; Clapham and Seipt 1991; Agler et al. 1992; Zanardelli et al. 1998; Notarbartolo-di-Sciara et al. 2003), although tagging and tracking data (Watkins et al. 1981, 1984; 1996; Gunnlaugsson 2007) have also shown considerable within- and between seasons movements, s.a. within the area between Iceland and Greenland (C1 and C2 breeding populations in this exercise) and from Canadian markings (W).

In SC/M08/RMP2 presented at the first intersessional meeting on NA fin whales demonstrated site fidelity, that might gradually change with time, within the whaling grounds west of Iceland (small area WI). This information is on a finer scale than what is captured in the IST work but is of qualitative significance.

Fin whale mark recoveries between areas in the NA are much later to turn up than between season recoveries within an area indicating site fidelity in that movement between areas is gradual in time. Hypothesis IV does not adequately model such fidelity. Hypothesis IV has no dispersal but rather mixing of breeding stocks on the feeding grounds, so that in WI three breeding stocks mix. Animals from these breeding stocks are randomly assigned to the feeding areas in the modelled proportions each year, independent of where they were the year before (no memory).

When doubts were raised about the appropriateness of including hypothesis IV, it was stated in response that inclusion was preferable for completeness and that this hypothesis would receive lower plausibility, if not supported by the model fits to the data. That is in fact what the trials now show. The *Tag fit* (deviance) in trials based on hypothesis IV is higher than in any trials based on other high plausibility hypotheses (excluding trials where CPUE is also fitted). Hypothesis IV should because of its nature therefore be seen only as a sensitivity test, and the results obtained from that exercise do not support that it should be assigned high plausibility

REFERENCES

- Agler, B.A., Robertson, K.A., Dendanto, D., Katona, S.K., Allen, J.M., Frohock, S.E., Seipt, I.E. and Bowman, R.S. 1992. The use of photographic identification for studying individual fin whales (*Balaenoptera physalus*) in the Gulf of Maine. Rep. int. Whal. Commn 42:711-22.
- Clapham P.J. & I.E. Seipt 1991. Resightings of independent fin whales *Balaenoptera physalus* on maternal summer ranges. J. Mammalogy. 72 (4): 788-790.
- Gunnlaugsson Víkingsson 2007. Update on fin whale markings in Icelandic waters. SC/M08/RMP2.
- Notarbartolo-di-Sciara G., M. Zanardelli, M. Jahoda, S. Panigada, S. Airolidi 2003. The fin whale *Balaenoptera physalus* (L. 1758) in the Mediterranean Sea. *Mamm. Rev.* 33(2): 105-150.
- Seipt I.E., P.J. Clapham, C.A. Mayo and M.P. Hawvermale 1990. Population characteristics of individually identified fin whales *Balaenoptera physalus* in Massachusetts Bay. *Fish. Bull.* 88(2): 271-278.
- Watkins, W.A., Sigurjónsson, J., Wartzok, D., Maiefski, D.R., Howey, P.W. and Daher, M.A. 1996. Fin whale tracked by satellite off Iceland. *Mar. Mamm. Sci.* 12: 564-560.
- Watkins, William A., Karen E. Moore, Jóhann Sigurjónsson, Douglas Wartzok, Giuseppe Notarbartolo di Sciara - 1984 Fin whale (*Balaenoptera physalus*) tracked by radio in the Irminger Sea. *Rit Fiskideildar*, 8: 1-14.
- Watkins, William A., Karen E. Moore, Jóhann Sigurjónsson, Douglas Wartzok, Giuseppe Notarbartolo di Sciara - 1981 Finback whale, *Balaenoptera physalus*, traced by radio from Icelandic to Greenland waters. ICES C.M. 1981/N:16.
- Zanardelli M, Panigada S, Airolidi S, et al. 1998 Site fidelity, seasonal residence and sex ratio of fin whales (*Balaenoptera physalus*) in the Ligurian Sea feeding grounds 12, 124.

WHY THE INFORMATION IS CURRENTLY INSUFFICIENT TO REDUCE THE PLAUSIBILITY FOR STOCK STRUCTURE HYPOTHESIS VI FROM "HIGH" TO "MEDIUM" PLAUSIBILITY – BUTTERWORTH, DONOVAN, POLACHEK AND PUNT

The First Intersessional Workshop agreed that the mark-recapture data do not provide a basis to select among broad stock structure hypotheses, although they provide information on movements of fin whales at local scales. We note that this is supported by the objective function values for trials NF01-14 (see Appendix X). The trials based on stock structure hypothesis IV have objective function values (deviances) between 253-260 units whereas those based on stock structure hypotheses II, III, VI and VII have objective function values ranging between 245 and 262 (the objective function values for stock structure hypotheses I and V are not comparable with those for the other stock structure hypotheses because these hypotheses do not allow animals from W breeding stock to be found in *sub-area* EG and further east). We further note that stock structure hypothesis IV has fewer estimable parameters than the other stock structure hypotheses so a higher objective function value for this stock structure hypothesis is not unexpected based on model selection criteria such as AIC or AICc.

The ability to discriminate between hypotheses involving dispersal (permanent movement) and mixing (non-permanent movement) is difficult even with large samples. We note that one (of the few) recaptures than changed *sub-area*, did so within a year, consistent with a mixing hypothesis. Furthermore, the probability of an animal returning to its "home" *sub-area* is 0.9 for stock structure hypothesis IV, i.e. mimicking site-fidelity at the *sub-area* level quite adequately. A substantial number of recaptures which show clear evidence for dispersal rather than site-fidelity at the *sub-area* level would have been needed to have assigned stock hypothesis IV "medium" rather than "high" plausibility.

Appendix 5

PROPOSAL TO INVESTIGATE THE APPARENT ANOMALIES BETWEEN THE RESULTS OF ALLOZYME ANALYSES AND DNA-BASED ANALYSES

SHORT TITLE:

Investigate the apparent anomalies between the results of allozyme analyses and DNA-based analyses.

RELEVANT AGENDA ITEMS

RMP: *Implementation Simulation Trials* for North Atlantic fin and minke whales. It is also relevant to SD and potentially AWMP

BRIEF DESCRIPTION OF PROJECT AND ITS IMPORTANCE TO RMP

In the case of North Atlantic fin whales and North Atlantic minke whales different genetic methodologies have revealed highly contrasting results. Allozyme analyses conducted in the early 1990s by Danielsdottir and co-workers estimated very high degrees of genetic divergence between samples from western, Central and eastern North Atlantic fin whales and minke whales at several loci. These results are in sharp contrast to the DNA-based analyses (mitochondrial DNA and microsatellite loci) which so far have revealed low level population genetic structure among the North Atlantic regions.

The lack of congruence among different genetic analyses has important consequences for the *Implementation Simulation Trials* for North Atlantic fin whales which have to include stock hypotheses covering the full range of these contrasting genetic analyses.

The high levels of population structure indicated by the allozyme analyses may have two explanations; technical issues relating to differential treatment of samples during collection and storage across sampling regions; or the allozyme loci (which encode cellular enzymes) may be under divergent natural selection. The latter explanation has been suggested by Danielsdottir and co-workers, but a review of similar comparisons of DNA-based analyses with allozyme studies in other species indicates that the high degree of genetic divergence and the high percentage of allozyme loci under presumed selection is highly unusual. This observation points to the possibility of underlying technical issues resulting in the observed pattern of genetic differentiation. This latter possibility may be assessed by sequencing the DNA sequences, which (contrary to the late 1980s) are now known and sequenced in other mammals. If indeed the allozyme data are correctly identifying allozyme alleles resulting in amino acid replacements that alter the overall electrical charge of the enzyme encoded by the target loci, such mutations may be identified in the sequence of DNA nucleotides in the exons.

The project will determine the sequence of nucleotides at the exons encoding the most divergent allozymes identified in Danielsdottir *et al.*'s allozyme study of North Atlantic fin whales. Using the allozyme genotype data by Danielsdottir *et al.*, individuals will be selected such that sequence multiple copies of each allozyme allele are sampled. Genomic DNA extractions from ~50 of the fin whale samples used in the original allozyme study by Danielsdottir and co-workers are already available..

TIMETABLE

A completed report will be submitted as a paper to the next Scientific Committee meeting.

RESEARCHERS

The work will be conducted at the Department of Genetics, Microbiology and Toxicology (Stockholm University, Sweden) lead by Drs. Martine Bérubé and Per Palsbøll, in collaboration with the Icelandic Marine Research Institute.

ESTIMATED TOTAL COSTS

It is estimated that the salary and reagent costs for this analysis will amount to £14,500.

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 (see Fig. 1). 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 SC/60/Rep 3.

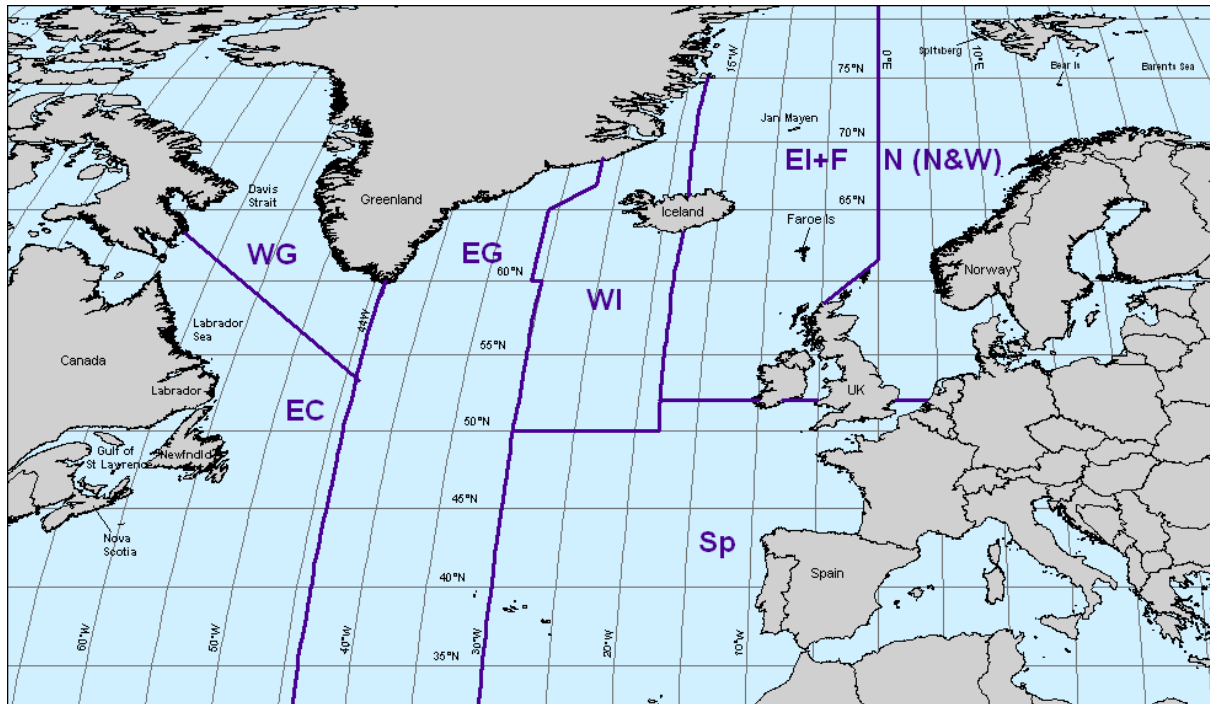


Fig. 1. Map of the North Atlantic showing the sub-areas defined for the North Atlantic Fin whales. [NB replace w. higher defn file for publication]

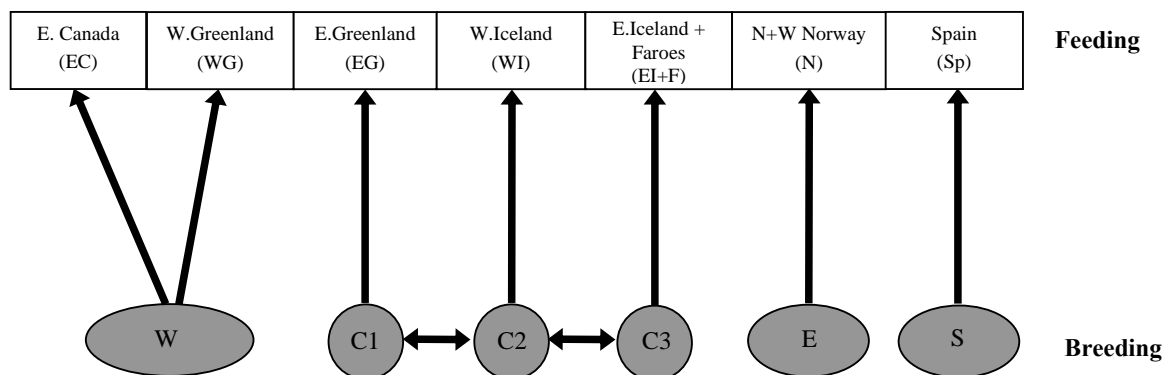
There are seven general hypotheses regarding stock structure, as illustrated in Fig 2:

- (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.

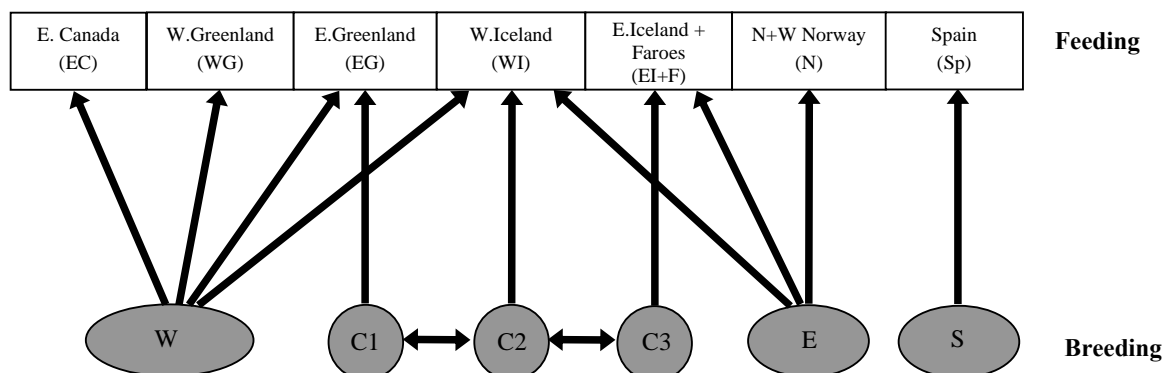
Possible sub-structure in the westernmost and easternmost regions has not been modelled (except as required by the nature of the abundance data) as the primary aim of these trials is not to investigate the full stock structure of fin whales in the North Atlantic, but rather to develop a broad set of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

Fig. 2. Stock structure hypotheses for North Atlantic Fin whales

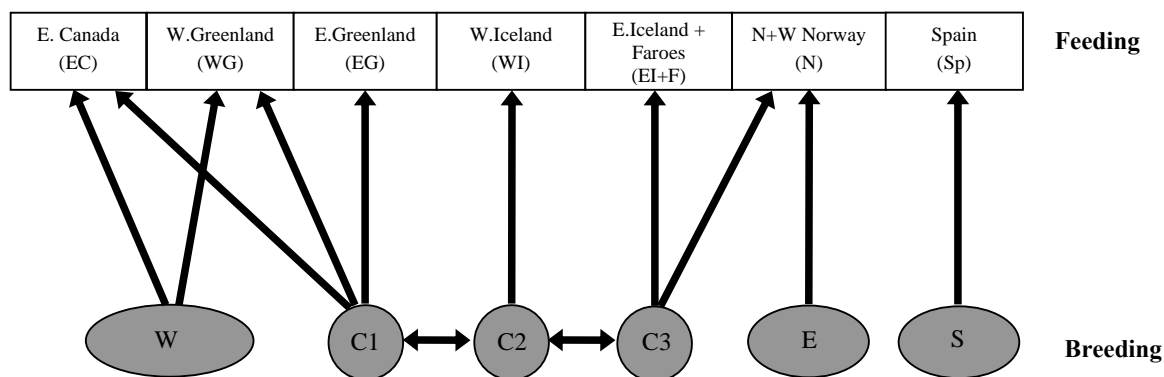
Hypothesis (I). Base case: 4 breeding stocks with separate feeding sub-areas



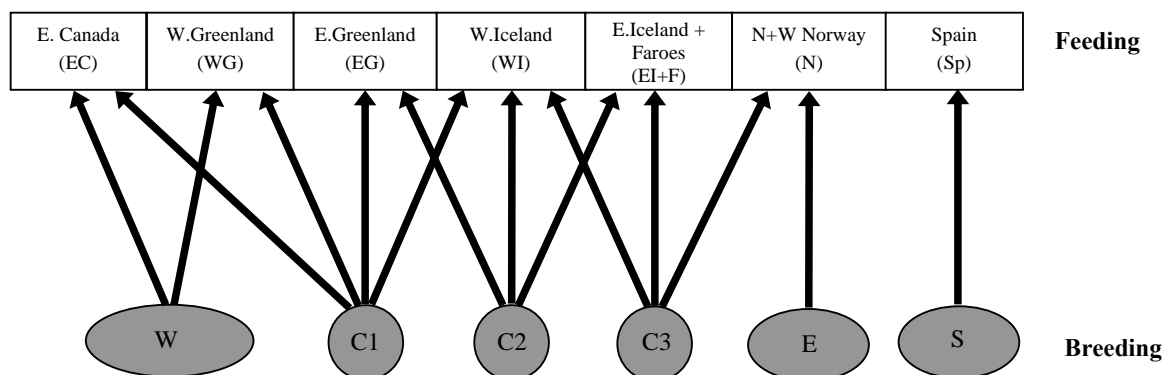
Hypothesis (II). 4 breeding stocks with the W and E stocks also feeding in the central sub-areas



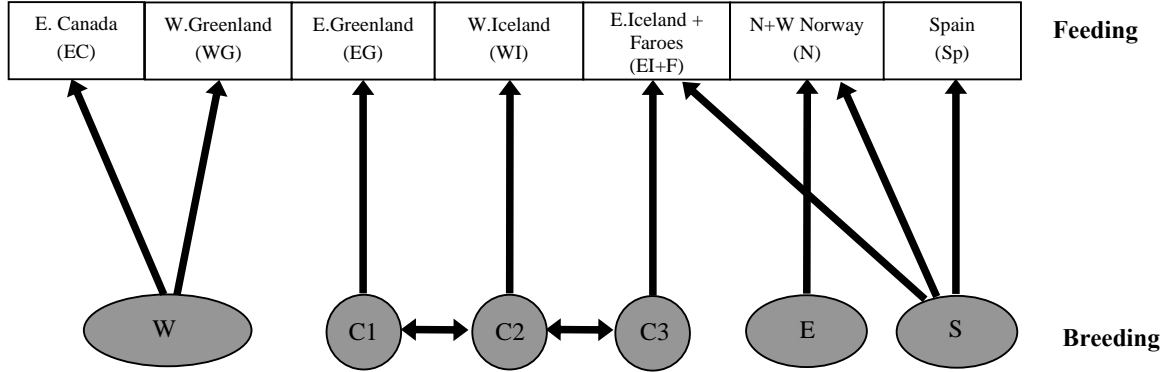
Hypothesis (III). 4 breeding stocks with the C stock feeding in the adjacent sub-areas



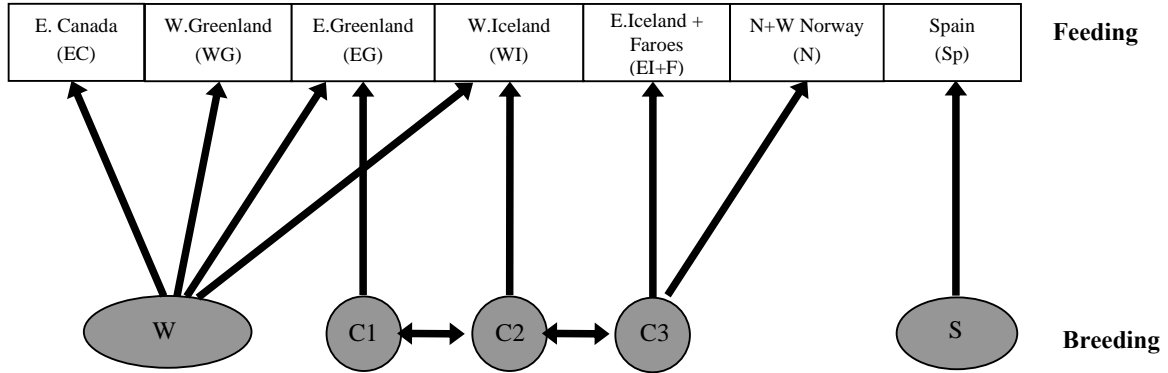
Hypothesis (IV). 4 breeding stocks but without interchange between the C sub-stocks



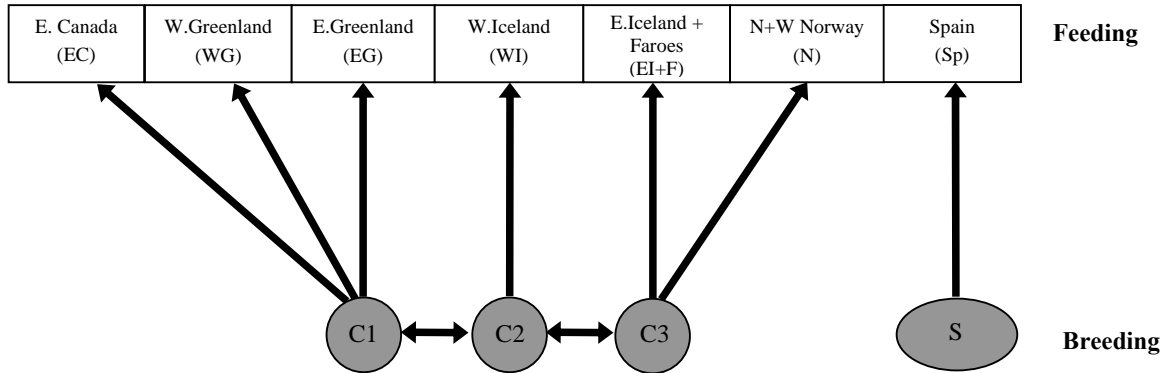
Hypothesis (V). 4 breeding stocks with the S stock feeding in the two adjacent sub-areas



Hypothesis (VI). 3 breeding stocks



Hypothesis (VII). 2 breeding stocks



B. Basic dynamics

The dynamics of the animals in stock/sub-stock j are governed by equations B.1(a) for the 'W' and 'E' stocks for which there is no dispersal (permanent movement) between stocks and by Equations B.1(b) for the 'C1', 'C2' and 'C3' sub-stocks:

$$N_{t+1,a}^{g,j} = \begin{cases} 0.5b_{t+1}^j & \text{if } a = 0 \\ (N_{t,a-1}^{g,j} - C_{t,a-1}^{g,j})\tilde{S} & \text{if } 1 \leq a < x \\ (N_{t,x}^{g,j} - C_{t,x}^{g,j})\tilde{S} + (N_{t,x-1}^{g,j} - C_{t,x-1}^{g,j})\tilde{S} & \text{if } a = x \end{cases} \quad (\text{B.1a})$$

$$N_{t+1,a}^{g,j} = \begin{cases} 0.5b_{t+1}^j & \text{if } a = 0 \\ \sum_{j \neq j'} [(1 - D^{j,j'}) (N_{t,a-1}^{g,j} - C_{t,a-1}^{g,j})\tilde{S} + D^{j',j} (N_{t,a-1}^{g,j'} - C_{t,a-1}^{g,j'})\tilde{S}] & \text{if } 1 \leq a < x \\ \sum_{j \neq j'} [(1 - D^{j,j'}) (N_{t,x}^{g,j} - C_{t,x}^{g,j} + N_{t,x-1}^{g,j} - C_{t,x-1}^{g,j})\tilde{S} + D^{j',j} (N_{t,x}^{g,j'} - C_{t,x}^{g,j'} + N_{t,x-1}^{g,j'} - C_{t,x-1}^{g,j'})\tilde{S}] & \text{if } a = x \end{cases} \quad (\text{B.1b})$$

where $N_{t,a}^{g,j}$ is the number of animals of gender g and age a in stock/sub-stock j at the start of year t ;
 $C_{t,a}^{g,j}$ is the catch (in number) of animals of gender g and age a in stock/sub-stock j during year t (whaling is assumed to take place in a pulse at the start of each year);
 b_t^j is the number of calves born to females from stock/sub-stock j at the start of year t ;
 \tilde{S} is the survival rate = e^{-M} where M is the instantaneous rate of natural mortality (assumed to be independent of stock, age and sex);
 x is the maximum age (treated as a plus-group); and
 $D^{j,j'}$ is the dispersal rate (i.e. the probability of an animal moving permanently) from sub-stock j to j' (note: there is only dispersal between the C1 and C2 sub-stocks and between the C2 and C3 sub-stocks).

Note that year $t=0$, for which catch limits might first be set, corresponds to 2009.

C. Births

Density-dependence is assumed to act on the female component of the 'mature' population. The convention of referring to the mature population is used here, although this actually refers to animals that have reached the age of first parturition.

$$b_t^j = B^j N_t^{f,j} \{1 + A^j (1 - (N_t^{f,j} / K^{f,j})^{z^j})\} \quad (C.1)$$

where B^j is the average number of births (of both sexes) per year for a mature female in stock/sub-stock j in the pristine population;
 A^j is the resilience parameter for stock/sub-stock j ;
 z^j is the degree of compensation for stock/sub-stock j ;
 $N_t^{f,j}$ is the number of 'mature' females in stock/sub-stock j at the start of year t .

$$N_t^{f,j} = \sum_{a=a_m}^x N_{t,a}^{f,j} \quad (C.2)$$

a_m is the age-at-first-parturition; and

$K^{f,j}$ is the number of mature females in stock/sub-stock j in the pristine (pre-exploitation, written as $t=-\infty$) population:

$$K^{f,j} = \sum_{a=a_m}^x N_{-\infty,a}^{f,j} \quad (C.3)$$

The values of the parameters A^j and z^j for each stock/sub-stock are calculated from the values for $MSYL^j$ and $MSYR^j$ (Punt, 1999). Their calculation assumes harvesting equal proportions of males and females.

D. Catches

It is assumed that whales are homogeneously distributed across a sub-area. The catch limit for a sub-area is therefore allocated to stocks/sub-stocks by sex and age relative to their true density within that sub-area and a mixing matrix V , i.e.:

$$C_{t,a}^{g,j} = \sum_k F_t^{g,k} V_t^{j,k} S_a^g N_{t,a}^{g,j} \quad (D.1)$$

$$F_t^{g,k} = \frac{C_t^{g,k}}{\sum_{j'} V_t^{j',k} \sum_a S_a^g N_{t,a}^{g,j'}} \quad (D.2)$$

where $F_t^{g,k}$ is the exploitation rate in sub-area k on fully recruited ($S_a^g \rightarrow 1$) animals of gender g during year t ;
 S_a^g is the selectivity on animals of gender g and age a :

$$S_a^g = (1 + e^{-(a-a_{50}^g)/\delta^g})^{-1} \quad (D.3)$$

a_{50}^g, δ^g are the parameters of the (logistic) selectivity ogive for gender g ;

$C_t^{g,k}$ is the catch of animals of gender g in sub-area k during year t ; and

$V_t^{j,k}$ is the fraction of animals in stock/sub-stock j that is in sub-area k during year t .

In these trials the mixing matrix (V) is independent of year, sex and age (although the control program retains the option for dependency on year).

The catches by sub-area and year are set to one of three historical (pre-2009) series ('best', 'low' and 'high') as listed in Adjunct 1. The 'best' series includes an estimated lost whale rate of 30% in the early period (up to 1916) and allocates whales not identified to species based on the species proportions for the nearest group of years by operation or by sub-area depending on the available data. In the 'low' series none of the unspecified whales are considered fin whales whilst for the 'high' series all of the unspecified whales are taken to be fin whales. Lost whale rates of 20% and 50% are used for the 'low' and 'high' series respectively. Further details of the assumptions used are included in Adjunct 1.

Future catches are determined using the RMP. There are no incidental catches. The sex ratio for historic catches of unknown sex and for future catches is assumed to be 50:50.

Sensitivity to the position of the northern part of the boundary between the WI and EI/F sub-areas is investigated in robustness trials NF23 and 24, by including all catches taken north of Iceland between 14-18W into the WI area.

E. Mixing

The entries in the mixing matrix V are selected to model the distribution of each stock/sub-stock at the time when the catch is removed / when the surveys are conducted. Mixing is deterministic in all these North Atlantic fin whale trials. Table 1 lists the mixing matrices for each of the stock structure hypotheses. (The problem of a mismatch between survey area and model sub-area, and the issue of surveyed whales moving out of the area before catching occurs is addressed in trials with process error due to boundary mis-specification (see trials NF23 and 24) and alternative survey strategies (trials NF25-28)

Table 1
The mixing matrices. The γ s indicate that the entry concerned is to be estimated during the conditioning process.

	Feeding Area	Stock W	Sub-stock C1	Sub-stock C2	Sub-stock C2	Stock E	Stock S
HYPOTHESIS I	CE	γ	-	-	-	-	-
	WG	$1-\gamma$	-	-	-	-	-
	EG	-	1	-	-	-	-
	WI	-	-	1	-	-	-
	EI,F	-	-	-	1	-	-
	N	-	-	-	-	1	-
	SP	-	-	-	-	-	1
HYPOTHESIS II	CE	0.88γ	-	-	-	-	-
	WG	$0.88(1-\gamma)$	-	-	-	-	-
	EG	0.10	1	-	-	-	-
	WI	0.02	-	1	-	0.02	-
	EI,F	-	-	-	1	0.10	-
	N	-	-	-	-	0.88	-
	SP	-	-	-	-	-	1
HYPOTHESIS III	CE	γ	0.10γ	-	-	-	-
	WG	$1-\gamma$	$0.10(1-\gamma)$	-	-	-	-
	EG	-	0.90	-	-	-	-
	WI	-	-	1	-	-	-
	EI,F	-	-	-	0.90	-	-
	N	-	-	-	0.10	1	-
	SP	-	-	-	-	-	1
HYPOTHESIS IV	CE	γ	0.05γ	-	-	-	-
	WG	$1-\gamma$	$0.05(1-\gamma)$	-	-	-	-
	EG	-	0.90	0.05	-	-	-
	WI	-	0.05	0.90	0.05	-	-
	EI,F	-	-	0.05	0.90	-	-
	N	-	-	-	0.05	1	-
	SP	-	-	-	-	-	1
HYPOTHESIS V	CE	γ	-	-	-	-	-
	WG	$1-\gamma$	-	-	-	-	-
	EG	-	1	-	-	-	-
	WI	-	-	1	-	-	-
	EI,F	-	-	-	1	-	0.02
	N	-	-	-	-	1	0.10
	SP	-	-	-	-	-	0.88
HYPOTHESIS VI	CE	0.88γ	-	-	-	n/a	-
	WG	$0.88(1-\gamma)$	-	-	-	n/a	-
	EG	0.10	1	-	-	n/a	-
	WI	0.02	-	1	-	n/a	-
	EI,F	-	-	-	γ_2	n/a	-
	N	-	-	-	$1-\gamma_2$	n/a	-
	SP	-	-	-	-	n/a	1
HYPOTHESIS VII	CE	n/a	γ	-	-	n/a	-
	WG	n/a	$1-\gamma-\gamma_3$	-	-	n/a	-
	EG	n/a	γ_3	-	-	n/a	-
	WI	n/a	-	1	-	n/a	-
	EI,F	n/a	-	-	γ_2	n/a	-
	N	n/a	-	-	$1-\gamma_2$	n/a	-
	SP	n/a	-	-	-	n/a	1

F. Generation of Data

The actual historical estimates of absolute abundance (and their associated CVs) provided to the RMP are listed in Table 2. The proposed plan for future surveys is given in Table 3. The trials assume that it takes two years for the results of a sighting survey to become available to be used by the management procedure, i.e. a survey conducted in 2009 could first be used for setting the catch limit in 2011.

Table 2 The estimates of abundance and their sampling standard errors (see Annex H of SC/60/Rep 3 for details)

Sub-area	Year	Estimate	Sampling CV
EC	2007	2808*	0.302
WG	1987	1100	0.40
WG	2005	3218	0.43
WG	2007	4656	0.46
EG	1988	5269	0.221
EG	1995	8412	0.288
EG	2001	11706	0.194
WI	1988	4243	0.229
WI	1995	6800	0.218
WI	2001	6565	0.194
El+F	1987	5261	0.277
El+F	1995	6647	0.288
El+F	2001	7490	0.255
N	1995	3964	0.21
N	1999	3749	0.24
Sp	1989	17355	0.265

* the 2007 EC area estimate of 2808 has not been used as it is uncorrected; the estimate from the IWC/NAMCO workshop is used until a new estimate is available.

Table 3 Sighting survey plan

Season	EG	Sub-area WI	El/F
2007	Yes	Yes	-
2008-12	-	-	-
2013	Yes	Yes	Yes
2014-18	-	-	-
2019	Yes	Yes	Yes
2020-24	-	-	-
2025	Yes	Yes	Yes
And so on in this pattern			

The future estimates of abundance for a survey area (a sub-area for these trials) (say survey area E) are generated using the formula:

$$\hat{P} = PYw / \mu = P^* \beta^2 Yw \quad (\text{F.1})$$

where Y is a lognormal random variable $Y = e^\varepsilon$ where $\varepsilon \sim N(0; \sigma_\varepsilon^2)$ and $\sigma_\varepsilon^2 = \ln(1 + \alpha^2)$;
 w is a Poisson random variable with $E(w) = \text{var}(w) = \mu = (P/P^*) / \beta^2$, Y and w are independent;
 P is the current total (1+) population size in survey area E:

$$P = P_t^E = \sum_{k \in E} \sum_j V_{t,j,k} \sum_g \sum_{a \geq 1} N_{t,a}^{g,j} \quad (\text{F.2})$$

P^* is the reference population level, and is equal to the total (1+) population size in the survey area prior to the commencement of exploitation in the area being surveyed; and

F is the set of sub-areas making up survey area E.

Note that under the approximation $CV^2(ab) = CV^2(a) + CV^2(b)$, $E(\hat{P}) = P$ and $CV^2(\hat{P}) = \alpha^2 + \beta^2 P^* / P$. For consistency with the first stage screening trials for a single stock (IWC, 1991, p.109; IWC 1994, p.85), the ratio $\alpha^2 : \beta^2 = 0.12 : 0.025$, so that:

$$CV^2(\hat{P}) = \tau(0.12 + 0.025 P^* / P) \quad (\text{F.3})$$

The value of τ is calculated from the survey sampling CV's of earlier surveys in area E. If $\overline{CV^2}$ is the average value of CV^2 estimated for each of these surveys, and \bar{P} is the average value of the total (1+) population sizes in area E in the years of these surveys, then:

$$\tau = \overline{CV^2} / (0.12 + 0.025 P^* / \bar{P}) \quad (\text{F.4})$$

Note therefore that:

$$\alpha^2 = 0.12\tau \quad \beta^2 = 0.025\tau \quad (\text{F.5})$$

The above equations apply in the absence of additional variance. If this is present with a CV of CV_{add} , then the following adjustment is made:

$$\sigma_\varepsilon^2 = \ln(1 + \alpha^2 + CV_{add}^2) \quad (\text{F.6})$$

An estimate of the CV is generated for each sighting survey estimate of abundance \hat{P} :

$$CV(\hat{P})_{est}^2 = \sigma^2 \chi^2 / n \quad (F.7)$$

where $\sigma^2 = \ell n(1 + \alpha^2 + \beta^2 P^* / \hat{P})$, and

χ^2 is a random number from a Chi-square distribution with n degrees of freedom (where $n=10$ as used for NP minke trials; IWC, 2004).

Two alternative survey strategies will be investigated in the robustness trials:

1. In trials NF25 and 26 future surveys will cover only the WI sub-area but with greater survey sampling intensity. This is implemented by changing $n \rightarrow 3n$, $\alpha^2 \rightarrow \alpha^2/3$ and $\beta^2 \rightarrow \beta^2/3$ corresponding to a tripling of this intensity. The additional variance contribution to the estimate (CV_{add}) will remain unchanged.
2. In trials NF27 and 28 future surveys in WI and EI/F will not cover the strata to the South of 60N. The proportion covered is estimated from past surveys using data in Annex H of SC/60/Rep 3.

G. Parameters and conditioning

The values for the biological and technological parameters are listed in Table 4.

Table 4 The values for the biological and technological parameters that are fixed

Parameter	Value
Plus group age, x	25 yrs
Natural mortality, M	0.08yr ⁻¹ (see also below)
Age-at-first-parturition, a_m	Knife-edged at age 6
Selectivity	
Males	$a_{50} = 3.6\text{yrs}$, $\delta = 0.57$
Females	$a_{50} = 4.1\text{yrs}$, $\delta = 1.0$
Maximum Sustainable Yield Level, $MSYL$	0.6 in terms of mature female component of the population

The natural mortality rate M is initially set to 0.08yr⁻¹ for most trials including the baseline; this value may be adjusted (possibly in a trial-specific manner) in the light of comparisons with model predictions for the catch curve slopes reported in Annex J of SC/60/Rep 3. However, to allow for the possibility of dome-shaped selectivity, and noting that the Comprehensive Assessment meeting (IWC 1992) used a value of $M=0.04\text{yr}^{-1}$, robustness tests NF39 and NF40 use $M=0.04$ and a selectivity that decreases by 4% per year for ages above 8 (see Item 4.3 of SC/60/Rep 3).

The 'free' parameters of the above model are the initial (pre-exploitation) sizes of each of the sub-stocks/stocks, the values that determine the mixing matrices (i.e. the γ parameters) and the dispersion rates between C1 and C2 and between C2 and C3. The process used to select these 'free' parameters is known as conditioning. The conditioning process involves first generating 100 sets of 'target' data as detailed in steps (a) to (d) below, and then fitting the population model to each (in the spirit of a bootstrap). The number of animals in sub-area k at the start of year t is calculated starting with guessed values of the initial population sizes and projecting the operating model forward to 2008 in order to obtain values of abundance etc. for comparison with the generated data¹.

The information used in the conditioning process is as follows.

- (a) The 'target' values for the historical abundance by sub-area are generated using the formula:

$$P_t^k = O_t^k \exp[\mu_t^k - (\sigma_t^k)^2 / 2]; \mu_t^k \sim N[0; (\sigma_t^k)^2] \quad (G.1)$$

where P_t^k is the abundance for sub-area k in year t

O_t^k is the actual survey estimate for sub-area k in year t (Tables 2 or 5); and

σ_t^k is the CV is O_t^k .

As some historic abundance estimates do not cover the full sub-area, the data used in conditioning are pro-rated upwards in robustness trials NF29 and NF30. The revised estimates are listed in Table 5 (see also Adjunct 2). (These revised estimates will not be available to the CLA).

Table 5 The revised (pro-rated) abundance estimates and their sampling standard errors (see Adjunct 2 for details)

Sub-area	Year	Estimate	Sampling CV
EG	1988	5269	0.221
EG	1995	10152	0.288
EG	2001	14225	0.194
WI	1988	4243	0.229
WI	1995	7363	0.218
WI	2001	7430	0.194
EI+F	1987	5261	0.277
EI+F	1995	6762	0.288
EI+F	2001	8758	0.255

¹ In order to check that the conditioning exercise has been successfully achieved, plots such as those shown in IWC, 2003, p473-80 will be examined, together with time-trajectories of the fraction of each stock in each sub-area.

- (b) Dispersal rate. The model allows dispersal between sub-stocks C1 and C2 and sub-stocks C2 and C3. To ensure equilibrium in the pristine population:

$$K^{1+,C1}D^{C1,C2} = K^{1+,C2}D^{C2,C1} \quad \text{and} \quad K^{1+,C2}D^{C2,C3} = K^{1+,C3}D^{C3,C2} \quad (\text{G.2})$$

where
$$K^{1+,j} = \sum_{a=1}^x (N_{-\infty,a}^{m,j} + N_{-\infty,a}^{f,j}) \quad (\text{G.3})$$

- (c) A 'target' for the numbers of animals tagged and recaptured is generated by selecting records at random and with replacement from the tag-recapture data (see Table 6). The objective function used to include the tagging data when conditioning is given below. The tag recapture data are assumed to be negative binomially (rather than Poisson) distributed to account for possible non-randomness in the tagging / recapture process. The dynamics of tagged animals are essentially the same as those of untagged animals, except that account needs to be taken of tagging. The following equations are used to determine the number of tagged animals of age a (for ages less than x) and gender g in stock/sub-stock j at the start of year $t+1$ originally tagged in sub-area k , $T_{t+1,a}^{g,j,k}$ (tagging is assumed to take place halfway through the fishing season):

For stocks with no dispersal:
$$T_{t+1,a}^{g,j,k} = T_{t,a-1}^{g,j,k} (1 - \sum_{k'} V_t^{j,k'} S_{a-1}^{g,k'}) \Omega_{2+} e^{-M} + Q_{t,a-1}^{g,j,k} (\Omega_1 e^{-M})^{1/2} \quad (\text{G.4a})$$

For stocks with dispersal:
$$T_{t+1,a}^{g,j,k} = \tilde{T}_{t+1,a}^{g,j,k} + \sum_{j' \neq j} \{ D^{j',j} \tilde{T}_{t+1,a}^{g,j'} - D^{j,j'} \tilde{T}_{t+1,a}^{g,j} \} \quad (\text{G.4b})$$

where $Q_{t,a}^{g,j,k}$ is the number of animals of age a and gender g in stock/sub-stock j that were tagged in sub-area k during year t

$$Q_{t,a}^{g,j,k} = \frac{(Q_t^k - SS_t^k / \Psi) C_t^{g,k}}{C_t^{t,k} + C_t^{m,k}} \frac{V_t^{j,k} N_{t,a}^{g,j}}{\sum_j V_t^{j,k} \sum_{a'} N_{t,a'}^{g,j'}} \quad (\text{G.5})$$

Q_t^k is the number of releases during year t in sub-area k ;

SS_t^k is the number of whales recovered in the same season as the tags were released in sub-area k ;

$\tilde{T}_{t+1,a}^{g,j,k}$ is defined as for $T_{t+1,a}^{g,j,k}$ in the no dispersion case (i.e. is set using equation G.4a);

Ψ is the reporting rate parameter (assumed to be independent of sub-area); and

Ω_1 and Ω_{2+} are the rates of tag-loss in year 1 and years 2 on (both are assumed to be unity for the baseline analyses).

The number of 'recruits' by age, sex and sub-stock to the tagged population therefore depends on the actual number tagged, assuming that an animal to be tagged is selected at random from the catch. Account is taken in Equation G.4 of mortality (both natural and fishing) from the time of tagging until the end of the year.

The model predicted number of animals recaptured during year t in sub-area k that were originally tagged in sub-area k' , $U_t^{k,k'}$ is given by:

$$U_t^{k,k'} = \Psi \left(\sum_g \sum_j \sum_a T_{t,a}^{g,j,k'} V_t^{j,k} S_a^g F_t^{g,k} \right) \quad (\text{G.6})$$

Same season recoveries are removed from the population, accounting for tag-reporting, but are not included in the likelihood function (i.e. they are included in Eqn G.4 but not G.6). The mark reporting rate Ψ is assumed to equal 1 but treated as estimable for the tags released in Canada, except for trials NF01x and NF02x. A loss rate of 0 is assumed in the base case. A loss rate of 0.2yr^{-1} in yr 1 (i.e. $\Omega_1 = e^{-0.2}$), and 0.1 thereafter (i.e. $\Omega_{2+} = e^{-0.1}$) is tested in trials NF33-38.

Table 6a Summary of the fin whales marked (recorded as 'hits') and recovered in the North Atlantic. 3 marks that were not recorded as 'hits' but which were recovered are excluded. The 1 whale marked by Canada in 1968 and recovered the same day is also excluded.

Year	C	WG	EG	WI	El/F	No	Sp
1965	0	0	0	13	0	0	0
1966	78	0	0	0	0	0	0
1967	54	5	8	0	0	0	0
1968	0	0	15	2	0	0	0
1969	45	0	0	0	0	0	0
1970	3	0	3	1	0	0	0
1971	19	0	2	0	0	0	0
1972	59	0	0	3	0	0	0
1973	12	3	3	0	0	0	0
1974	0	0	0	0	0	0	0
1975	0	0	0	0	0	0	0
1976	2	0	0	0	0	0	0
1977	0	0	0	0	0	0	0
1978	0	0	0	0	0	24	0
1979	27	3	0	34	0	0	0
1980	0	8	0	11	0	0	0
1981	0	4	26	62	0	0	3
1982	0	0	0	52	14	0	2
1983	0	0	5	10	0	0	17
1984	0	0	32	0	7	0	0
1985	0	0	0	0	0	0	0
1986	0	1	0	0	0	0	0
Total	300	24	94	188	21	24	22

Table 6b Summary of the Fin whales recovered in the North Atlantic. (highlights need to be confirmed)

Release Recovery								Release Recovery							
MarkNo	Area	Yr	Area	Yr	Sx	Yrs to rec	Note:	MarkNo	Area	Yr	Area	Yr	Sx	Yrs to rec	Note:
34	C	1966	C	1966	F	0		40278	EL/F	1982	EL/F	1982	F	0	
67	C	1966	C	1966	M	0		16110	WI	1965	WI	1966	M	1	9
16/410	C	1966	C	1966	M	0		16131	WI	1965	WI	1966	M	1	
5/410	C	1966	C	1966	M	0		16132	WI	1965	WI	1973	M	8	
C 177	C	1966	C	1967	F	1		16133	WI	1965	WI	1966	M	1	
C 319	C	1966	C	1967	M	1		16135	WI	1965	WI	1972	M	7	
94	C	1966	C	1967	M	1		15815	WI	1972	WI	1972	M	0	
3/410	C	1966	C	1967	M	1		36282	WI	1979	WI	1980	F	1	10
63	C	1966	C	1967	M	1		36289	WI	1979	WI	1979	F	0	
72	C	1966	C	1968	F	2		36298	WI	1979	WI	1982	?	3	
15456	C	1966	C	1968	F	2		36310	WI	1979	WI	1980	M	1	
89	C	1966	C	1968	M	2		X74	WI	1979	WI	1981	?	2	
C 164	C	1966	C	1968	M	2		29436	WI	1979	WI	1983	M	4	
15466	C	1966	C	1968	M	2		36389	WI	1980	WI	1982	F	2	
70	C	1966	C	1968	M	2		36392	WI	1980	WI	1980	M	0	
86	C	1966	C	1969		3	1	36221	WI	1980	WI	1984	F	4	
56	C	1966	C	1968		2		29465	WI	1981	WI	1982	F	1	
C 154	C	1966	C	1968		2		38176	WI	1981	WI	1984	M	3	
73	C	1966	C	1968		2		38182	WI	1981	WI	1982	F	1	11
97	C	1966	C	1969	M	3	2	38184	WI	1981	WI	1981	F	0	
85	C	1966	C	1969	F	3		38320	WI	1981	WI	1985	M	4	
3	C	1966	C	1969	M	3		38202	WI	1981	WI	1984	?	3	
55	C	1966	C	1969	M	3		38195	WI	1981	WI	1981	M	0	12
10/410	C	1966	C	1968		2	3	38199	WI	1981	WI	1984	F	3	
48	C	1966	C	1970	F	4		38201	WI	1981	WI	1985	F	4	
58	C	1966	C	1970	F	4		38204	WI	1981	WI	1982	M	1	
C 318	C	1966	C	1970	M	4		38316	WI	1981	WI	1981	F	0	
C 183	C	1966	C	1971	M	5		38193	WI	1981	WI	1982	M	1	
809	C	1967	C	1967	F	0		38217	WI	1981	WI	1983	?	2	
816	C	1967	C	1968	F	1		38213	WI	1981	WI	1984	F	3	
753	C	1967	C	1971	M	4	4	38216	WI	1981	WI	1981	M	0	
807	C	1967	C	1972	F	5		38241	WI	1981	WI	1983	M	2	
912	C	1967	C	1969	M	2	5	38255	WI	1981	WI	1983	F	2	
15481	C	1968	C	1968	F	0	15	38261	WI	1981	WI	1985	M	4	
1083	C	1969	C	1971	F	2		40796	WI	1981	WI	1982	F	1	
926	C	1970	C	1970	F	0		24824	WI	1982	WI	1984	M	2	
1756	C	1971	C	1972	F	1		24826	WI	1982	WI	1982	M	0	
1296	C	1972	C	1972	M	0		24828	WI	1982	WI	1982	M	0	
1291	C	1972	C	1972	M	0	6	24834	WI	1982	WI	1984	F	2	
c1866	C	1979	WI	1988	F	9		24842	WI	1982	WI	1984	M	2	
16144	EG	1968	WI	1969	M	1		24851	WI	1982	WI	1984	M	2	
16150	EG	1968	WI	1968	F	0		24868	WI	1982	WI	1982	M	0	
15565	EG	1968	WI	1977	F	9		24865	WI	1982	WI	1987	M	5	13
15600	EG	1973	WI	1983	F	10		39794	WI	1982	WI	1983	M	1	
38254	EG	1981	WG	1989	F	8		39806	WI	1982	WI	1989	F	7	14
39875	EG	1984	WI	1986		2	7	39815	WI	1982	WI	1985	M	3	
39876	EG	1984	WI	1988	M	4	8	39829	WI	1983	WI	1988	F	5	
39881	EG	1984	WI	1988	M	4	8	39837	WI	1983	WI	1989	M	6	

Notes

- 1 Found in 1968 (in cooker?) but given as 1 year recovery so recovery year set as 1967
- 2 Also recovered 1967 tag 912 from this whale
- 3 Found in 1969 (in cooker?) but given as 2 year recovery so recovery year set as 1968
- 4 $\frac{3}{4}$
- 5 ? 1 year check?? Also recovered 1966 tag 97 from this whale
- 6 1293 Same cruise
- 7 Found in cooking pot; prior to this season
- 8 39881 & 39876 recovered in same whale but not thought to be same whale on firing
- 9 Whale double tagged; 2nd tag (16111) also recovered
- 10 Whale double tagged; 2nd tag (36283) also recovered
- 11 Whale double tagged; 2nd tag (38179) also recovered
- 12 Tag no. uncertain. 38195 & 6 both fired in 1981. Discrepancy re which was recovered
- 13 Check: recovery date given as 1987 in IMS but 1986 in Icelandic data
- 14 Female in IMS but male in Icelandic data
- 15 1 mark only, recovered in the same/next day. Not used in conditioning.

- (e) In the base case, CPUE data will be used qualitatively to compare with model output rather than being included directly in the likelihood calculation. In addition trials NF31 and NF32 will investigate the effect of including all the CPUE series (West Iceland 1962-87, East Iceland 1904-13 (see Appendix I) and West Iceland 1902-14 (Gunnlaugsson series 2)) in the likelihood calculation. The CPUE series are listed in Table 7.

Table 7. CPUE series for North Atlantic fin whales.

Earlier period			Later period				
East Iceland		West Iceland	West Iceland				
Year	CPUE $\hat{=}$ 5	CPUE $\hat{=}$ 6	Year	CPUE $\hat{=}$ 1	CPUE $\hat{=}$ 2	CPUE $\hat{=}$ 3	CPUE $\hat{=}$ 4
1902	-	24.8	1962	0.1398	0.1512	0.1048	-
1903	-	21.2	1963	0.1363	0.0841	0.0671	-
1904	1.195	22.9	1964	0.0770	0.0551	0.0492	-
1905	1.621	28.3	1965	0.1979	0.1519	0.1204	-
1906	0.894	18.2	1966	0.1150	0.1083	0.0863	0.1310
1907	1.122	16.0	1967	0.1040	0.1280	0.1798	0.1350
1908	0.971	16.5	1968	0.1548	0.0990	0.1314	0.1672
1909	1.228	25.4	1969	0.0541	0.0880	0.0691	0.0495
1910	0.733	18.4	1970	0.1040	0.1596	0.1466	0.1282
1911	0.739	16.9	1971	0.0824	0.0591	0.0523	0.0703
1912	-	9.9	1972	0.0836	0.0718	0.0648	0.0601
1913	0.496	5.8	1973	0.0785	0.0853	0.0708	0.0791
1914	-	7.4	1974	0.0810	0.1134	0.0861	0.1132
			1975	0.1115	0.0958	0.0779	0.1011
			1976	0.1067	0.0909	0.0993	0.0779
			1977	0.0296	0.0651	0.0443	0.0390
			1978	0.0507	0.0583	0.0732	0.0675
			1979	0.1817	0.1494	0.1389	0.1276
			1980	0.0891	0.0933	0.1317	0.1220
			1981	0.1572	0.1134	0.1333	0.1271
			1982	0.1677	0.1190	0.1094	0.0974
			1983	0.0804	-	0.0597	0.0837
			1984	0.1169	-	0.1233	0.1283
			1985	0.1170	-	0.0777	0.0857
			1986	-	-	0.0744	0.0856
			1987	-	-	0.1792	0.0990

Table 8. The variance-covariance matrix for the late CLUE series obtained by quadratically detrending the log-transformed data (Butterworth and Punt 1992).

	1	2	3	4
1	0.171	0.089	0.102	0.118
2	0.089	0.103	0.105	0.076
3	0.102	0.105	0.156	0.104
4	0.118	0.076	0.104	0.127

(f) Calculation of likelihood

The likelihood function consists of up to three components (depending on whether the CPUE data are used when conditioning trials). Equations G.7 – G.8, G.12 and 14 list the negative of the logarithm of the objective function for each of these three components.

a) Abundance estimates

$$L_1 = 0.5 \sum_k \sum_t \frac{1}{(\sigma_t^k)^2} (P_t^k / \hat{P}_t^k)^2 \quad (\text{G.7})$$

where \hat{P}_t^k is the model estimate of the number of animals aged 1 and older at the start of year t .

b) Tagging data

$$L_2 = -\ell n \prod_t \prod_{k'} \prod_k \frac{\Gamma(U_t^{k,k'} + \tilde{U}_t^{k,k'})}{\Gamma(\tilde{U}_t^{k,k'} + 1) \Gamma(U_t^{k,k'})} \left(\frac{\lambda}{1 + \lambda} \right)^{U_t^{k,k'}} \left(\frac{1}{1 + \lambda} \right)^{\tilde{U}_t^{k,k'}} \quad (\text{G.8})$$

where $\tilde{U}_t^{k,k'}$ is the observed of animals recaptured during year t in sub-area k that were originally tagged in sub-area k' .

c) CPUE data

The i th CPUE series is assumed to be proportional to the selected abundance in the corresponding area k and year t .

$$CPUE_t^{k,i} = q_i N_t^{k,e} \quad (\text{G.9})$$

$$N_t^{k,e} = \sum_j V_t^{j,k} \sum_g \sum_a S_a^g N_{t,a}^{g,j} \quad (\text{G.10})$$

The catchability coefficient q^i for CPUE series i is estimated by its maximum likelihood value, which is given by:

$$\ln \hat{q}_i = \frac{\sum_t (\ln CPUE_t^{k,i} - \ln N_t^{k,e})}{n^i} \quad (G.11)$$

where n^i is the number of data points for CPUE series i .

The negative log-likelihood for the later period CPUE series ($i=1$ to 4) over 1966 to 1982 is given by:

$$-\ln L^{CPUE1} = 0.5 \sum_t \boldsymbol{\eta}_t [\mathbf{V}^{-1}] \boldsymbol{\eta}_t^T \quad (G.12)$$

where \mathbf{V}^{-1} is the inverse of the variance-covariance matrix \mathbf{V} (Table 8) for the late series CPUE indices, and $\boldsymbol{\eta}_t$ is a vector comprised of four elements, the k th element of which is:

$$\boldsymbol{\eta}_t^i = \ln CPUE_t^i - \ln q_i N_t^{WI,e} \quad (G.13)$$

This method applies to the years in which values from all four series are available (1966-1982). Where there are values available from only three (1962-1965 and 1983-1985) or two (1986-1987) of the series, the contributions to $-\ln L^{CPUE1}$ are similar but \mathbf{V} and $\boldsymbol{\eta}_t$ are reduced by removing the row(s) and column(s) for which no values are available.

For the earlier period CPUE series ($i=5$ or 6) the negative log-likelihoods are:

$$-\ln L^{CPUE2} = \sum_{i=5}^6 \left(\frac{\sum_t [\ln CPUE_t^{k,i} - \ln(q_i N_t^{k,e})]^2}{2\sigma_i^2} \right) \quad (G.14)$$

where values of $\sigma_5 = 0.228$ and $\sigma_6 = 0.251$ were obtained by quadratic detrending of these data.

H. Trials

The *Implementation Simulation Trials* for the North Atlantic Fin whales are listed in Table 9. All trials are based on the assumption that $g(0)=1$.

I. Management Options

The following management options will be considered.

Management options based on calculating catch limits by *Small Area*:

- (1) Sub-areas WI, EG+WI/EF+F is a *Small Area* and catch limits are set by *Small Area*. All future catches are taken from the WI sub-area.

Management options based on applying catch cascading:

- (2) Sub-areas WI, EI/F and EG are taken to be *Small Areas* and sub-area WI+EI/F+WG is taken to be a *Combination area*. Sub-areas WI are *Small Areas*, with *catch-cascading* applied.

The simulated application of the RMP is based on using the "best" catch series (see Adjunct 1).

J. Output Statistics

Population-size and continuing catch statistics are produced for each stock/sub-stock and catch-related statistics for each sub-area.

- (1) Total catch (TC) distribution: (a) median; (b) 5th value; (c) 95th value.
- (2) Initial mature female population size ($P_{initial}$) distribution: (a) median; (b) 5th value; (c) 95th value.
- (3) Final mature female population size (P_{final}) distribution: (a) median; (b) 5th value; (c) 95th value.
- (4) Lowest mature female population size (P_{lowest}) distribution: (a) median; (b) 5th value; (c) 95th value.
- (5) Average catch by sub-area over the first ten years of the 100 year management period: (a) median; (b) 5th value; (c) 95th value.
- (6) Average catch by sub-area over the last ten years of the 100 year management period: (a) median; (b) 5th value; (c) 95th value.

K. References

IWC 1992

Butterworth and Punt 1992

Adjunct 1

The Catch Series used in the trials (L=low, B=best, H=high)

To come

Table 9. The *Implementation Simulation Trials* for North Atlantic fin whales.

Trial No.	Stock Structure Hypothesis	$MSYR_{mat}$	No. of Stocks	Catch series	Boundaries	Future surveys	Mark loss rate	Other	Trial Weight	Notes
NF01	I	1%	4	Best	Baseline	EG,WI,El+F	0	-	M	Base case: 4 stocks, separate feeding areas
NF01b	I	2.5%	4	Best	Baseline	EG,WI,El+F	0	MSYR 2.5%	H	Base case: 4 stocks, separate feeding areas
NF02	I	4%	4	Best	Baseline	EG,WI,El+F	0	-	H	Base case: 4 stocks, separate feeding areas
NF03	II	1%	4	Best	Baseline	EG,WI,El+F	0	-	M	4 stocks; 'W' & 'E' feed in central sub-areas
NF03b	II	2.5%	4	Best	Baseline	EG,WI,El+F	0	MSYR 2.5%	H	4 stocks; 'W' & 'E' feed in central sub-areas
NF04	II	4%	4	Best	Baseline	EG,WI,El+F	0	-	H	4 stocks; 'W' & 'E' feed in central sub-areas
NF05	III	1%	4	Best	Baseline	EG,WI,El+F	0	-	M	4 stocks; 'C' feeds in adjacent sub-areas
NF05b	III	2.5%	4	Best	Baseline	EG,WI,El+F	0	MSYR 2.5%	H	4 stocks; 'C' feeds in adjacent sub-areas
NF06	III	4%	4	Best	Baseline	EG,WI,El+F	0	-	H	4 stocks; 'C' feeds in adjacent sub-areas
NF07	IV	1%	4	Best	Baseline	EG,WI,El+F	0	-	M	4 stocks without sub-stock interchange
NF07b	IV	2.5%	4	Best	Baseline	EG,WI,El+F	0	MSYR 2.5%	H	4 stocks without sub-stock interchange
NF08	IV	4%	4	Best	Baseline	EG,WI,El+F	0	-	H	4 stocks without sub-stock interchange
NF09	V	1%	4	Best	Baseline	EG,WI,El+F	0	-	M	4 stocks as in I but 'S' in adjacent sub-areas
NF09b	V	2.5%	4	Best	Baseline	EG,WI,El+F	0	MSYR 2.5%	H	4 stocks as in I but 'S' in adjacent sub-areas
NF10	V	4%	4	Best	Baseline	EG,WI,El+F	0	-	H	4 stocks as in I but 'S' in adjacent sub-areas
NF11	VI	1%	3	Best	Baseline	EG,WI,El+F	0	-	M	3 stocks (no 'E' stock)
NF11b	VI	2.5%	3	Best	Baseline	EG,WI,El+F	0	MSYR 2.5%	H	3 stocks (no 'E' stock)
NF12	VI	4%	3	Best	Baseline	EG,WI,El+F	0	-	H	3 stocks (no 'E' stock)
NF13	VII	1%	2	Best	Baseline	EG,WI,El+F	0	-	L	2 stocks (no 'W' or 'E' stock)
NF13b	VII	2.4%	2	Best	Baseline	EG,WI,El+F	0	MSYR 2.5%	M	2 stocks (no 'W' or 'E' stock)
NF14	VII	4%	2	Best	Baseline	EG,WI,El+F	0	-	M	2 stocks (no 'W' or 'E' stock)
NF15	I	1%	4	High	Baseline	EG,WI,El+F	0	-	M	Hypothesis I; High historic catch series
NF16	I	4%	4	High	Baseline	EG,WI,El+F	0	-	H	Hypothesis I; High historic catch series
NF17	III	1%	4	High	Baseline	EG,WI,El+F	0	-	M	Hypothesis III; High historic catch series
NF18	III	4%	4	High	Baseline	EG,WI,El+F	0	-	H	Hypothesis III; High historic catch series
NF47	IV	2.5%	4	High	Baseline	EG,WI,El+F	0	MSYR 2.5%	H	Hypothesis IV; High historic catch series
NF48	IV	4%	4	High	Baseline	EG,WI,El+F	0	-	H	Hypothesis IV; ; High historic catch series
NF19	I	1%	4	Low	Baseline	EG,WI,El+F	0	-	L	Hypothesis I; Low historic catch series
NF20	I	4%	4	Low	Baseline	EG,WI,El+F	0	-	L	Hypothesis I; Low historic catch series
NF21	III	1%	4	Low	Baseline	EG,WI,El+F	0	-	L	Hypothesis III; Low historic catch series
NF22	III	4%	4	Low	Baseline	EG,WI,El+F	0	-	L	Hypothesis III; Low historic catch series
NF23	III	1%	4	Best	NI catch from WI	EG,WI,El+F	0	-	M	N Iceland catch inc. in WI sub-area
NF24	III	4%	4	Best	NI catch from WI	EG,WI,El+F	0	-	H	N Iceland catch inc. in WI sub-area
NF25	III	1%	4	Best	Baseline	WI	0	-	M	Survey WI only with greater precision
NF26	III	4%	4	Best	Baseline	WI	0	-	H	Survey WI only with greater precision
NF27	III	1%	4	Best	Baseline	N 60°N	0	-	M	WI & El+F surveys exc. S. 60°N strata
NF28	III	4%	4	Best	Baseline	N 60°N	0	-	H	WI & El+F surveys exc. S. 60°N strata
NF29	III	1%	4	Best	Baseline	EG,WI,El+F	0	Pro-rate abund.	M	Pro-rate abundance data for conditioning
NF30	III	4%	4	Best	Baseline	EG,WI,El+F	0	Pro-rate abund.	M	Pro-rate abundance data for conditioning
NF31	III	1%	4	Best	Baseline	EG,WI,El+F	0	Fit to CPUE	M	Inc. CPUE data in the likelihood calculation
NF32	III	4%	4	Best	Baseline	EG,WI,El+F	0	Fit to CPUE	M	Inc. CPUE data in the likelihood calculation
NF33	I	1%	4	Best	Baseline	EG,WI,El+F	0.2 → 0.1	-	M	Mark loss =20% in yr 1; 10%/yr thereafter
NF34	I	4%	4	Best	Baseline	EG,WI,El+F	0.2 → 0.1	-	H	Mark loss =20% in yr 1; 10%/yr thereafter
NF35	III	1%	4	Best	Baseline	EG,WI,El+F	0.2 → 0.1	-	M	Mark loss =20% in yr 1; 10%/yr thereafter
NF36	III	4%	4	Best	Baseline	EG,WI,El+F	0.2 → 0.1	-	H	Mark loss =20% in yr 1; 10%/yr thereafter
NF37	IV	1%	4	Best	Baseline	EG,WI,El+F	0.2 → 0.1	-	M	Mark loss =20% in yr 1; 10%/yr thereafter
NF38	IV	4%	4	Best	Baseline	EG,WI,El+F	0.2 → 0.1	-	H	Mark loss =20% in yr 1; 10%/yr thereafter
NF39	I	1%	4	Best	Baseline	EG,WI,El+F	0	Selectivity decr	M	Selectivity decr. 4%/yr after age 8; $M=0.04$
NF40	I	4%	4	Best	Baseline	EG,WI,El+F	0	Selectivity decr	H	Selectivity decr. 4%/yr after age 8; $M=0.04$
NF41	I	1%	4	Best	Baseline	EG,WI,El+F	0	Wt tag likelihd	M	Tag likelihood weight = * 10
NF42	I	4%	4	Best	Baseline	EG,WI,El+F	0	Wt tag likelihd	M	Tag likelihood weight = * 10
NF43	I	1%	4	Best	Baseline	EG,WI,El+F	0	C2->EG	M	C2 substock enters EG beginning yr 1985
NF44	I	4%	4	Best	Baseline	EG,WI,El+F	0	C2->EG	H	C2 substock enters EG beginning yr 1985
NF45	III	1%	4	Best	Baseline	EG,WI,El+F	0	C2->EG	M	C2 substock enters EG beginning yr 1985
NF46	III	4%	4	Best	Baseline	EG,WI,El+F	0	C2->EG	H	C2 substock enters EG beginning yr 1985
NF01x	I	1%	4	Best	Baseline	EG,WI,El+F	0	Fix C tag rep	L	Fix Canada tag reporting rate = 1
NF02x	I	4%	4	Best	Baseline	EG,WI,El+F	0	Fix C tag rep	L	Fix Canada tag reporting rate = 1

Adjunct 2
Survey abundance pro-rating
Rebecca Rademeyer

Some historic abundance estimates from the NAS surveys used in the North Atlantic fin trial conditioning do not cover the full sub-areas (East Greenland, West Iceland and East Iceland/Faroes). Robustness trials (trials 29 and 30) have been included in which the data used in conditioning are pro-rated for these sub-areas only. The abundance indices have simply been pro-rated by assuming the same density in and out of the surveyed region (Gunnlaugsson, 2008).

Table 1 gives the NAS region estimates used to compute the final sub-areas estimates. The original and pro-rated estimates are given. Table 2 compares the final estimates used in the conditioning trials. These have been calculated as described in Annex H (SC/60/Rep3).

Table 1

East Greenland					
Year	Region	N	pro-rated N	Area covered	pro-rated by
1987	B-West	1750		82331	
1989	B-West	2329		82331	
1995	B-West	7812		77682	
2001	B-West	7736		88694	
1989	A-West	3274		263980	1.00
1995	A-West	600	2340	67706	3.90
2001	A-West	3970	6489	161551	1.63
West Iceland					
Year	Region	N	pro-rated N	Area covered	pro-rated by
1987	B-East	1857		109971	
1989	B-East	3677		92854	
1995	B-East	5915		101081	
2001	B-East	6285		102740	
1989	A-East	1595		213039	1.00
1995	A-East	885	1448	130217	1.64
2001	A-East	280	1145	52131	4.09
East Iceland/Faroe Islands					
Year	Region	N	pro-rated N	Area covered	pro-rated by
1987	EGI	1050		145783	
1995	EGI	4145		127219	
2001	EGI	5405		254076	
1987	WN-SPB	675		271255	1.00
1995	WN-SPB	1594	1709	204222	1.33
2001	WN-SPB	2085	3353	136278	1.99

Table 2

East Greenland		
Year	N	pro-rated N
1988	5269	5269
1995	8412	10152
2001	11706	14225
West Iceland		
Year	N	pro-rated N
1988	4243	4243
1995	6800	7363
2001	6565	7430
East Iceland/Faroe Islands		
Year	N	pro-rated N
1987	5261	5261
1995	6647	6762
2001	7490	8758

Pike, D. and Gunnlaugsson, T. 2006. Regional estimates of density and abundance of fin whales (*Balaenoptera physalus*) from Icelandic and Faroese North Atlantic sightings surveys. Paper SC/M06/FW18 and SC/14/FW/18 presented to the joint IWC/NAMMCO workshop, 'Catch history, stock structure and abundance of North Atlantic fin whales', 23-26 March 2006, Reykjavik, Iceland. 12pp.

Gunnlaugsson, T. 2008. NA fin whale abundance by RMP IST areas. SC/60/RMP WP4. 2pp.

Appendix 7

NORTH ATLANTIC MINKE WHALES RMP IMPLEMENTATION REVIEW

Members: Allison, Apostolaki, Bannister, Bjørge, Breiwick, Butterworth, Bøthun, Cañadas, Cooke, Donovan, Grønvik, Gunnlaugsson, Hammond, Koski, Kitakado, Leaper, Miller, Miyashita, Okada, Palsbøll, Palka, Pampoulie, Pastene, Polacheck, Punt, Shimada, Skaug, Vikingsson, Walløe, Øien.

1. INTRODUCTORY REMARKS

Cooke was elected Chair. Hammond, Palsbøll, Skaug and Punt acted as rapporteurs. The adopted agenda is given as Annex 1. Relevant documents available to the sub-committee were identified. Datasets available for any new *Implementation Simulation Trials* were also identified.

2. SUMMARY OF PREVIOUS IMPLEMENTATIONS/IMPLEMENTATION REVIEWS FOR NA MINKE WHALES

2.1 Initial implementation in 1993

Implementation Simulation Trials were developed for North Atlantic minke whales between 1990 and 1993. They arose from the model for multi-stock robustness trials of mixed coastal and pelagic whaling. The full specifications of the trials are given in RIWC 43: 189-195 – Annex I, Appendix 4. A summary is given below.

The North Atlantic was divided into ten management *sub-areas* for which catches were to be set. Three breeding stocks were modelled: Western, Central and Eastern. Each stock had a number of sub-stocks (WG, WC, CIC, CIP, CG, CM, EN, EC, ES and EB) with its own preferred feeding ground or “home” area, coinciding exactly with the *sub-areas*. Uncertainties in the appropriate location of the boundaries were taken into account by “mixing matrices” that defined in which *sub-areas* (in addition to its “home” *sub-area*) each sub-stock could feed (in “yes, no, maybe” form) and the proportion of each sub-stock that would be found in each *sub-area*. Other factors tested in the 16 *Implementation Simulation Trials* were MSY(mat) rates of 1% or 4%, three sets of initial year (1989) population sizes in each *sub-area*, whether or not catches could be taken in *sub-area* CIP, and different versions of the matrices defining the proportion of sub-stock found in each *sub-area* when catching takes place (catch mixing matrix), and the proportion of each sub-stock in each *sub-area* when abundance is estimated (sightings mixing matrix).

Small Areas were set equal to *sub-areas*, and *Medium Areas* were set equal to the three stock areas Western, Central and Eastern. Three different management options (variants) were considered: (1) application of the CLA to *Small Areas* only; (2) Catch-cascading over the Central and Eastern *Medium Areas*; and (3) Catch-cascading over the Eastern *Medium Area* and over the CIC+CG+CM *Combination Area* (treating the CIP *Small Area* separately). The results of the *Implementation Simulation Trials* are given in RIWC 43: 167-185 (Annex I, Appendix 2, Table 2) and described in RIWC 44: 48-49. Catch-cascading over the Central and Eastern *Medium Areas* consistently outperformed the other variants in all trials in terms of average catches. The conservation-related performance of this variant was also satisfactory in almost all trials. Only in two trials were the lower 5%-ile of the final population sizes below the nominal protection level of 54% and then only by a fairly small margin (to 50.1% in the worse case). The Committee therefore recommended implementation of the RMP with Catch-cascading over the Central and Eastern *Medium Areas* for the North Atlantic minke whales.

2.2 Implementation Review in 2003

In 2003, the Committee conducted an *Implementation Review* (JCRM (suppl) 6: 12-13; 88-89; 171-183) at which it reviewed new information on stock structure and estimates of abundance.

On stock structure, the Committee assessed the extent to which the new information indicated a change to the area boundaries and implementation options recommended in 1993. The new genetic information continued to show that genetic differentiation was greater between the three putative stocks (Eastern, Central, Western) than within them. Data to assess structure within these stocks were available only for the Eastern stock. Genetic differentiation among Eastern sub-areas was generally low, but was statistically significant in several cases, including between the North Sea and the area immediately to the north (although not between the North Sea and areas further north). Circumstantial evidence from pollutant levels, isotope ratios, and fatty acid analysis was consistent with a distinction between the North Sea and other areas in terms of feeding. There was a significant genetic difference between the Barents Sea and areas to the west, which was maximised by a boundary at 28° E. No genetic evidence was found to support a distinction between the Vestfjorden area (EC *Small Area*) and surrounding areas. No significant genetic differences were found between the Svalbard area (ES *Small Area*) and areas to the south but there were operational considerations favouring retention of this area as a management area.

The Committee considered that the new abundance estimates from Norwegian surveys, the 1994 SCANS estimate for the North Sea, and most of the Icelandic shipboard and aerial survey estimates met the requirements for use in *Implementation Simulation Trials* and also in the RMP. Some of the Icelandic data required further analyses to resolve problems identified before they could be used at all. Details for all abundance estimates considered are given in JCRM (Suppl) 6: 178.

Concerning management areas and implementation options, the Committee recommended that the *Medium Areas* should remain unchanged, but that the following changes should be made to *Small Area* boundaries: move the northern border of the EN *Small Areas* from 65° to 62° N; amend the EB *Small Area* by creating a new western boundary at 28° E south to the Norwegian coast; eliminate the EC *Small Area* as initially defined and merge it into a new EW *Small Area*. Catch-cascading at the *Medium Area* level remained the preferred management option.

A limited set of additional *Implementation Simulation Trials* was specified to examine the effects of including additional variance into the framework used in the original trials. The results indicated that the trials conducted in 1992 had already adequately captured an appropriate level of additional variance.

The Committee noted that these trials accounted for some degree of lifetime site fidelity in feeding behaviour, but not heritable site fidelity that could lead to genetic differences within *Medium Areas*. The Committee recommended that this issue be revisited at the next *Implementation Review*, taking any new stock structure information into account.

3. STOCK STRUCTURE

3.1 Review of previous stock structure

The current *Implementation Simulation Trials* for North Atlantic minke whales are based on there being three stocks of minke whales in the North Atlantic. Each stock consists of sub-stocks in which there is no heritability in site fidelity (although animals aged 1 and older are assumed to exhibit site fidelity). The range of stock structure hypotheses included whether the CM sub-stock was part of the Central or Eastern stocks, whether the EN sub-stock was a stock, and whether the CIP sub-stock was part of the Western or Central stocks

Previous genetic analyses aimed at elucidating the stock structure of minke whales in the North Atlantic include analyses of the partitioning of genetic variation at allozyme loci (Danielsdottir *et al.* 1992, 1995), multi-locus fingerprinting (Arnason and Spillaert 1991), as well as mitochondrial (mt) and microsatellite DNA (Palsbøll 1989; Palsbøll *et al.* 1991; Andersen *et al.* 2003; IWC 2004). In summary, the allozyme data detected a strong signal of spatial structure between the western, central and eastern North Atlantic. Some, but much lower levels, of population genetic structure have been detected between and within North Atlantic areas in DNA-based analyses (Arnason and Spillaert 1991; Andersen *et al.* 2003).

3.2 Review of recent data analyses

3.2.1 New analyses

SC/60/PFI10 presented the results of a genetic analysis of genotypic data collected from 16 microsatellite loci as well as mtDNA control region sequence data from samples collected in six regions within the North Atlantic: coastal area off Norway, off Spitsbergen, the North Sea, the Barents Sea, off West Greenland and off Iceland. Both classes of genetic markers yielded congruent results, suggesting limited heterogeneity in the spatial partitioning of the genetic diversity within and among the areas sampled. A larger regional scale assessment of the partition of genetic diversity among the four areas defined by Andersen *et al.* (2003) was also performed, comprising samples from West Greenland, the Central Atlantic, the northeast Atlantic and the North Sea. This analysis also failed to detect any statistically significant degree of genetic heterogeneity among these current management areas for North Atlantic minke whales. A minimum spanning network estimation of the mtDNA haplotype revealed the presence of two distinct groups of mtDNA control region haplotypes as previously described by Palsbøll *et al.* (1991). However, no spatial structure was observed with regard to the distribution of these two mtDNA control region haplotype groups.

An assessment was conducted comparing the partition of genetic diversity at the 16 microsatellite loci between the two mtDNA control region haplotype groups to assess whether they represent individuals from different breeding populations. This partition yielded an estimate of F_{ST} of 0.0013, which differed significantly from zero ($P < 0.01$). This estimate is lower than observed among some regional comparisons. An F_{ST} of 0.0013 translates into an effective number of 192 migrants per generation assuming population genetic equilibrium. The 95 and 99% confidence intervals of the F_{ST} ranged from 0.0000 to 0.0002 and from 0.0000 to 0.0030 respectively (Table 1). Overall these results suggest that the two mtDNA control region haplotype groups may not necessarily represent different breeding populations, but rather a single panmictic population.

It was noted that the mtDNA mismatch distribution in SC/60/PFI10 is compatible with exponential population growth over recent evolutionary time. This observation could be taken to imply that the current North Atlantic minke whale populations were founded recently and are thus not in population genetic equilibrium. Low F_{ST} estimates may therefore reflect a recent population divergence rather than high levels of gene flow.

The sub-committee recommended that the data used in SC/60/PFI10, and particularly the readily comparable mtDNA nucleotide sequences, should be included in a combined analysis with the mtDNA control region sequences collected as part of the Norwegian minke whale DNA register. Skaug advised that this was planned in the future.

SC/60/PFI1 provided an analysis of the genetic data from the Norwegian minke whale catches for the period 2003-2006. The analysis involved a comparison of the *Small Areas* within the *Eastern Medium Area*, and the *CM Small Area* within the *Central Medium Area*. The finer geographical stratification employed in the *Implementation Review* conducted in 2003 was also considered. No significant degree of genetic differentiation among subareas was detected, neither for the mtDNA nor for the microsatellite loci. This conclusion was in contrast to the previous analysis conducted in 2003 based on genetic data from the 1997-2002 catches. Those analyses detected a significant degree of heterogeneity in the mtDNA data for females between the *Central* and *Eastern Medium Areas*, and a significant degree of genetic divergence between animals caught east and west of 28°E along the coast of Finnmark, whereas no such heterogeneity was detected in the 2003-2006 data. A change in laboratory in 2003 was identified as a possible explanation for the difference in results between the analyses based on the 2003-06 and 1992-2002 data. Laboratory techniques have improved over time, and it is possible that the lack of homogeneity found in the 1997-2002 data was caused by laboratory errors.

The sub-committee discussed the effect of data sets generated under different conditions and/or in different laboratories. It noted that some past inferences of temporal or spatial structure in population genetic data had later proved to be caused by technical errors. It acknowledged that this might also be the case for the genetic data generated during the early years for the Norwegian minke whale DNA register. However, the sub-committee also recognised that care should be taken when discarding past conclusions and that this should be based upon objective and transparent criteria. Skaug explained that efforts were underway to check and validate all raw data to create a single data set for future analysis.

4. ABUNDANCE ESTIMATES

The sub-committee reviewed the abundance estimates available for minke whales in the North Atlantic, focusing on the most recent estimates. It evaluated whether the estimates could be used when conditioning *Implementation Simulation Trials* and for use when applying the RMP. Table 2 is a summary of the deliberations of the sub-committee. The following sections provide more detail for each *Small* and *Medium Area*.

4.1 Review of new abundance estimates (since 2003 *Implementation Review*)

4.1.1. Northeast Atlantic (Norwegian Sea and Barents Seas)

SC/60/PFI4 presented an estimate of abundance for minke whales in the Northeast Atlantic, based on partial surveys conducted during 2002-2007 and use of the method in Skaug *et al.* (2004). Two vessels each equipped with two independent observer platforms, surveyed an area approximately corresponding to a *Small Area* as used in the RMP implementation for North Atlantic minke whales each year. The total abundance for the areas covered during 2002-2007 is 103,000 (CV 0.16). Of these, 79,000 (CV 0.16) were within the *Eastern Medium Area*. These estimates are in accordance with the corresponding estimates from the previous survey period 1996-2001. Inter-annual variation in the spatial distribution of minke whales arising from partial coverage has not yet been incorporated.

The method of analysis, which was developed around 1995, has now been applied to a series of four survey periods. It was suggested that it is time for a review of the methodology, and the following issues were identified:

- (1) Neyman Scott process estimation/stability;
- (2) bias correction method;
- (3) heterogeneity and lack of fit in Bernoulli trials;
- (4) duplication identification procedure;
- (5) timing of sighting (improve recording);
- (6) measurement error model, including observer specific effects;
- (7) dive time data (are there area effects?).

There is ongoing work, relating to (3) and (7), to quantify the effect of different sources of heterogeneity. The sub-committee recommended that other recently developed analysis methods should be applied to the survey data for the North Atlantic minke whales for comparison purposes.

The abundance estimate in SC/60/PFI4 has not been corrected for additional variance, and the component relating to the Neyman-Scott model may be subject to revision. Hence, the variance estimates presented in SC/60/PFI4 will be revised. The sub-committee agreed that the estimates in SC/60/PFI4 meet the requirements for conditioning trials, but not for use in the RMP until the further work indicated had been completed.

SC/60/PFI5 presented an analysis of the distance and angle experiments conducted as an integrated part of the Norwegian multiyear surveys. The aim of the experiments was to evaluate the precision and bias when naked eye distance and angle board readings are conducted. The experiment was conducted in conditions as close as possible to actual survey conditions. Several error models were developed to describe the observation process in the experiment. The results from these models were compared with data from duplicates in the sighting survey. Observations of radial distances below 1,000m seemed to be fairly unbiased, but were underestimated substantially when the whale was actually further than 1,000m. The biased observed angles can be described by the angular velocity between the vessel and the object. The observed variance in duplicate observations in the survey and the experiment were in the same range as the variance estimated from comparing observations against readings from the radar for the log normal model for radial distances. For observations of angles, the duplicates in surveys gave an estimate of variance that was around twice as high as the estimates from the experiment. This may be explained by large time lags in the survey data.

The sub-committee noted that the estimated variance of the sighting radial distance error, based on duplicate sightings, is smaller in the survey than in the buoy experiments. This was contrary to expectation as it is usually easier to estimate the position to a fixed object of known size than a whale which is at surface only for a short period. The most likely explanation is that there is a selection bias in the survey data, in that cues with a large error in position for one of the observer platforms will not be recognised as a duplicate by the duplicate identification rule.

The duplicate identification rule has been subject to minor revision over the years, but the main principles of the procedure developed in 1995 remain, and it may be time for a review. The procedure accepts a large time difference between observers when either of the observers sees the whale for the first time. It was noted that the internal parameter settings in the procedure have been tuned so as to obtain a balance between the two types of errors involved in duplicate identification (SC/54/RMP5). The sub-committee felt that there is scope for technical improvements in field methods for time and distance/angle estimation. The method used for angle and distance estimation in the surveys has remained unchanged over the years. New methods, based for example on video techniques, have not been applied nor are observer specific effects related to distance and angle estimation part of the model. The sub-committee suggested that inclusion of these factors may improve the model.

SC/60/PFI8 presented results from a dive time experiment on a minke whale off Spitsbergen in August 2007 and included a table summarising all dive time data collected by radio tagging methodology over 1989-2007. This minke whale was followed over five days and showed mean half-hour intersurfacing intervals varying between 30-100s and a mean blow rate of 62 blows/hour, which is in accordance with data collected previously. One minke whale was also satellite tagged in the same general area and both whales seemed to adopt a pattern of rapid movement between several possible feeding areas within a larger general area.

The sub-committee noted that the Committee recommended in 1996 that more dive time data should be collected. The recommendation has partly been followed in that there are now 19 dive time series, but there was disagreement within the sub-committee whether these series had sufficient spatial coverage to be representative of the whole survey area. In particular, it was noted that five of these were from outside the EN *Small Area*. Four of those five had a surfacing rate in excess of 60 blows per hour compared to only two of the 14 series for the EW *Small Area* (the surfacing rate for all 19 whales was 48.5 blows per hour). It was noted that in methods applied to Antarctic minke whales the effective mean dive time is estimated from survey data along with the other parameters of the hazard probability model (SC/F08/A2; SC/F08/A8). Application of this approach to the Norwegian survey data could be informative with respect to the appropriateness of surfacing rate estimates used in the abundance estimates.

Only the most recent dive time series are used to estimate the mean dive time in SC/60/PFI4. The rationale for this was not clear, and it was noted that this differs from previous practice. The sub-committee recommended that all previous abundance estimates should be updated, using the new information about mean dive time, for the next *Implementation Review*. It was noted that this would probably have very little effect on the abundance estimates.

4.1.2 North Sea

Hammond presented new information on abundance from surveys of European Atlantic waters in 2005 (SCANS-II 2008) and 2007 (CODA; Macleod *et al.* 2008). The surveys in 2005 covered all continental shelf waters of the European Atlantic, including the North Sea, from 36° to 62° N. The surveys in 2007 extended coverage to offshore waters from 42.5° to 62° N; the western boundary was the same as the eastern boundary of TNASS. Data collection and analysis methods used were essentially the same as in the SCANS survey in 1994 (Hammond *et al.* 2002), estimates from which have previously been accepted by the Committee (JCRM 6: 177). For 2005, data from the shipboard surveys were analysed using mark-recapture distance methods to account for $g(0) < 1$ and responsive movement. A total of 58 tracker, 60 primary and 18 duplicate sightings gave an estimate of abundance for all shipboard survey blocks of 13,281 (CV=0.36). The 15 sightings from the aerial surveys were analysed using conventional line transect methods but partially corrected using an estimate of availability bias of 0.106 (CV=0.66) from Witting (2005) to give an estimate of 5,333 (CV=0.55). The total minke whale abundance estimate in 2005 was 18,614 (CV=0.30). Details of the 2005 analysis are given in Burt *et al.* (2008). The surveys in 2007 (all shipboard) generated 22 sightings which were analysed using conventional distance sampling methods to give an estimate of 6,765 (CV=0.99). Details of the 2007 analysis are given in Macleod *et al.* (2008).

The sub-committee agreed that the abundance estimates obtained from the shipboard part of SCANS 2005 meet the requirements for conditioning trials and for use in the RMP, and that the corresponding aerial surveys meet the requirements for conditioning trials, but their status with the respect to use in RMP is not clear because they have not been fully corrected for $g(0)$.

4.1.3 CM (Jan Mayen) area

An abundance estimate for the CM *Small Area* was presented in SC/60/PFI4. The estimate was comparable to that for the previous period from the Norwegian surveys, but it was noted that the proportion of the CM *Small Area* covered has varied between survey periods (partial coverage during the 1988-89 and 1995 Norwegian surveys and full coverage in 1995 by the Norwegian survey combined with the Icelandic component of NASS-95 (Borchers *et al.*, 1997), and full coverage in 1997 by the Norwegian surveys), which makes it difficult to interpret the apparent increasing trend in this *Small Area*.

4.1.4 Iceland coastal

SC/60/PFI12 reported on the Icelandic aerial survey component of the T-NASS project, a continuation of a series of surveys covering Icelandic shelf waters first conducted in 1986, but using nearly identical design and methodology in 1987, 1995 and 2001, and with the same cruise leader acting as control observer as in

2001. The primary target species in all the surveys has been the common minke whale (*Balaenoptera acutorostrata*) with humpback whales (*Megaptera novaeangliae*) a secondary target along with harbour porpoise (*Phocoena phocoena*) in this latest survey (June - July 2007). The 2007 survey was flown at an altitude of 600 ft (183m), the same altitude used in SCANS and other dedicated harbour porpoise surveys. The survey was flown at 750 ft (229m) in previous years. The survey speed cannot be reduced and was unchanged. Cue counting methods were used for baleen whales while standard line transect procedures were used for other species. The latest survey achieved 79% of planned coverage under acceptable conditions. A total of 431 unique sightings was made, including 70 groups of minke whales, 119 unique sightings of harbour porpoises, 58 sightings of humpback whales and 109 sightings of white-beaked dolphins (*Lagenorhynchus acutus*). The general distribution pattern of most species was similar to that in previous surveys, with some exceptions. Minke whales occurred in lower numbers and were absent from some nearshore areas where they were abundant in previous surveys. In particular, they were absent from areas where sandeel has been observed as the dominant food item. In recent years, pronounced changes have occurred in oceanographic conditions and relative distribution and abundance of several species of fish including capelin. Recruitment of sandeel was extremely low in 2005 and 2006 resulting in breeding failure of seabirds. Harbour porpoise sightings were made in all nearshore blocks in much higher numbers than before because an experienced harbour porpoise observer was employed on this survey.

The abundance estimate using data from both primary observers was 10,680 (95% CI 5,873-17,121) (CV 0.29). The primary observer who made most of the harbour porpoise sightings made much fewer minke whale sightings made in particular within 200m of the plane, and, no duplicates with the control observer that would enable estimation of distance error and $g(0)$. The other primary observer had experience from partial surveys conducted under the Icelandic Research Program during 2003-05 to detect seasonal abundance changes as well as on a survey off West Greenland in September 2005. This observer duplicated all sightings within short radial distances and had low distance estimation error. The distance estimates by this observer tended to be greater than those made by the control observer. The abundance estimate for minke whales using this observer alone and standard cue counting methods was 15,055 (95% CI 6,357, 27,278) (CV 0.36). This observer may have overestimated distances to some degree and the $g(0)$ for this observer may have been lower than 1 although that is not apparent from the limited duplicate sighting data.

The change in survey altitude would have resulted in a 44% reduction in the effective area searched if observers searched within the same declination angle as in 2001, but the effective search area was estimated to be just 15% smaller in 2007 than in 2001, indicating that the observers compensated for lower altitude by changing their searching behaviour. The decrease in the estimate compared to 2001 is unlikely to be an artefact of changes in survey methods alone. There is some evidence that minke whale density was increasing over the course of the survey, suggesting that the peak in seasonal abundance might have been missed.

The sub-committee noted that the reason advanced for excluding data from one of the observers was that this observer did not detect any minke whales within 200m of the trackline and duplicated none of the minke whales detected by the control observer, precluding estimation of distance error or $g(0)$. Gunnlaugsson pointed out that the counts from the two primary observers were significantly different at the 5% level and the duplicate counts were significantly different at the 1% level. Other members responded that the significance of differences in counts may also be overestimated due to clumping of whales.

The sub-committee noted that this observer did make observations of other species (particularly harbour porpoise) close to the trackline. There was no reason to suspect problems in species identification, nor any other obvious reason why this observer should have had a reduced ability to detect minke whales close to the trackline. Despite the difference in detections and the inability to estimate distance error or $g(0)$ for this observer, the sub-committee agreed that there was no *a priori* reason to exclude these data.

The sub-committee agreed that the abundance estimate of 10,680 (CV=0.29) based on data from both observers meets the requirements for use in conditioning trials and for use in the RMP. Gunnlaugsson believed that the estimate of 15,055 (CV=0.36) based on data from the observer for whom it was possible to estimate $g(0)$ also meets these requirements, noting that the lower estimate is incompletely corrected for $g(0)$.

On this latter point, the sub-committee referred to its discussions relating to the use of a series of estimates in the RMP that had or had not been corrected for a known source of bias (Annex D, Item 5.4).

4.1.5 Other Small Areas in the Central Medium Areas

SC/60/For info 34 presented a cruise report for TNASS 2007 in the Denmark Strait south west of Iceland. No attempt had been made to obtain an abundance estimate for this area due to very low realised effort in areas off north Iceland and along the east Greenland coast, and the limited number of minke whale sightings. It was noted that exclusion of surveys that yielded a low number of sightings could lead to the abundance estimates used for the RMP being biased. It was suggested that an abundance estimate could be constructed from the pooled dataset, using a stratified detected function. The usefulness of having data from all surveys conducted available in a database was noted, so that a meta-analysis can be conducted in the future.

4.1.6 West Greenland

Donovan summarised the AWMP discussions, where an aerial survey estimate of 10,800 (CV=0.71) (JCRM 10 p. 126) had been accepted. A shipboard estimate had not been accepted.

4.1.7 Western North Atlantic

The US conducted an aerial survey in August 2006 using the circle-back method that resulted in an estimate of 3,312 (CV=0.74) minke whales in the Gulf of Maine, Bay of Fundy, and western Scotian shelf (a similar area to previous surveys). This estimate included an estimate of $g(0)$ for perception bias (Waring et al. 2007). The sub-committee agreed that this estimate meets the requirements for conditioning trials. However, it is not necessary that these surveys meet the requirements for the RMP because they are not part of the stocks that are the focus of the whaling operations being considered in this *Implementation Review*.

Shipboard (US only) and aerial (US and Canada) surveys covering waters from North Carolina, US to Labrador, Canada were conducted during July-August 2007. Estimates of minke whale abundance based on the surveys will be available by the 2009 SC meeting.

4.2 Review of previously accepted or revised abundance estimates

4.2.1 Northeast Atlantic (Norwegian Sea and Barents Seas)

The sub-committee confirmed that the 1988-89, 1995 and 1996-2001 abundance estimates still meet the requirements for conditioning trials and for use in the RMP.

4.2.2 North Sea

The sub-committee confirmed that the 1994 SCANS abundance estimate for minke whales still meets the requirements for conditioning trials and the RMP. With respect to the RMP, the requirements regarding data submitted to the IWC, and cruise reports and associated documents, were not met because they were not required at the time of the survey.

4.2.3 CM (Jan Mayen) area

The sub-committee confirmed that the 1987, 1988-89, 1995 and 1997 Norwegian/Icelandic abundance estimates meet the requirements for conditioning trials and for use in the RMP.

4.2.4 Iceland coastal

SC/60/For Info36 presented a reanalysis of the data from the 1987 and 2001 aerial surveys in Icelandic coastal areas (CIC *Small Area*). Previous analysis of these data by Hiby et. al. (1989) was based on a normal distance measurement error model. A Gamma model produced a substantially lower AIC in the new analysis and was hence preferred. The resulting distance- and $g(0)$ -corrected estimate with Beaufort sea state as an explanatory variable was 24,532 (CV 0.32) (13,399-44,916, 95% CI).

The authors of SC/60/ForInfo36 considered the best estimate from the 2001 survey should be based only on the data from the side of the plane on which the primary observer who had more duplicates with the control observer (co-pilot) operated. In this case, distance errors are small enough to be ignored, and $g(0)$ can be taken as 1.0 because detection at distance zero is virtually certain for this observer. This estimate is 43,633 (0.19) (30,148-63,149 95% CI.) The sub-committee agreed that these abundance estimates meet the requirements for conditioning trials and for use in the RMP.

4.2.5 Remainder of Central Area

The Committee had previously agreed that the Icelandic shipboard surveys in 1987-89, 1995 and 2001 met the requirements for conditioning trials if the abundance estimates are considered minimum estimates. The two earlier abundance surveys were conducted before the Requirements were established, and the latest survey was conducted when Iceland was not a member country of the IWC. It is expected that future surveys and analyses will follow the IWC guidelines established for abundance surveys more closely. The IWC guidelines call for distance estimation experiments to be conducted during the cruise, but this was not done on the 2001 survey. The sub-committee agreed that the estimates could be regarded as provisionally acceptable for use in the RMP, provided the concern raised in item 4.1.5 is addressed and determined not to be a problem.

4.2.6 West Greenland

The sub-committee confirmed that the 1987-88 and 1993 Greenland aerial surveys meet the requirements for conditioning trials. It is not necessary that these surveys meet the requirements for the RMP because they are not used when setting commercial catch limits.

5. IMPLEMENTATION TRIALS

5.1 Review of Previous Trials

See Item 2.1.

5.2 Consideration of whether new Trials are needed

The review of new information on stock structure and abundance did not reveal any new hypotheses which are not captured qualitatively by the existing set of 16 trials. The sub-committee noted that the factors included in the current sets of trials are similar to those included in the most recent sets of *Implementation Simulation Trials* (western North Pacific Bryde's whales, and North Atlantic fin whales). However, the North Atlantic *Implementation Simulation Trials* were developed before the *Requirements and Guidelines for Implementations* (JCRM 7(Suppl.): 84-92) were adopted and, as such, the current set of trials does not follow the *Requirements and Guidelines* exactly. For example, it was noted that the approach for selecting the values for the parameters of the operating model (conditioning) did not involve fitting the operating model to the available information on, for example, abundance and movement from mark-recapture data. These trials do, however, follow the intent of the *Requirements and Guidelines*. The sub-committee therefore agreed that it was not necessary to modify the existing trials for the current *Implementation Review*, but that the next *Implementation Review* in 2013 should be based on following the *Guidelines and Requirements*. The sub-subcommittee agreed that there was a need to modify the *Guidelines and Requirements* to reflect that it will be necessary to update *Implementation Simulation Trials* periodically to reflect changes in the methodology of how to evaluate management procedures using simulation, and requested Donovan to provide draft text for consideration of the next meeting of the Committee.

The sub-committee noted that following the *Requirements and Guidelines for Implementations* for North Atlantic minke whales would require adequate resources (personal and financial) and, ideally, the results of new research focused on selecting among stock hypotheses and parameterising the operating model. The sub-committee suggested that the Norwegian and Icelandic scientists develop an initial broad set of stock structure hypotheses which could form the basis for focusing and prioritising future research for use in the next *Implementation Review*. This set of hypotheses should include whether there is dispersal among sub-stocks as well as mixing of stocks.

The sub-committee identified the following research topics which should enhance the 2013 *Implementation Review*:

1. Apply non-genetic methods to further elucidate stock structure and assess movement and dispersal rates, using methods such as microchemistry, tracking of individual whales, and *Discovery*-type marking.
2. Analyse the spatial distribution of close relatives and individuals (identified by genetic analyses) to assess whether there is evidence for site-fidelity.
3. Explore whether data can be collected to explore temporal effects, including variation in the time it takes for animals to migrate through each sub-area.
4. Evaluate the implications of population expansion on the use of genetics data.
5. Undertake DNA sequence-based analyses to assess if the high degree of genetic divergence detected at allozyme loci is evident in the DNA sequences that encode the allozymes.

6. RMP IMPLEMENTATION OPTIONS

6.1 Management areas

6.1.1 Review of choices made in previous Implementation/Implementation Review

The Committee had recommended that the *Medium Areas* should remain unchanged from their original specification in 1993 during the *Implementation Review* in 2003. Changes were made to the original *Small Area* boundaries as follows (JCRM 6 (suppl): 171).

- the northern border of the EN *Small Area* was moved from 65° to 62° N;
- the EB *Small Area* was amended by creating a new western boundary at 28° E south to the Norwegian coast;
- the EC *Small Area* was eliminated and merged into a new EW *Small Area*.

The previous *Implementation Review* noted that evidence for the need and/or the location of these boundaries was not particularly strong.

6.1.2 Consideration of alternative management areas

6.1.2.1 Medium Areas

The sub-committee recommended that the *Medium Areas* remain unchanged.

6.1.2.2 Small Areas

Walløe proposed that the boundary between the EW and EB *Small Areas* that had been introduced in 2003 should be removed. He noted that there was weak evidence for introducing it in the first place and the new information presented under Item 3 showed that there was now no evidence for it. Although there was no evidence for a boundary between ES and EW/EB *Small Areas*, he believed that it was appropriate to keep this boundary for precautionary reasons.

The sub-committee had an extended discussion on the merits or otherwise of this proposal. Three main points were discussed.

- (1) The analysis of catches in 2003-2006 presented in SC/60/PF11 found no genetic difference between whales east and west of 28° N, in contrast to the result found from analysis of catches in 1997-2002. The sub-committee agreed that it was important to determine whether this difference was due to improvements in laboratory techniques, i.e. that the earlier result was an artefact, as suggested might be the case by the author. Following some discussion, a Working Group (Skaug, Palsbøll and Butterworth) was established to attempt to clarify this through further analysis of the data. In particular, attempts would be made to identify whether the difference found in the earlier analysis resulted from just a few individuals. This Working Group would report to the sub-committee later in the meeting. If the differences east and west of 28° N were found to be an artefact, then attention would focus on the following points.
- (2) The sub-committee discussed the distribution of catches and abundance in *Small Areas* EB and EW. Catches were generally taken from along the coast of northern Norway, but the abundance estimates were for the entire areas. If animals were not distributed throughout the *Small Areas*, the genetic data may be from only a small part of the range and uncertainty would remain about stock structure in these areas. In this case, removing the boundary between EB and EW *Small Areas* could be a cause for concern. Appropriate members were requested to extract the relevant information from available documents and prepare a Working Paper to present to the sub-committee later in the meeting.
- (3) The sub-committee recalled the analysis of close relatives previously presented by Skaug (SC/57/SD2). Skaug reported that there were approximately 25 pairs of close relatives in the whole eastern North Atlantic dataset. Analyses had been unable to reject the hypothesis that close relatives were found closer together than unrelated animals. Furthermore, there were also instances of close relatives being found in different *Small Areas* and even in different *Medium Areas* in some cases. Skaug agreed to revisit these analyses with the aim of clarifying the question of differences east and west of 28° N and to report to the sub-committee later in the meeting.

The sub-committee agreed that a decision on whether or not to remove the boundary between *Small Areas* EB and EW would be deferred until the results of the above work were available.

6.2 Catch-capping and catch-cascading

The present RMP implementation includes catch-cascading (but no catch-capping) at the *Medium Area* level. No information was available to indicate a change to this, so the sub-committee recommended that catch-cascading be retained.

7. Adoption of report

The report was adopted during the meetings of the RMP sub-committee. The sub-committee thanked Cooke for his excellent chairmanship and the rapporteurs for their work.

References

- Andersen, L. W., E. W. Born, 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. *Marine Ecology-Progress Series* **247**: 263-280.
- Arnason and Spillaert 1991
- (Borchers et al., 1997
- Burt, ML, Borchers, DL & Samarra, F (2008). Design-based abundance estimates from SCANS-II. Appendix D3.4 to SCANS-II (2008) – see below.
- Hammond, P.S., Berggren, P., Benke, H., Borchers, D.L., Collet, A., Heide-Jørgensen, M.P., Heimlich, S., Hiby, A.R., Leopold, M.F. & Øien, N. (2002). Abundance of harbour porpoises and other cetaceans in the North Sea and adjacent waters. *Journal of Applied Ecology* **39**: 361-376.
- Macleod, K, Burt, ML, Cañadas, A, Santos, B, Uriarte, A, Van Canneyt, O, Vázquez, JA & Hammond, PS (2008). Preliminary abundance estimates of cetaceans in offshore European Atlantic waters. Paper SC/60/O2 presented to the 2008 meeting of the IWC Scientific Committee, Santiago de Chile.
- SCANS-II (2008). Small Cetaceans in the European Atlantic and North Sea. Final Report to the European Commission under project LIFE04NAT/GB/000245. Available from SMRU, Gatty Marine Laboratory, University of St Andrews, St Andrews, Fife, KY16 8LB, UK.
- Witting, L. (2005). Aerial image estimation of minke whale surface time. Paper SC/57/AWMP1 presented to the 2005 meeting of the IWC Scientific Committee, Ulsan, South Korea.
- Danielsdottir, A. K., E. J. Duke, et al. (1992). Genetic variation at enzyme loci in North Atlantic minke whales, *Balaenoptera acutorostrata*. *Biochemical Genetics* **30**(3/4): 189-204.
- Danielsdottir A.K., Halldorsson, S.D., Gudlaugsdottir, S., Arnason, A. (1995). Genetoc variation in northeastern Atlantic minke whales (*Balaenoptera acutorostrata*). In: Whales, seals and man, eds. Blix, A.S., Walløe, L., Ulltang, Ø, pp105-118
- Hiby et al (1989)
- IWC (2004). Report of the Sub-Committee on the Revised Management Procedure 2003. *J. Cetacean Res. Management* **4**(Suppl).
- Macleod et al. 2008
- Palsbøll et al. (1991)
- Palsbøll, P. J. (1989). Restriction fragment pattern analysis of mitochondrial DNA in the North Atlantic minke whale, *Balaenoptera acutorostrata*. *Department of Genetics*. Copenhagen, Institute of Molecular Biology, University of Copenhagen: 42 pp.
- Skaug, H.J., Øien, N., Schweder, T. and G. Bøthun 2004. Abundance of minke whales (*Balaenoptera acutorostrata*) in the Northeastern Atlantic; *Can. J. Fish. Aquat. Sci.* **61**: 870-86.
- Skaug et al (2005) SC/57/SD2
- (Waring et al. 2007)
- Add references from Table 2

Table 1. F_{ST} value and associated 95% and 99% CIs, for the two haplotype groups detected with the minimum spanning mtDNA haplotype network (Fig. 1 of SC/60/PFI10).

	<i>Average</i>	<i>95% CI</i>		<i>99% CI</i>	
F_{ST}	0.0013	0.0000	0.0020	0.0000	0.0030

Adjunct 1. North Atlantic minke whales RMP Implementation Review -Draft Agenda

1. Introductory items
 - 1.1. Election of Chair
 - 1.2. Appointment of rapporteurs
 - 1.3. Adoption of agenda
 - 1.4. Review of documents
 - 1.5. Review of data sets available for the Implementation Review
2. Stock structure
 - 2.1. Review of previous stock structure
 - 2.2. Review of recent data analyses
 - 2.2.1. New analyses
 - 2.2.2. Other published analyses
 - 2.3. Consideration of new hypotheses
 - 2.3.1. Specification of subareas
 - 2.3.2. Dynamics of stocks and substocks in relation to subareas
3. RMP Implementation options
 - 3.1 Management areas
 - 3.1.1. Review of choices made in previous Implementation Review areas and their basis
 - 3.1.2. Consideration of alternatives
 - 3.1.2.1. Medium Areas
 - 3.1.2.2. Small Areas
 - 3.2. Catch-capping and Catch-cascading
 - 3.2.1. Review of previous recommendations
 - 3.2.2. Consideration of alternatives
4. Implementation Trials
 - 4.1. Review of previous Trials
 - 4.2. Consideration of whether new Trials are necessary
 - 4.3. Specification of Trials (in broad outline only)
 - 4.4. Appointment of subgroup to detail specification of Trials
5. Abundance estimates
 - 5.1. Review of new abundance estimates (since 2003 Implementation Review)
 - 5.1.1. Northeast Atlantic (Norwegian Sea and Barents Seas)
 - 5.1.2. North Sea
 - 5.1.3. CM (Jan Mayen) area
 - 5.1.4. Coastal Iceland
 - 5.1.5. Remainder of Central Small Area
 - 5.1.6. West Greenland
 - 5.1.7. Western North Atlantic
 - 5.2. Review of previously accepted or revised abundance estimates
 - 5.2.1. Northeast Atlantic (Norwegian Sea and Barents Seas)
 - 5.2.2. North Sea
 - 5.2.3. CM (Jan Mayen) area
 - 5.2.4. Coastal Iceland
 - 5.2.5. Remainder of Central Small Area
 - 5.2.6. West Greenland
 - 5.2.7. Western North Atlantic
 - 5.3. Identification of estimates acceptable for use in RMP and/or conditioning trials
 - 5.3.1. Northeast Atlantic (Norwegian Sea and Barents Seas)
 - 5.3.2. North Sea
 - 5.3.3. CM (Jan Mayen) area
 - 5.3.4. Coastal Iceland
 - 5.3.5. Remainder of Central Small Area
 - 5.3.6. West Greenland
 - 5.3.7. Western North Atlantic

Table 2

For each *Small Area*, a summary of available abundance estimates and their confidence, characteristics of the associated survey, references and whether the abundance estimate meets requirements for use in conditioning trials and/or the RMP.

<i>Small Area(s)</i>	<i>Year(s)</i>	<i>Organiser/ programme</i>	<i>Platform</i>	<i>Reference(s) for estimates</i>	<i>Data status</i>	<i>Abundance and CI</i>	<i>Meets requirements for conditioning trials</i>	<i>Meets requirements for use in the RMP</i>
Northeast Atlantic								
ES, EB, EC, EN	1988-89	Norway/NASS	Ship	Schweder <i>et al.</i> (1997)	Submitted, avail.	63,730 (CV=0.19)	Yes	Yes
ES, EB, EC, EN	1995	Norway/NILS	Ship	Schweder <i>et al.</i> (1997)	Submitted, avail.	112,125 (CV=0.10)	Yes	Yes
ES, EB, EC, EN	1996-2001	Norway/NILS	Ship	Skaug <i>et al.</i> (2004)	Submitted, avail.	80,487 (CV=0.15)	Yes	Yes
ES, EB, EW, EN	2002-2007	Norway/NILS	Ship	Bøthun <i>et al.</i> (2004)	Submitted, avail.	78,572 (CV=0.16)	Yes	No
NS (part of EN)	1994	SCANS	Ship	Hammond <i>et al.</i> (2002)	Available ¹	8,445 (CV=0.24)	Yes	Yes ¹
EN	2005	SCANS-II	Ship	SCANS-II (2008)	Available	18,614 (CV=0.3)	Yes	Yes
Central North Atlantic								
CM	1987	Norway/Iceland	Ship	Øien (2000)	Submitted, avail.	5,609 (CV=0.26)	Yes	Yes
CM	1988-89	Norway	Ship	Schweder <i>et al.</i> (1997)	Submitted, avail.	2,650 (CV=0.48) (No NVS)	Yes	Yes
CM	1995	Norway/Iceland	Ship	Schweder <i>et al.</i> (1997) + Borchers <i>et al.</i> (1998)	Submitted, avail.	6,174 (CV=0.36) (No NVS) 12,043 (CV=0.28) (Combined Norway & Iceland)	Yes ²	Yes
CM	1997	Norway/NILS	Ship	Skaug <i>et al.</i> (2004)	Submitted, avail.	26,718 (CV=0.14)	Yes	Yes
CM	2005	Norway/NILS	Ship	Bøthun <i>et al.</i> (2008)	Submitted, avail.	24,890 (CV=0.45)	Yes	No
CIC	1987	Iceland/NASS	Aircraft	Borchers <i>et al.</i> (2008)	Submitted, avail.	24,532 (CV 0.32) ⁴	Yes	Yes
CIC	1995	Iceland/NASS	Aircraft	Borchers <i>et al.</i> (1997)	Submitted, avail.	Not estimated	No	No
CIC	2001	Iceland/NASS	Aircraft	Borchers <i>et al.</i> (2008)	Submitted, avail.	43,633 (CV=0.19)	Yes	Yes
CIC	2007	Iceland/NASS	Aircraft	Pike <i>et al.</i> (2008)	Submitted, avail.	10,680 (CV 0.29)	Yes	Yes
CG, CIP	1987-89	Iceland	Ship	IWC (1993) p.66	Submitted, avail.	9,986 (CV=0.22)	Yes ²	Yes
CG, CIP	1995	Iceland/NASS	Ship	Pike <i>et al.</i> (2003b)	Submitted, avail.	Approx. stratum 9 – 4,854 (CV=0.27)	Yes ²	Yes
CG, CIP	2001	Iceland/NASS	Ship	Gunnlaugsson <i>et al.</i> (2002), Pike <i>et al.</i> (2003a)	Submitted, avail.	23,592 (CV=0.26)	Yes ²	Yes ³
Western North Atlantic								
WG	1987-88	Greenland	Aircraft	IWC (1990) p.43	Submitted? Not required	3,266 (CV=0.31) ⁴	Yes	Not required
WG	1993	Greenland	Aircraft	Larsen (1995); Hedley <i>et al.</i> (1997)	Submitted? Not required	8,371 (95% CI: 2,400-16,900); 6,342 (95% CI: 2,942-13,855)	Yes	Not required
WG	2007	Greenland	Aircraft	Heide Jørgensen <i>et al.</i>	???	???	???	???
WC: G. of Maine	1995-99	USA	Ship	Waring <i>et al.</i> (2002)	Not requested	1995: 2,790 (CV=0.32); 1998: 2,998 (CV=0.19)	Yes	Not requested
WC: G. of St. L.	1995-96	Canada	Aircraft	Kingsley and Reeves (1998)	Not requested	1,020 (SE=280)	No	Not requested
WC: G. of Maine.	2006	USA	Aircraft	Waring <i>et al.</i> (2007)	Not requested	3,312 (CV=0.74)	Yes	Not requested

¹Available from RUWPA. ²Used as minimum estimate (no g(0)). ³Yes, unless concerns raised in report are determined to be a problem. ⁴Partial coverage of area.

Appendix 8

A CLOSER LOOK AT THE INHOMOGENEITY AROUND 28°E FOR NA MINKE WHALES

Hans Skaug

At the Implementation Review for NA minke whales held in Berlin in 2003 a significant degree of heterogeneity was detected at mtDNA haplotype frequencies between female animals caught east and west of 28°E, respectively, along the coast of Finnmark. The present working paper investigates further the possible cause of this result, more precisely if the effect was due to samples from a specific year, or a particular mtDNA haplotype.

The basis for the introduction of a Small area boundary at 28°E was hypothesis H14 in Table 4 in IWC (2004). The sampling site 6^E is east of 28°E, while the sampling site 5+6^W constitutes the area west of 28°E.

The analysis conducted in 2003 did not include calculation of F_{ST} like statistics. These have now been calculated using the program Hetero (P. Palsbøll, personal communication) and are shown in Table 1. The F_{ST} values are all very small, and it is only the chi-square test that is significant at a 5% level.

When data from 1998 are excluded, the heterogeneity disappears (Table 2), but when looking at data only from 1998 there is no significant heterogeneity. Neither do individuals from 1998 (pooling east and west of 28°E) differ significantly from individuals in the other years (p-value 0.77).

Figure 1 shows the effect of leaving out individual mtDNA haplotypes one at the time. It is seen that there are few haplotypes which, when removed from dataset, increase the p-value appreciably.

Conclusion

The F_{ST} values are very low, and unlikely to be biologically significant. Neither are the hypothesis tests significant. The whole basis for the 28°E line has been pinned down to an effect caused by individuals caught in 1998. It is however, not clear exactly what is special about the 1998 individuals.

Table 1 Fst-like statistics and corresponding p-values for the hypothesis H14 in Table 4 in IWC (2004) .

	Statistic	p-value
Kst	-0.000452	<0.704300
Kst*	-0.000053	<0.432000
Hst	0.000747	<0.067400
X^2	84.483	<0.012700

Table 2 The effect of excluding data from individual years one-at-the-time, and using only data from single years. The right-most two columns give sample sizes.

	X^2 statistic	p-value	n (6 ^E)	n (5+6 ^W)
All years	84.483	0.011	604	389
All -1997	73.204	0.077	453	364
All -1998	63.752	0.181	426	346
All -1999	76.102	0.038	510	318
All -2000	75.029	0.024	560	317
All -2001	83.864	0.006	567	314
All -2002	73.467	0.019	504	286
Only 1997	13.537	0.909	151	25
Only 1998	33.835	0.441	178	43
Only 1999	26.269	0.622	94	71
Only 2000	25.571	0.525	44	72
Only 2001	28.342	0.467	37	75
Only 2002	28.495	0.912	100	103

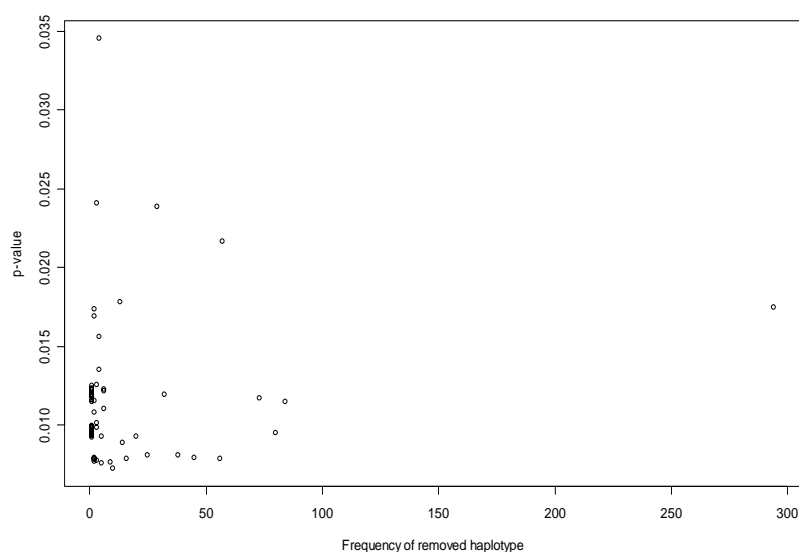


Fig. 1. Effect on p-value when leaving out individual haplotypes (jack-knifing haplotypes). Each point represents a hypothesis test with all individuals having a given haplotypes left out.

Appendix 9

CATCH POSITION FOR PAIRS OF RELATED INDIVIDUALS

Hans Skaug

When searching the Norwegian minke whale DNA-register from 1997-2002, 27 pairs of related individuals (dyads) have been identified (SD/57/SD2). Many of these were parent-offspring pairs. Figure 1 shows the position of related individuals, while Table 1 summarises Figure 1 at a Small Area level.

Table 1. Comparison of catch positions (Small area) members of pairs of related individuals detected in SD/57/SD2. Each cell gives the number of dyads for a particular *Small Area* combination, so for instance there were 4 dyads for which one member was caught in EW while the other member was caught in EN.

	EN	EW	EB	ES	CM
EN	0				
EW	3	4			
EB	2	4	2		
ES	2	4	2	1	
CM	0	1	0	1	1

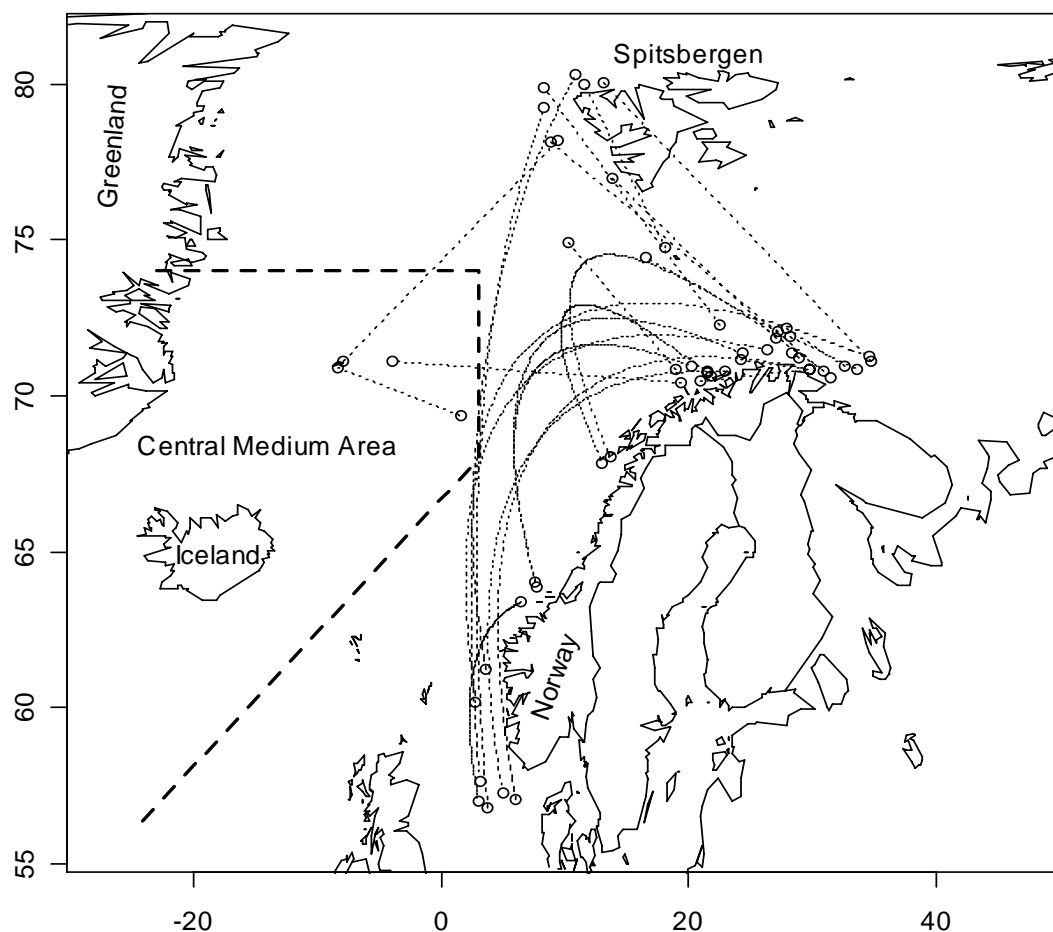


Fig. 2 Capture locations (circles) of pairs of related individuals. Related individuals are connected by dotted lines. The thick dashed line indicates the border between the Central and Eastern Medium Areas. Sea areas outside the southern part of Norway are referred to as the North Sea

REFERENCE

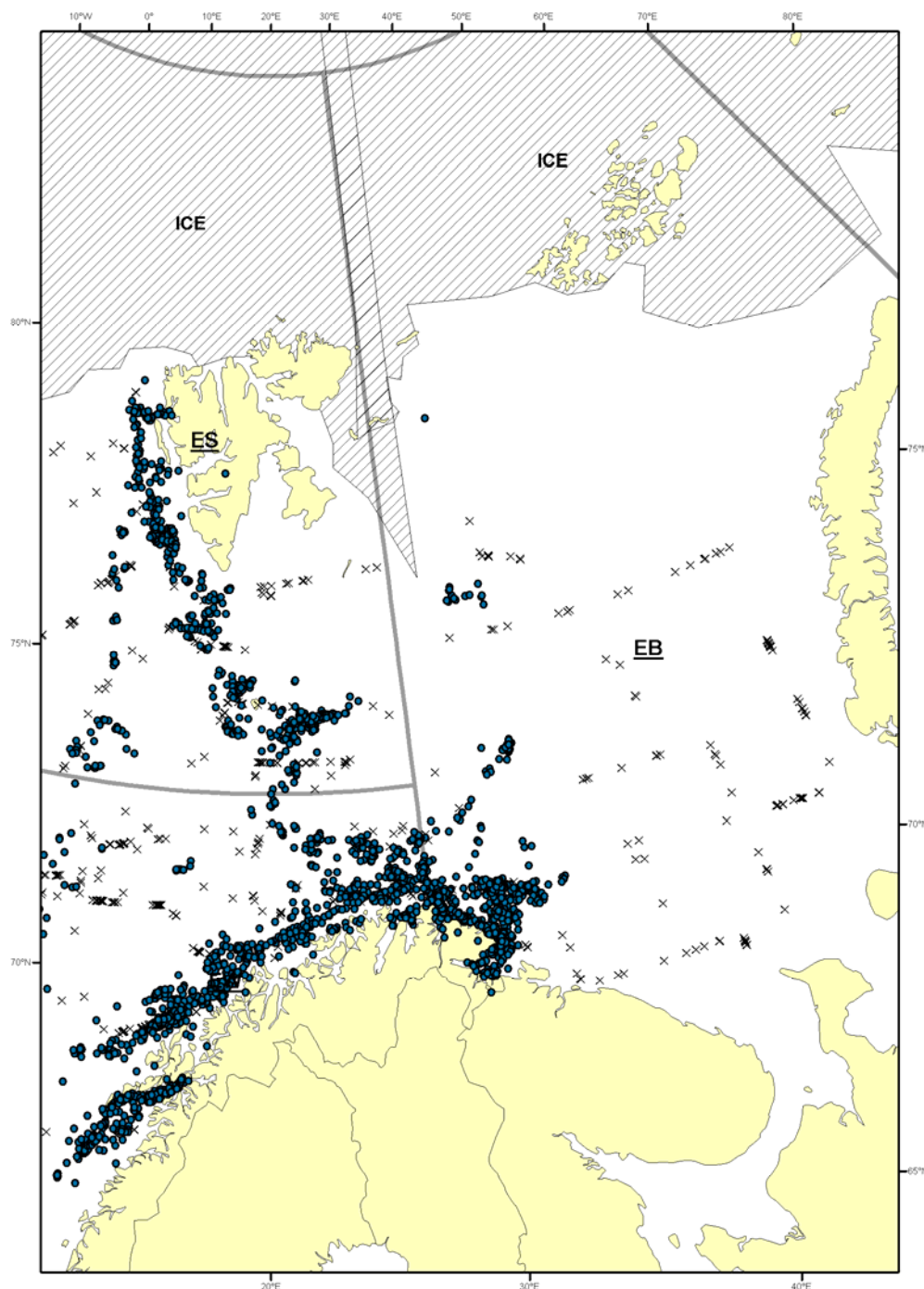
Skaug, H. J. Palsbøll, P. J., Bérubé, M., Rew, M. B., (2005), "Application of high resolution DNA profiling to management of Northeastern Atlantic minke whales", Paper SC/57/SD2 presented to 57th Scientific Committee of the International Whaling Commission.

Appendix 10

DISTRIBUITION OF MINKE WHALES RELATIVE TO CATCHES, WITH SPECIAL REFERENCE TO THE EASTERN BARENTS SEA

L.G. Bøthun and N. Øien

The figure below shows (1) the distribution of minke whale sightings over the most recent NILS survey period 2002-2007 (x – crosses), and (2) the distribution of catches 2002-2006 (• - filled circles). While sightings are found all over the area, catches are limited to within Norwegian EEZ and to areas where the whalers have experienced reasonable densities of whales to occur and, not at least, are logistically accessible by the relatively small vessels used in this fishery. In practice this means that catches usually are taken in coastal waters. Presently, however, Russian EEZ excludes Norwegian whalers from areas explored earlier in the Barents Sea, usually limited only by ice conditions. The usual situation in the Barents Sea is that the northern and northeastern parts are closed by ice, although the ice extension varies a lot between years. The indicated line is the 28°E longitude (present boundary between Small Management Areas EW/ES and EB). As such, it can be said that genetic data from the eastern Barents Sea now are mainly confined to samples collected off northern Norway and from the northern Barents Sea within the Norwegian EEZ.



Appendix 11

PROPOSAL TO CONTINUE AUGMENTATION OF THE COMMITTEE'S COMPUTING CAPABILITIES WITH RESPECT TO RMP AN AWMP IMPLEMENTATIONS

Relevant Agenda Items(s):
Annex D, Item 3.

Brief description of project and why it is necessary to the Committee

There is a need for extra computational support for new and ongoing *Implementations*. Without this, the Committee will be unable to meet the strict timetable agreed in the Requirements and Guidelines for *Implementations*. This project will involve using the programming capabilities in this field of research staff at the University of Cape Town to provide direct programming support to Allison and the relevant sub-committees. In the first instance this will apply to the North Atlantic fin whale *Implementation*. The programmers involved will work under the supervision and guidance of Allison, Butterworth and Punt to implement the decisions of the relevant sub-committees and the Committee with respect to *Implementations* and *Implementation Reviews*.

Timetable

For the envisaged period up to and including the 2009 Annual Meeting the tasks will comprise:

- (1) assisting with coding and running of the *Implementation Simulation Trials* agreed at the present meeting and development of the inputs needed to apply the criteria used to assess conservation performance;
- (2) participation in the Second Intersessional Fin Whale Workshop to amend/run software as required;
- (3) continue software development with as required before SC 2009; and
- (4) participation in SC/61 in 2009 to work with Allison to amend/run software as required.

Researchers' name

Primarily Dr C. Cunningham and Mrs R Rademeyer, with additional support from other research staff at the University of Cape Town as appropriate

Estimated total cost with breakdown as needed (e.g. salary, equipment)

Total budget £20,000

Salary: £15,000

Travel and subsistence: three people to attend the Second Intersessional Fin Whale Workshop, and the 2009 Annual Meeting.