

areas. It was agreed that both the inclusion of age-dependent mixing and the exclusion of it would be given high plausibility.

Additional process error: It was agreed that the inclusion of additional process error would be given high plausibility.

Stochastic mixing: It was agreed that stochastic mixing of two stocks in sub-area 1 would be given medium plausibility.

Alternative boundary: The default in trials is that the boundary between 1W and 1E is at the survey boundary. Alternative boundary allows for the stock boundary to be in locations other than the survey boundary. These alternative boundaries were all given medium plausibility.

Low and High catch series: The Low catch series and the High catch series are specified to account for uncertainty in the catch series, mainly due to uncertain species identification between Bryde's and sei whales, along with the possibility that the true catches are higher than the reported catches (Kasuya and Brownell, 2001). In discussion, it was suggested by Perrin that the High catch series was equally plausible as the reported catch series, and both should have high plausibility. As reported previously in IWC (2006), Kasuya and Brownell (2001) had noted the total actual catches off the Ogasawara Islands might be 1.6 times the reported catches but the original records have been lost and are not available. Therefore, it is not possible to examine this issue any further to elucidate which catch series is more likely, and consequently both catch records should be accorded high plausibility. This ensures that the performance of both catch series (Best and High) will be held to the same standards in trials. The sub-committee **agreed** that both the Best and High catch series would be given high plausibility.

3.1.6 Data/research to reduce hypotheses

Under this item the sub-committee noted its earlier discussions under Item 3.1.1, and in particular under Item 3.1.5.1, hypothesis 4.

3.1.7 Specification of operational features and management variants

The following four management options will be considered:

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

- (1) sub-areas 1W, 1E¹ and 2 are *Small Areas* and catch limits are set by *Small Area*;
- (2) sub-area 2 is taken to be a *Small Area* and the complete sub-area 1 is treated as a *Small Area*. For this management option, all of the future catches in sub-area 1 are taken from sub-area 1W.

Management options based on applying catch cascading:

- (3) sub-area 2 is taken to be a *Small Area* and sub-area 1 is taken to be a *Combination Area*. Sub-areas 1W and 1E are *Small Areas*, with *catch-cascading* applied;

- (4) sub-areas 1 and 2 (combined) are taken to be a *Combination Area*, and sub-area 2 and sub-areas in 1W and 1E are *Small Areas*, with *catch-cascading* applied.

The simulation application of the RMP is based on using the 'best' catch series (see Table 2).

3.1.8 Specification and classification of final trials

The full list of specified trials, including the weights of each trial given by the lowest plausibility of any component, is found in Appendix 6, table 6.

3.1.9 Work plan

In accordance with the 'Requirements and Guidelines for Implementations' (IWC, 2005) plans were made for the second intersessional Workshop for the WNP Bryde's whale *Implementation*. Japan offered to host the meeting, as for the first intersessional Workshop, to be convened by Kawahara. The cost will be the same as for the first workshop.

3.2 North Atlantic fin whales

3.2.1 Report of the joint NAMMCO/IWC Scientific Workshop

Walløe presented the report of the Joint NAMMCO/IWC Scientific Workshop on the catch history, stock structure and abundance of North Atlantic fin whales (SC/58/Rep3). The main objective of the Workshop was to consider the available information on stock structure, catch history, biological parameters and abundance and trends in order to advance the fin whale assessments ongoing in the two organisations.

Several papers on stock structure, based on both genetic and non-genetic data, were presented at the Workshop. A number of key factors emerged that require further work before a full understanding of the contribution of the genetic work to the elaboration of stock structure in the North Atlantic fin whales can be completed, and these were given as recommendations for work to be completed before the IWC meeting in St. Kitts. The Workshop then went on to consider the hypotheses with respect to feeding areas, using the schematic figures of IWC (2005) as a guide. It is important to stress that the figures are schematic and the location of the 'breeding stocks' is not intended to suggest any specific geographical location. The Workshop considered each of the figures in turn and modified them where appropriate. The Workshop noted that in many cases the discriminatory evidence is weak. The results of these discussions are given in SC/58/Rep3, fig. 1. The Workshop agreed that pressures of time meant that it had not been possible to fully consider the need for possible further scenarios (e.g. incorporating possible north-south structure, alternative links and/or strength of links between breeding stocks and feeding areas, or finer structure within feeding areas).

The Workshop received a complete review of estimates of biological parameters for fin whales, including age and length at sexual maturity, asymptotic length, length at age five, age at recruitment, mortality rate, ovulation rate and interval and the proportion pregnant in the mature female catch. It was agreed that there was nothing in the review to necessitate change to the parameter values used previously by both the IWC (IWC, 1992b) and NAMMCO (NAMMCO, 2000; 2001; 2004) Scientific Committees.

A number of papers detailing catch series for the northeast and central Atlantic were presented to the Workshop. It was agreed that there was sufficient uncertainty in the catches, in particular in years when the fin whale catch was estimated

¹ Defined to be 140°E-165°E and 165°-180° irrespective of the true boundary used to define the structure of the populations in the operating model.

from the total catch by species proportion and in years when the struck and lost rate was thought to be appreciable, to warrant development of alternative catch series. It was agreed that the information in the catch series will be used as a basis to develop a 'high' and a 'low' series containing the maximum and minimum catches, however this work could not be completed at the Workshop. In addition the Workshop considered papers detailing various Catch Per Unit Effort (CPUE) indices for the Icelandic, Norwegian and Faroese fin whaling operations, and provided a series of recommendations for improvement and better documentation of these indices. It was considered particularly important that papers proposing CPUE series provide adequate documentation of the rationale behind any assumptions made and values chosen and consideration of alternative values and assumptions to capture uncertainty/possible bias. It was recommended that priority be given to investigating whether appropriate CPUE series could be developed for the 'early' (pre-1915) Icelandic whaling operations and Faroese whaling after the 1st World War.

Several papers detailing abundance estimates from international and Norwegian surveys carried out in the northeast and central North Atlantic since 1987, as well as recent Canadian and Greenlandic surveys, were presented at the Workshop. The Workshop found the estimates from the North Atlantic Sighting Survey (NASS) and Norwegian surveys for the central and northeast Atlantic to be acceptable for use in assessments and agreed that for general purposes the best estimate of current abundance in the central North Atlantic (including the Faroes) is 25,800 (CV=0.125) for the year 2001. The best estimate for the eastern North Atlantic is 4,100 (CV=0.210) from the 1996-2001 survey series. These estimates are based on the assumption that $g(0)=1$. Estimates of $g(0)$ from recent NASS and Norwegian surveys were presented and fall in the range of 0.7 to 0.9 depending on whether the estimate is for the single or combined platforms. It was considered that for the purposes of assessment the assumption of $g(0)=1$ was adequate.

The Workshop noted that estimated abundance in the area west and southwest of Iceland increased at an annual rate of 10% (95% CI: 6% – 14%) between 1987 and 2001. This is the area where nearly all fin whaling has been conducted since 1915. Estimated abundance in the whole East Greenland/Iceland (EGI) area has increased at 3% (95% CI: –1% – 7%) per year, i.e. this rate of increase is not significant at the 5% level. There was no evidence of any trend in abundance in the eastern North Atlantic.

A new assessment model of the EGI fin whale population, modelled as four subpopulations with movement between areas was presented. The model is sex- and age-structured, and is fitted to CPUE, sightings survey abundance split by area, and mark-recapture data using both maximum likelihood and Bayesian approaches. For the base case and most sensitivity tests, the overall recruited population is increasing and above 80% (base case 84%) of pre-exploitation abundance. The Workshop could not draw firm conclusions from this modelling exercise, but noted that the more complex models involving two or more spatial components did fit the historical and modern CPUE and abundance data better than single homogeneous stock models.

The Workshop provided a series of recommendations for future work that are detailed in its report (SC/58/Rep3, item 10). It was agreed that all documents submitted to the respective Scientific Committees pertaining to the

assessment of fin whales in the North Atlantic and the reports of the respective Committees, would be exchanged in the future. The first joint meeting between the NAMMCO and IWC Scientific Committees was considered successful, efficient and productive, and it was hoped that this level of cooperation on issues of common importance could be continued.

In the sub-committee's discussion of the joint Workshop report, Aguilar noted that most evidence suggested that Mediterranean fin whales were a separate population with little or no exchange with other North Atlantic groups. Records from past whaling operations as well as more recent studies indicate that fin whale densities in the Strait of Gibraltar area were low historically and are so now. Nevertheless evidence from satellite tagging and stable isotope ratios (Guinet *et al.*, 2005) indicates that some exchange between the Mediterranean and the Atlantic through the Strait does occur.

3.2.2 Report of the intersessional Working Group

Víkingsson reported on the work of the Intersessional Working Group on North Atlantic Fin Whales. The Working Group met briefly in St Kitts, but Víkingsson reported mainly on a meeting held in connection with the Joint NAMMCO/IWC Scientific Workshop (see Item 3.2.1). The conclusions of the Intersessional Working Group are included where relevant under Item 3.2.3 below.

3.2.3 Progress on completion of the pre-implementation assessment

3.2.3.1 PLAUSIBLE STOCK STRUCTURE HYPOTHESES

The sub-committee noted that plausible stock hypotheses need only to be specified in broad detail at this stage, that they should be consistent with the data and inclusive enough that it is deemed unlikely that new data collected during the *Implementation* process will suggest a major new hypothesis. New analyses conducted subsequent to the Joint Workshop are detailed below.

SC/58/PFI6 presented results from the population genetic structure analysis of two datasets that were calibrated and combined by Bérubé and Danfælsdóttir and contain genetic data of six microsatellite loci (genotypes) and one mtDNA locus (control region sequences). The main objective of this study was to assess further the population genetic structure of North Atlantic fin whales at their feeding locations by combining datasets and therefore enlarge the dataset presented in Bérubé *et al.* (1998). The sample sizes were increased for West Greenland, Iceland and Spain and the geographical coverage was extended by adding new locations, such as Norway and the Faroe Islands. The combined datasets consist of a total of 649 samples from eight North Atlantic fin whale feeding locations: Gulf of Maine ($n=31$); Gulf of St. Lawrence ($n=109$); West Greenland ($n=56$); Iceland ($n=129$); Faroe Islands (19); Norway (38); Spain ($n=92$); and the Mediterranean Sea ($n=74$) and in addition as reference samples, samples from the Sea of Cortez ($n=75$), in the Gulf of California and the North Pacific Ocean ($n=13$). The combined samples from the North Atlantic and the Mediterranean Sea as well as the combined samples from the North Atlantic (excluding the Mediterranean Sea for the microsatellite loci), deviated significantly from Hardy-Weinberg genotypic proportions due to heterozygote deficiency. Deviations were also observed among the samples collected in the Gulf of St. Lawrence and off the Faroe Islands but they were not statistically significant after applying the sequential Bonferroni test. The Slatkin linearised F_{ST} homogeneity

tests, based on the microsatellite loci data within and among the North Atlantic and Mediterranean Sea samples, revealed significant between the different sample years of the Faroe Islands samples, but it should be noted that sample sizes were low. The Faroe Islands samples were the most divergent samples from the remaining North Atlantic Ocean sampling localities (estimates of F_{ST} ranged from 0.005 to 0.113 among the North Atlantic localities). One possible explanation may be some level of pod structure in fin whales, but each pod would have to have large geographic ranges to explain the overall low level of genetic structure across the North Atlantic. The Faroe Island samples differ from the samples collected in other areas by being collected more or less at the same position in and in a very short time (over a few hours). In all other areas only one or two samples may have been collected at the same time and place. Future data analyses and sample collection need take this possibility into consideration. Significant heterogeneity was also detected between sampling localities in the North Atlantic and Mediterranean Sea against the Sea of Cortez (estimates of F_{ST} ranged from 0.325 to 0.528). The *BayesAss* estimation (Wilson and Rannala, 2003) that was undertaken as the rate of current dispersal may be of more immediate management concern than the average rate of gene flow over evolutionary time. The probability that an individual was an immigrant indicated that between 17% and 33% of the individuals in each population are immigrants which suggested large amounts of gene flow among all putative populations/stocks. The amount of migration rates between locations suggested that movement of animals between locations were predominantly unidirectional. The point estimates revealed that 20 percent or more of individuals in a single area are immigrants. Such exchange rates are in a range where populations are likely to be demographically correlated, and perhaps should not be viewed as demographically or genetically independent populations. A total of 35 polymorphic sites were detected defining 78 haplotypes of the mtDNA control region sequence data. The estimates of the nucleotide diversity at all North Atlantic sampling localities were all within the same range (0.012-0.014). The nucleotide diversity observed in the Mediterranean Sea and in the North Pacific Ocean samples were significantly lower than any of the observed values at North Atlantic sampling localities. In addition, the nucleotide diversity of 0.001 estimated in the samples from the Sea of Cortez was exceptionally low, and significantly lower than in any other sampling localities. Based on the mtDNA data, significant levels of heterogeneity were detected among some of the North Atlantic samples and also between the Mediterranean Sea and all North Atlantic samples. Significant levels of heterogeneity were detected between Sea of Cortez and all the North Atlantic/Mediterranean Sea sampling localities as well as between North Pacific and all the North Atlantic/Mediterranean Sea sampling localities. However, estimates of genetic divergence among the North Atlantic (and Mediterranean Sea) sampling localities were all very low and [as for nuclear DNA] suggesting high levels of exchange between sampling areas.

SC/58/PFI6 concluded that the genetic analyses based upon nuclear as well as mitochondrial loci all suggested high levels of gene flow among all North Atlantic sampling areas; although both allele and haplotype frequencies were statistically different among the majority of the sampling areas, the actual level of divergence is very low. The estimated migration rates were in a range where populations are likely to be demographically correlated, and perhaps

should not be viewed as demographically or genetically independent populations. The analyses ignored the signal of exponential population expansions detected in the North Atlantic samples by Bérubé *et al.* (1998). Hence, the high degree of genetic similarity among the North Atlantic sampling areas may be due to recent divergence rather than high gene flow. However, the *BayesAss* analyses suggest differently. The number of migrants estimated from the F_{ST} estimates is on the order of 30 migrants per generation. While this rate may initially seem much lower, it should be kept in mind that the estimate is an estimate of the effective number of migrants and hence should be related to the effective population size, which may be lower than the census population size. In addition, the ~30 migrants per generation is between each pair of populations, which results in a much larger number of immigrants once summed for all connected populations.

In discussion the sub-committee noted that the methodology used in the *BayesAss* software is relatively new and has not been tested on a wide range of scenarios, particularly ones where the level of differentiation is as low as that found in North Atlantic fin whales. The estimated levels of immigration may be upwardly biased under this circumstance. Donovan noted that this program is being tested with simulated datasets under the TOSSM project.

All samples came from feeding grounds, not from the breeding grounds, the location of which is uncertain. A degree of mixing of different stocks on the feeding grounds might be expected and is indicated by other genetic analyses. The methodology used in *BayesAss* has not been tested under these circumstances, and it was therefore not clear if dispersal between feeding areas or alternatively the degree of mixing of discrete stocks on the feeding areas was being estimated. Samples from the breeding grounds would be useful in this regard but are not yet available.

SC/58/PFI7 presented results of the genetic analyses of two fin whale datasets that aimed to study further the temporal and micro- and macrogeographical population structure of North Atlantic fin whales sampled at different feeding grounds. At the joint Workshop the interpretation of P -values, when values of F_{ST} were very small, was discussed. The Workshop agreed that this topic required further investigation and discussion and referred the matter to a working group consisting of Skaug, Kitakado and Butterworth, in consultation with Palsbøll, Daniëlsdóttir and Pastene. In particular it noted that it was important when presenting results of F_{ST} values that CI be calculated (e.g. using bootstrapping) for new and previously published data where significant differences have been reported (Árnason *et al.*, 1992; Daniëlsdóttir *et al.*, 2006; 1991; 1992; 2005). The first dataset was on the genetic variation at nine microsatellite loci in 1,022 fin whales sampled at five North Atlantic areas; i.e. West off Iceland ($n=900$), Spain ($n=39$), Norway ($n=54$), West off Greenland ($n=16$) and East off Canada ($n=13$). The data were based on further statistical analysis of data presented in Daniëlsdóttir *et al.* (Daniëlsdóttir *et al.*, 2006; 2005). The new statistical programs applied included CI's of F_{ST} (as suggested at the joint Workshop), number of migrants per generation (N_m) and graphical illustration of potential 'populations' as in Waples and Gaggiotti (2006). There was significant heterogeneity within all samples, except the West Greenland samples, all due to heterozygote deficiency. Various genetic analyses resulted in significant genetic heterogeneity among the Icelandic samples, revealing temporal and seasonal differences in the samples from the years 1981-89. The level of genetic differentiation was low among the 13 samples

($F_{ST} \sim 0.004$, $p < 0.05$). As before, greatest significant differences were observed between the Newfoundland Canadian samples and the other locations. The CIs of the pairwise F_{ST} comparisons varied considerably. When looking at the lower value of the 95% CI of the F_{ST} values, it reduced the number of the significant pairwise comparisons down from 26 to 10 of 78 comparisons made, two were comparisons between Icelandic sample years and eight were involving the Newfoundland Canadian and Icelandic samples. However, if the higher value was considered, all comparisons were significant. According to the graphical illustration of potential 'populations' as in Waples and Gaggiotti (2006) the number of groups should be five. The first consisting of Icelandic sample years (Iceland 1982, 1984-88), Norway, Spain and West Greenland. Then each of IC81, IC83, IC89 and Newfoundland Canada as separate groups. As previously suggested, there might be variations in herds at feeding locations in the different sample years from Iceland, contributing to the heterogeneity within and among years and feeding locations or there could be disproportional mixing of different breeding units at the feeding grounds both in time and space.

The second dataset is on the microsatellite genetic variation in 226 fin whales sampled in five North Atlantic areas; i.e. off West Iceland, Norway, Spain and West Greenland, a total of: 129, 54, 39 and 16 samples, respectively. The analyses are based on genotypes at 16 microsatellite loci. More number of samples is to be screened so only preliminary statistical analysis of this dataset was presented.

The sub-committee noted in discussion that the significant heterogeneity between sampling years seen at Iceland and the Faroes suggested either temporal variation in the summer distribution of stocks and/or that different proportional mixtures of stocks were being sampled on the feeding grounds. Such year to year differences may exist in other areas as well but the temporal resolution of the sampling is not sufficient to detect them. The situation at the Faroes was exceptional in that the samples were collected in single events over a short period of time. Therefore it is possible that single 'herds' of related individuals may have been sampled in each event.

There was some discussion over the issue of the use of simple P values vs bootstrap confidence intervals for pairwise F_{ST} comparisons. Although it was generally agreed that providing confidence intervals for F_{ST} values is to be encouraged, it was pointed out that the P value from a standard test of heterogeneity provides a more direct test of the null hypothesis that all samples have been drawn from the same population.

SC/58/PFI8 presented results of new statistical analyses of three old fin whale allozyme and carbonic anhydrase datasets previously published in Árnason *et al.* (1992) Daniélsdóttir *et al.* (1991; 1992). At the joint NAMMCO/IWC Scientific Workshop the interpretation of P -values, when values of F_{ST} were very small, was discussed. The first dataset is on the genetic variation at 11 variable allozyme loci in 328 fin whales sampled in two North Atlantic areas; i.e. off West Iceland and Spain, a total of: 283 (Iceland 1985-88) and 46 (Spain 1985) samples, respectively. The data is based on further analysis of genotypes at 11 allozyme loci: *Ada*, *Ak-1*, *Gpd*, *Ldh-A*, *Mdh-S*, *Mpi-1*, *Pep-A*, *Pgm-1*, *Pgi* and *Sod-A*. The new statistical programs applied included F_{ST} , CIs of F_{ST} , N_m , PCA, multidimensional scaling (MDS), *STRUCTURE* and graphical illustration of potential 'populations' as in Waples

and Gaggiotti (2006). There was significant heterogeneity within each sample and overall samples, all due to heterozygote deficiency. Various genetic analyses on the dataset resulted in high significant genetic heterogeneity among the Icelandic and Spanish samples, and temporal differences in the Icelandic samples from the years 1981-88 ($F_{ST} \sim 0.078$, $p < 0.0001$) as well as differences between Icelandic and Spanish samples ($F_{ST} \sim 0.094$, $p < 0.0001$). Divergence between Icelandic sample years was less than between Icelandic and Spanish samples. The Spanish samples were overall the most divergent of the samples and with lower N_m than among the Icelandic sample years. The CIs of the pairwise F_{ST} varied considerably and were larger in comparisons of larger F_{ST} (i.e. between Icelandic and Spanish samples than between Icelandic sample years). This could indicate that the observed level genetic divergence between groups is less than concluded before from the previous results of high F_{ST} and significance between groups, however when considering the lower CI values, all comparisons remained significant. Based on Nei's (1978) genetic distances, multidimensional scaling (MDS) analysis revealed genetic divergence with a stress value of 0.0229 between axes 1 and 2. The *STRUCTURE* analysis indicated two groups among the samples. As previously suggested, there might be variations in herds at feeding locations in the different sample years of Iceland, contributing to the heterogeneity within and among years and feeding locations. The genetic heterogeneity within and between temporal Icelandic samples and geographical samples, in addition to the likelihood of number of breeding units estimated in *STRUCTURE*, are both in agreement with the hypothesis that the North Atlantic fin whale is genetically structured on the feeding grounds and different breeding units might mix disproportionally at the feeding grounds both in time and space. The heterogeneity among Icelandic samples years could therefore also be disproportional mixing of two breeding units represented in the different years.

The second dataset (II) is on the genetic variation at five allozyme loci (*Ak-2*, *Est*, *Ldh-A*, *Mdh-S* and *Pgi*) of 67 fin whales from three North Atlantic areas; i.e. Newfoundland Canada ($n=24$), Norway ($n=19$) and off West Iceland ($n=24$). There were statistical significant heterogeneity within the pooled samples and genetic divergences were found among Newfoundland Canadian, Norwegian and Icelandic samples ($F_{ST} \sim 0.343$, $P < 0.0001$). All three F_{ST} pair-wise comparisons varied considerably in their CIs indicating variation in the estimation of significant comparisons from two to all significant comparisons of three made and reducing the earlier level of observed genetic differentiation. The *STRUCTURE* analysis indicated three clusters among the samples. The results from this study based on allozyme loci indicate that the fin whale samples from the feeding grounds off Iceland, Norway, Spain and Newfoundland Canada are significantly heterogenous, but genetic divergence is high between groups. The genetic heterogeneity within and between the samples in addition with the likelihood of number of breeding units estimated in *STRUCTURE* both are in agreement with the hypothesis that the North Atlantic fin whale is genetically structured on the feeding grounds and different breeding units might mix disproportionally at the feeding grounds.

The level of genetic differentiation was higher for the allozyme than the microsatellite data (Bérubé *et al.*, 1998; Daniélsdóttir *et al.*, 2005; 2006; Sigurjónsson and Gunnlaugsson, 2006; SC/58/PFI6). To better estimate the

true unbiased geneflow among the samples, further analyses need to include estimation on effective population size (N_e) to have a better estimate of effective number of migrants per generation (N_m), *BayesAss* to estimate current migration rates and *MIGRATE* to estimate historical migration rates.

The third dataset (III) is on the *Ca* locus genotype variation in 1,159 fin whales sampled in two North Atlantic areas; i.e. off Spain (1983 and 1984) and West Iceland (1971 and 1981-89), a total of 26 and 1,133 samples, respectively. There was heterogeneity in two Icelandic sample years, but no overall significant heterogeneity was observed at this locus within or among samples ($F_{ST} \sim 0.003$, $P > 0.05$). The Spanish 1983 samples showed greatest overall F_{ST} values compared to all other locations and the least number of migrants, N_m .

Skaug presented SC/58/PFI9 which detailed the screening of a dataset consisting of 15 microsatellite loci from 226 fin whales from several North Atlantic locations for closely related individuals. Five pairs of individuals were identified as being closely related, four of which were consistent with a parent-offspring relationship. Two of these parent-offspring pairs had been conjectured to be mother-calf pairs when the biopsies were obtained. Of the two pairs that were not sampled at the same location, one showed a linkage between North Norway and the area west of Svalbard, and the other between North Norway and West Iceland.

The sub-committee agreed that this method shows promise for identifying relatives in genetic samples and can assist in the interpretation of analyses related to stock boundaries and degree of mixing among areas. It was noted that the number of matches of closely related individuals would increase with sample size, and the certainty of detection with the number of microsatellite loci included in the analysis. In response to a query, Skaug noted that it would be possible to determine if the number of related individuals in a sample was greater or less than expected given the assumption of random mixing.

Kitakado presented the results of a preliminary analysis using a new method aimed at simultaneous estimation of mixing proportions and genetic differentiation for stocks for North Atlantic fin whales. The method uses individual genotypes at multiple loci and does not require the presence of baseline stocks. An integrated likelihood function with elimination of nuisance parameters was employed to estimate the parameters, and then the maximum values under one and two stock scenarios were compared to determine the likely number of stocks. To investigate model performance, a simulation study was conducted under the one stock scenario and with two simulated stocks with $F_{ST} = 0.1$. The model successfully discriminated the 1 and 2 stock situations. For analysis for fin whales, the same data were used as in SC/58/PFI7 (226 individual's genotypes at 17 microsatellite loci). The result was consistent with one stock in the area. Kitakado emphasised the preliminary nature of this analysis and that further investigations are required.

In response to a query, Kitakado noted that while the method is similar to *STRUCTURE* in that it estimates the number of genetic stocks present in a sample without reference to sample origin, the estimation methods employed are different. In addition this method provides explicit parameters for mixing proportions of the putative stocks identified.

The F_{ST} used in the simulation study was much higher than that commonly observed between fin whale sampling areas. The ability of the model to detect population structure when the populations are so weakly differentiated has not

been tested. The sub-committee considered this method promising and **recommended** that Kitakado continue simulation testing of the model under levels of differentiation observed in whale populations. In addition the method should be applied to other species and stocks for which stock structure is better known, such as bowhead and gray whales.

Conclusions

The Report of the Joint NAMMCO/IWC Scientific Workshop (SC/58/Rep3) provided a range of stock hypotheses and recommendations for further genetic work to refine or suggest new ones. The sub-committee was gratified to see that much of this work had been accomplished and thanked the authors of SC/58/PFI6-8 and the members of the intersessional Working Group for their hard work in fulfilling these recommendations in the short period since the joint Workshop. Considering the new information brought forward, the sub-committee found no reason to modify any of the existing stock hypotheses, or to suggest new ones.

3.2.3.2 PRELIMINARY INVESTIGATION OF EXPERIMENTAL WAYS TO DISTINGUISH AMONG COMPETING HYPOTHESES

It was noted that recommendations for further analytical work to distinguish among competing stock hypotheses should be provided at this meeting so that the work could be carried out in time for the first intersessional meeting for the *Implementation Assessment*, if it proceeds.

Photo-id work was identified as a potentially useful method, but it was noted that there are only two catalogues available, for the Gulf of Maine and the Mediterranean. Robbins agreed to compile all information on photo-identification for the sub-committee.

The sub-committee agreed that obtaining samples for genetic analysis from the breeding grounds would be very valuable for identifying fin whale stocks, which might then be distinguishable on the feeding grounds. However the location(s) of the breeding grounds are presently unknown. Satellite tags applied late in the season on the feeding ground might be very useful in identifying fin whale breeding areas. In addition such applications could provide information on migration routes and movements between feeding areas. However it was recognised that the rate of success in fin whale tagging, in terms of tag functioning and duration, had been low in previous attempts, and that these issues must be resolved before tagging could proceed on a large scale.

The new analytical methods for genetic data used in SC/58/PFI6 (*BayesAss*), SC/58/PFI7 and SC/58/PFI8 (*STRUCTURE*), and in the report of the intersessional Workshop, were considered promising, but in all cases they should be tested using simulated datasets showing similar levels of genetic variation to that observed in fin whales. It was hoped that this might occur under the TOSSM project but the sub-committee recognised that the results might not be available for the prospective *Implementation Assessment*.

3.2.3.3 DISPERSAL RATES

F_{ST} values and other data provided by genetic studies will need to be used to produce realistic ranges of dispersal rates for input into trials. The sub-committee noted that dispersal rates refer to permanent movement of individuals between breeding stocks and differ from mixing proportions which refer to situations where more than one breeding stock feeds in a particular area; trials need estimates of both these quantities. This work requires careful consideration and

must be completed before the first intersessional Workshop once an *Implementation* has begun. The issue was referred to an intersessional Working Group consisting of Palsbøll, Skaug and Waples.

3.2.3.4 ABUNDANCE ESTIMATES (INCLUDING $g(0)$ ISSUES AND PLANS FOR FUTURE SURVEYS)

Víkingsson confirmed that all survey data will become available in the IWC database as per the data availability guidelines. It was concluded that these were of sufficient temporal and spatial resolution to calculate abundance estimates both on the scale of the sub-areas that would be likely to be used in conditioning simulation trials and for use in the *CLA*.

It had been noted at the Joint Workshop (SC/58/Rep3) that no recent abundance data are available for the American coastline. However Palka informed the intersessional Working Group that there are estimates available for the Gulf of Maine-Bay of Fundy region and that these could be made available to the Scientific Committee.

Abundance estimates from the 1987, 1989, 1995 and 2001 NASS as well as the 1996-2001 Norwegian surveys were reviewed by the Joint Workshop and found to be of sufficient quality for use in simulation trials and in the *CLA*. The issue of $g(0)$ for fin whale ship surveys was also examined by the joint Workshop, which concluded that $g(0)$ was close to 1 and the assumption of $g(0)=1$ would be sufficient for trials.

The sub-committee **concurred** with these conclusions of the Joint Workshop.

Víkingsson informed the sub-committee that a new survey would be carried out in 2007 and that Iceland planned to continue large-scale surveys at 5-6 year intervals. Plans for the Trans North Atlantic Sightings Survey (TNASS, see Item 4.2), which will cover a large part of the northern North Atlantic and includes the participation of Norway, the Faroe Islands, the Russian Federation, Iceland, Greenland and Canada, were provided in SC/58/O21. A synoptic redfish survey will take place in 2007, coordinated by the ICES Study Group on Redfish Stocks, with international participation from several countries including Iceland. The Icelandic vessel will be used as a cetacean survey platform. The sub-committee **endorsed** this collaborative effort and **recommended** that the Commission encourage the relevant governments participating in the international redfish survey to include a cetacean component in the survey.

3.2.3.5 CATCH DATA (INCLUDING ALTERNATIVE SERIES)

Allison confirmed that the catch history for North Atlantic fin whales was sufficiently well known to allow a catch series to be developed for use in trials, and that work on this task was in progress. This compilation will include notations on data quality and available ancillary information. There are sufficient uncertainties in the catch series (allocation of catches between species, catch location, struck and lost) to anticipate the use of alternative catch series, and the compilation of catch data will be used to develop such alternative series.

SC/58/PFI4 presented CPUE series for fin whales during the early modern whaling operation in Iceland (1883-1915) that have been revised from Sigurjónsson and Gunnlaugsson (1988), based on the recommendations drawn up at the joint Workshop. The series are split by the west (Vestfjord) and East coast operation. The FpBM (fin whales per boat month) series for the East coast is based on individual catch records from 1904 to 1913 restricted to the period 14th May to 11th

August. This series might be used only from 1907 when fin whale catches exceeded 50% of the total. Individual catch records are too limited for the Vestfjord operation so total fin whale catch per boat (FpB) has to be used. Fin whale catches exceed 50% continuously from 1902, which is considered a reasonable starting point in this case. The operational range expanded over time and in particular in the last year in 1915 when a large part of the catches were taken on the Greenland side of the Iceland-Greenland midline, which suggests that this year should not be included. Two alternatives in correcting for handling times are given for both series. The season length is generally not known in the Vestfjord operation, but is needed for this correction and is assumed to have been four months based on all information available. An uncorrected catch per boat series (CpB) is also presented and is considered a reasonable index for the Vestfjord operation although not accounting for handling times dampens the trend therein. Operational changes over time and limitations of the data are believed to be more likely to mask the real trend in the population.

The sub-committee thanked the authors for their work in responding to the recommendations of the joint Workshop.

3.2.3.6 FUTURE WHALING OPERATIONS

This RMP *Implementation* is requested by Iceland, and the only likely commercial whaling operation in the near future at least is on the traditional fin whaling grounds off west Iceland. The operational factors in this fishery have been described by Sigurjónsson (1988). Since the ban on whaling was imposed by the Icelandic parliament in 1915, Icelandic whaling for large whales has been limited to a single land station in Hvalfjörður, Faxaflói in West Iceland apart from limited catches from a single whaling station in northwest Iceland during 1935-1939. The whaling station in Hvalfjörður operated during 1948-89 and has been maintained so that future large whaling operations are likely to be restricted to this station. Company regulations restricted the whaling operation in various ways. Thus, the processing capacity of the factory limited the number of whaling vessels, operating at any one time to four and further restrictions on catch rates were imposed temporarily during busy periods (Rørvik *et al.*, 1976). The Hvalfjörður whaling station is the only one in Iceland and there are no plans to build whaling stations in other parts of Iceland. It can therefore be assumed that future whaling will only be conducted from this single land station and that the operating area of the whaling vessels will be restricted to the same area as during the commercial whaling 1948-85. The whaling area off Iceland during 1951-73 is shown in fig. 2 of SC/58/PFI5. Some of the catches were taken west of the present 200 n.miles EEZ for Iceland, but any future catches would likely be within this 200 n.miles limit. The whaling seasons from the whaling station in Hvalfjörður usually began in the latter half of May and ended near the end of September. Since 1968 the whaling season began in the first half of June (Read *et al.*, 2004). Future catches under the RMP would likely be confined to the period June-September.

The sub-committee noted that there are no plans to initiate commercial whaling for fin whales by other nations that caught fin whales in the North Atlantic prior to the onset of the moratorium such as Spain, the Faroes, Norway and Canada. The possibility of a very limited catch (5-10 animals) for scientific purposes off Norway and the Faroes in the medium future cannot be precluded and might thus be included as a sensitivity test (Bjarni Mikkelsen and Lars Walløe, pers. comm.).

3.2.3.7 OTHER ANTHROPOGENIC REMOVALS

SC/58/PFI5 summarised non-natural mortality of fin whales, other than direct catch, as compiled from National Progress Reports covering the period 1997-2004 (www.iwcoffice.org/sci_com/scprogress.htm). During this eight year period a total of 11 fin whales was reported killed from fisheries interactions, four in the North Atlantic and two in the Mediterranean (see table 1 of SC/58/PFI5). In the same period nine fin whales were reported killed or likely killed by ship strikes. Eight of these were in the North Atlantic.

Read *et al.* (2006) used bycatch statistics from the USA to make crude extrapolations to estimate global bycatch of large cetaceans. Of 201 reported bycatches in US waters during 1990-99, six were fin whales.

The sub-committee noted that since systematic monitoring of cetaceans was initiated in Iceland around 1980 there have been no reported bycatches of fin whales off Iceland, in contrast to many other species of cetaceans in this area. Only one stranding of a fin whale is reported for this period, a calf that stranded near a small boat harbour in 1994. The animal had wounds on the head that might have been caused by a ship strike (Marine Research Institute, Reykjavik, unpublished information). This is the only known example for fin whales off Iceland of anthropogenic mortality other than direct catch. Apart from a single bycatch off Ireland and a ship strike in the mid North Atlantic, it is the only example for the whole Northeastern Atlantic (east of West Greenland). Somewhat higher rates in the Western North Atlantic may be due to the apparently more coastal distribution of the species in this region.

Berggren informed the sub-committee that the sub-committee on estimation of bycatch and other human induced mortality had received some new information on ship strikes of fin whales in the Mediterranean (Anonymous, 2005; 1991) and the Strait of Gibraltar (SC/58/BC5) this year, which indicates that this source of mortality may be greater in this area than in others. However he emphasised that rate of reporting may be low in all areas. There is no information to suggest a high rate of lethal bycatch of fin whales in the North Atlantic.

The sub-committee recognised that although the efficiency of reporting schemes is difficult to evaluate with precision, it can be concluded from the available evidence that non-natural mortality of fin whales in the North Atlantic (outside the Mediterranean) is insignificant compared to abundance. The sub-committee concluded that there is no need to model incidental catches in the *ISTs*.

3.2.3.8 CONDITIONING (INCLUDING BIOLOGICAL PARAMETERS)

SC/58/PFI3 presented some new investigations of life history parameters based on data from biological samples of fin whales caught off Iceland from 1967-85 and scientific catches from 1986-89, originally presented in Lockyer and Sigurjónsson (2006). The classification of animals with respect to maturity and pregnancy stage when foetuses and/or ovaries were lost or damaged, that then had to be based on other measurements, is validated. Samples were collected only for different parts of the season in the first years and in two years appear selective with respect to size. The scientific catches show some differences from the commercial catches. The proportion pregnant changes over the season and with age, so the imbalance in the samples needs to be considered in estimates of pregnancy rate. The changes in fecundity with age are best demonstrated by comparing females with a different number of ovarian corpora. After the first pregnancy the females are estimated

to rest for 1.64yr. Of these the younger animals appear to rest for longer which indicates that early maturity may come at some cost. The resting period decreases to 1.37yr after 10-15 ovulations but then increases again to 1.74yr in animals after 21 or more ovulations, indicating reproductive senescence (also reported by Konráðsson *et al.*, 1991). In addition, no foetuses were found in the oldest animals that appeared to be pregnant from inspection of the ovaries. Fewer of the younger females caught were in the later stages of pregnancy, which implies that they need a longer time feeding to build up the energy required for pregnancy and lactation. The earlier findings of changes in the age at maturity based on the proportion mature and proportion of first ovulators, are confirmed and are in line with estimates based on transition phase readings in the ear plugs (IWC, 2005). Estimates of mortality are derived based on an assumption of constant cohort size. The estimate of natural mortality is 0-0.07. It is suggested that a high proportion of maturing animals in the most recent catches and changes in the age distribution of the catch can best be explained by an influx of immature animals.

The sub-committee thanked the authors for this compilation and noted that it will be of use in the *Implementation* process. It was agreed that the available biological data, including estimates of relevant biological parameters, was sufficient for *ISTs*.

3.2.4 Work plan

The sub-committee concluded that the only outstanding item to be completed before proceeding towards an *Implementation* was the development of a list of catches with associated ancillary information that would allow the development of a best and alternative catch series for use in simulation trials. Considerable progress towards this had been made at the joint Workshop and it was anticipated that this could be completed in time to begin an *Implementation* this year. However, it was considered impractical to begin the *Implementation* this year because of a lack of resources and the high workload of the Committee, which must complete the NP Bryde's whale *Implementation* as a priority. Therefore the sub-committee proposed that the *Implementation* for North Atlantic fin whales be initiated in 2007. It was emphasised that this delay in initiation of the *Implementation* was due to the priorities and workload of the Scientific Committee rather than a lack of sufficient preparation on the part of the initiating Member Government, Iceland.

In the interim period the sub-committee **recommended** the following priorities for further research:

- (1) completion of a comprehensive list of catches as noted above;
- (2) refinement and extension of genetic and other analyses to discriminate between existing stock hypotheses and to estimate mixing proportions and dispersal rates.

4. CONSIDERATION OF SURVEYS UNDER THE GUIDELINES AND REQUIREMENTS

4.1 Norwegian surveys

Walløe presented results from SC/58/RMP4, which was a report of a Norwegian 2005 survey for minke whales in *Small Management Area* CM around Jan Mayen. As part of a six-year programme over the period 2002-07 with the aim to get a new estimate of minke whale abundance in the Northeast Atlantic, the area around Jan Mayen in the Greenland Sea, the *Small Management Area* CM, was surveyed with two vessels during the summer 2005. There