

**Report of the Second Intersessional
Workshop to Prepare for the 2007
Bowhead Whale *Implementation Review***

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1. INTRODUCTORY ITEMS

The meeting was held from 12-17 January 2007 at the National Marine Mammal Laboratory (NMML), Seattle. The list of participants is given as Annex A.

1.1 Convenor's opening remarks

Donovan (Convenor) welcomed the participants to the Workshop. At the IWC meeting in Ulsan, a timetable of work to enable the *Implementation Review* for bowhead whales to be completed at the 2007 Annual Meeting was developed. The primary area of work to be considered at the *Review* related to the possibility that there was more than one stock of bowhead whales. The primary focus of the present Workshop was to build upon the work of the first Workshop (IWC, 2007) and the subsequent discussions at the 2006 Annual Meeting to finalise the development of stock structure hypotheses and the modelling framework.

1.2 Election of Chair

Donovan was elected Chair.

1.3 Appointment of rapporteurs

Taylor, Palsbøll, Punt and Donovan acted as rapporteurs.

1.4 Adoption of Agenda

The Agenda adopted is given as Annex B.

1.5 Documents available

The documents available (SC/J01/AWMP1-8) are given as Annex C. A summary of the available data is given as Annex D.

2. STOCK STRUCTURE HYPOTHESES

Palsbøll *et al.* (2006) advocated abandoning the current focus of rejecting panmixia as means of defining management units (MUs) as originally proposed by Moritz (1994), but instead use a population genetic estimate of dispersal among putative MUs and the uncertainty of the dispersal estimate(s) as means of determining if putative MUs should be divided or combined. Such an approach will require an understanding of how movement of individuals among putative MUs relates to genetic divergence, and determining (in each individual case) what the threshold level of exchange should be. The inclusion of the uncertainty of the estimate of dispersal among putative MUs permits a specific case to be labelled as resolved or not, and an assessment of how much more data are required in case of an unresolved case.

The Workshop supported the central points of Palsbøll *et al.* (2006): that *p*-values from hypothesis tests concerning panmixia had limitations in delineating stock structure and that estimates of dispersal were what was needed. The Workshop also recognised that there was no 'golden' level of genetic differentiation that defined a management unit *inter alia* because such units are defined for particular management objectives. It was noted that the magnitude of desired dispersal for the bowhead whale case remained undefined. Palsbøll *et al.* (2006) also cautioned about the assumption that populations are in equilibrium common to many analytical methods. Bowhead whales are known to be out of equilibrium, and this must be taken into account in any interpretation of results from such methods. The Workshop **agreed** that Palsbøll *et al.* (2006) was of broader relevance than simply to the present Workshop and **agreed** that it should be discussed by the Working Group on Stock Definition at the forthcoming Annual Meeting.

2.1 Short summary of the nine hypotheses agreed at the 2006 intersessional Workshop

The nine stock hypotheses from the 2006 intersessional meeting (figs 2-6 in IWC, 2007) were:

- (1) Baseline single stock;
- (2) Single stock with social structuring;
- (3) Single stock with 'Generational Gene Shift';
- (4) Single stock with feeding ground site fidelity;
- (5) Two-stocks – Chukchi Circuit-mixed;
- (6) Two-stocks – Chukchi Circuit-segregated;
- (7) Two-stocks – temporal segregation;
- (8) Two-stock – spatial segregation – St. Lawrence mixed; and
- (9) Two-stock – spatial segregation – St. Lawrence segregated;

Ignoring current dispersal for the 2-stock hypotheses, where dispersal is emigration, is a worst case scenario with respect to population dynamics as it allows no possibility for the rescue of a depleted small stock through immigration. The Workshop **agreed** to proceed assuming no recent dispersal between stocks.

2.2 Review of new and existing genetic information

2.2.1 Summary of new data available

SC/J07/AWMP2 summarises the new data submitted for microsatellite loci. A total of 349 individuals were available for both the old 11 loci and the new 24 loci. In addition, 65 individuals from the Sea of Okhotsk stock and 50 individuals from Igloodik, Canada (Baffin Bay stock) were available for the new loci only. Huebinger noted that an oversight was made in not submitting data for 50 samples from Igloodik, Canada. Permission was given by the data owner (Postma) and the data were provided to the

¹ Presented to the meeting as SC/59/Rep3.

Workshop. The full set of data available for the *Implementation Review* are listed on the IWC website (http://www.iwcoffice.org/sci_com/data_availability.htm).

The Workshop **agreed** that data sharing agreements should be put in place, along with definitions of reference data sets. A working group was established to develop a reference data set of individuals to be used for nuclear (microsatellite loci) and mtDNA from the total updated database. Analyses which employ other data than those contained in the reference data sets can then simply note any difference in the data set used.

Taylor noted that all new mtDNA sequences and Single Nucleotide Polymorphisms (SNP) data generated at Southwest Fisheries Science Center (SWFSC) were submitted according to the Data Availability Agreement (DAA).

2.2.2 Results of new analyses

MICROSATELLITE DATA

SC/J07/AWMP2 analysed 33 microsatellite loci for bowhead whales, including 22 new highly reliable markers. This research provides evidence that the conventional model that Bering-Chukchi-Beaufort (B-C-B) Seas bowhead whales have always been a single panmictic stock must be reconsidered. Although these bowhead whales are clearly genetically distinct from bowhead whales in the Sea of Okhotsk and Canada, SC/J07/AWMP2 also found patterns of genetic heterogeneity among the B-C-B Seas samples. These samples exhibit strong and widespread departure from Hardy-Weinberg equilibrium, including significant evidence of a historical bottleneck consistent with gene drift after commercial exploitation or thousands of years earlier. SC/J07/AWMP2 also detected significant evidence that whales of detectably different ancestry intermingle during some spatio-temporal portions of the annual migration but partially segregate in other portions. The most notable such pattern is seen in migratory pulses passing Barrow in the autumn, detected in part using a model assuming admixture. Estimates of F_{ST} associated with these findings of genetic structure in B-C-B Seas bowhead whales are extremely small compared to values for comparisons with the known separate stocks in the Sea of Okhotsk and Canada, and are also smaller than values obtained by separating suspected familial lineages within the B-C-B Seas samples. Therefore, SC/J07/AWMP2 concluded that B-C-B Seas bowhead whales may comprise a complex spatio-temporal aggregation of animals with mixed and variable ancestry with an unknown degree of non-random mating, whose degree of genetic heterogeneity is significantly lower than what was observed between spatially isolated stocks.

The Workshop noted that different criteria were used to eliminate samples with missing data for microsatellite loci for Canada and Okhotsk strata; for the B-C-B group both new and old markers were available (33) while only the new markers were available for the non-B-C-B samples (22). The rule of eliminating samples if data were missing for more than three markers could not, therefore, be equitably applied to all strata. The Workshop discussed the criteria that had been employed in discarding loci and **agreed** that general and clear guidelines for quality control and locus selection would be advantageous. The Workshop **agreed** to define reference sample sets to form the basis of analyses for SC/59. These reference sets would enable different groups of researchers to conduct directly comparable analyses. No restrictions were imposed on alternate analyses using different samples. All sets remove fetuses with mothers present. Three sets were **agreed**:

- (1) mtDNA with duplicate samples from St. Lawrence Island (SLI) bone/baleen removed;
- (2) microsatellite set for B-C-B samples (which have been run for 33 loci) omitting samples with four or greater missing loci;
- (3) microsatellite set for B-C-B, Okhotsk and Canada (which have been run for 22 loci) omitting samples with three or greater missing loci. The latter omits two Okhotsk samples (18981, 18986) and one Canada sample (BMIG-01).

The Workshop **agreed** to a reference microsatellite set in which three microsatellite loci was discarded. Locus TV18 was omitted because of short allele dominance (Jorde *et al.*, 2007). The other loci (BMY38 and BMY44) were omitted due to large heterozygote deficiencies suggestive of null alleles and also for possible stuttering in the former case. No consensus was reached regarding other loci despite lengthy consideration of TV7, the only remaining locus that originally was isolated from bottlenose dolphin. It was **agreed** that ideally analyses should be conducted using and excluding locus TV7.

The Workshop noted that there were several ways to screen for problematic markers and samples in addition to the use of software packages such as *MICRO-CHECKER* (van Oosterhout *et al.*, 2004) as was done in this case. These include laboratory checking for traits known to correlate with errors (stutter bands), comparisons of mother/calf/foetus pairs, and replication experiments. Huebinger (2006) noted that loci with extensive stutter had been discarded during the initial screening of suitable loci. In addition, all loci included in the analyses had been analysed in all available mother and foetus sample pairs ($n=8$). Replicate analyses of 10% (~30 samples) were undertaken for all the original 11 loci. The Workshop **agreed** that general data quality check guidelines would be desirable, but it was unclear which SC subcommittee (e.g. Stock ID or DNA) was the appropriate forum to develop such guidelines.

Suggestions to augment the positive finding for population bottleneck were to explore different settings for the two-step model, methods that permit determination of the timing of the putative bottleneck, as well as using different methods that estimated the bottleneck date including the Garza and Williamson (2001) method.

The Workshop considered the *STRUCTURE* results in SC/J07/AWMP2 and SC/J07/AWMP3, noting previous discussions in the Committee about general problems in the interpretation of the results from *STRUCTURE* (Falush *et al.*, 2003; Pritchard *et al.*, 2000). The Workshop **agreed** that these results suggested strong evidence for at least three stocks (i.e. one B-C-B stock) and weaker evidence for genetic differentiation within the B-C-B group. There was also general agreement that the posterior probabilities estimated by *STRUCTURE* were problematic. The Workshop **agreed** that understanding the level of differentiation implied by the results would be important and that results from TOSSM simulations would aid in the interpretation of the *STRUCTURE* results. It was suggested to assess if the putative components within B-C-B were in Hardy Weinberg equilibrium. LeDuc and Taylor (2004) suggested that in some analyses, *STRUCTURE* assigns individuals to one cluster that is in Hardy-Weinberg equilibrium, with the last cluster containing all those individuals that led to Hardy-Weinberg disequilibrium and accordingly this last cluster was found to be strongly out of equilibrium. Givens reported this to be the case in the B-C-

B samples, where one *STRUCTURE* cluster deviated significantly from the expected Hardy-Weinberg genotype frequencies equilibrium and the other not. It was noted that Hardy-Weinberg disequilibrium among the whales sampled during the middle of the autumn was consistent with some type of population or demographic structure. It was noted that this finding was found with a *STRUCTURE* model assuming no admixture, but not with a model assuming admixture. Others suggested using the degree of relatedness within various strata to test if strata differed in the degree of relatedness and it was noted that such calculations were planned.

Pastene suggested that from his experience with minke whales, there was value in comparing morphological traits between groupings suggested by genetic analyses even if estimates of F_{ST} were low. It was observed that the confidence intervals of the observed F_{ST} estimates included zero, which was inconsistent with inferring a marked Hardy-Weinberg disequilibrium. It was suggested that Fisher's exact test be employed with the new 22 loci only. Givens produced a table of heterozygote deficiency p -values split by new and old loci together with the number of individuals for which that locus was missing. The pattern noted above regarding F_{ST} was apparent throughout in both new and old markers and requires further explanation. The number of individuals with missing data was much higher for the old markers than the 22 new markers, with 80% of missing values attributed to the third of the loci that were the old markers. These and other additional results developed at the meeting are given as Annex D.

The Workshop discussed interpretation of the F_{ST} values and whether simple analytical models could be used to determine whether the lower values obtained for within B-C-B comparisons were consistent with dispersal rates low enough to warrant concern for AWMP purposes. The Workshop **agreed** that given the violation of assumptions of such simple models (populations of equal size in mutation-drift equilibrium) that such calculations were inadvisable.

SC/J07/AWMP3 conducted genetic analyses based on microsatellite samples of the B-C-B bowhead whales. A total of 35 currently available loci (11 old and 24 new) were analysed using *STRUCTURE* (Falush *et al.*, 2003; Pritchard *et al.*, 2000). Analyses were conducted under four possible combinations of assumptions; non-admixture or admixture, and independent or correlated allele frequencies among stocks. In general, the values of the marginal likelihood strongly suggested the possibility of multiple stocks in the B-C-B stock. Temporal stock structure at Barrow was also investigated based on results of assignment probabilities under the two-stock hypothesis of non-admixture with independent allele frequencies. The results suggested the possibility of temporal segregation between two different stocks at Barrow; in spring, a portion of the individuals of 'Stock 1' reach Barrow first, followed by individuals of 'Stock 2' in autumn, females of 'Stock 2' seem to reach Barrow first, followed by a migratory peak of 'Stock 1'. Furthermore, the results indicated that the hypothesis of mixing of two stocks cannot be discarded.

The Workshop noted that the temporal structure in SC/J07/AWMP3 was not supported by any p -values. The results in SC/J07/AWMP3 assuming non-admixture with independent allele frequencies did not show the pulsing pattern off Barrow during the autumn that was found in SC/J07/AWMP2, suggesting that the *STRUCTURE* results were sensitive to model choice. Furthermore, no significant evidence of spring pulsing at Barrow was found. Two technical differences between SC/J07/AWMP2 and

SC/J07/AWMP3 were noted: (1) SC/J07/AWMP3 used all the microsatellite loci whereas SC/J07/AWMP2 discarded two loci; and (2) SC/J07/AWMP2 included two distantly related groups (Canada and the Okhotsk), whereas SC/J07/AWMP3 was based on only the B-C-B and Okhotsk samples. It was noted that the authors of the *STRUCTURE* program suggested omitting distantly related groups if the stock structure question involved low levels of genetic heterogeneity. The Workshop **agreed** that conducting the analyses with and without more distantly related groups would be interesting to assess the magnitude of differentiation among groups and to provide a more detailed examination of potential subdivision within the B-C-B whales. It was also noted that no evidence had been provided about whether the magnitude of differentiation in SC/J07/AWMP3 was large enough to interpret the *STRUCTURE* clusters as separate stocks.

In this regard, the Workshop recognised the general difficulty facing the Committee in interpreting the results of genetic analyses in a management context. There is no absolute rule that can be applied with respect to measures of differentiation and determining whether one or more management stocks are present. This important issue is being addressed by the Testing of Spatial Structure Models (TOSSM) project but it will be some time before practical advice will become available

SC/J07/AWMP7 analysed a subset of the microsatellite loci data for Barrow. Loci Tv7, Tv18, Bmy38 and Bmy44 were excluded, as well as individuals with four or more unscored loci among the remaining 32 loci. The remaining 245 individuals were analysed with respect to genetic variability, heterozygote deficiency, and pair-wise genetic differences. Heterozygote deficiency (F_{IS}) is found to correlate negatively with genetic variation (H_S). This might reflect technical problems with the genotyping. It might also be due to a Wahlund effect since this effect is less likely to be visible in more variable loci which evolve at high rates. The data was partitioned into a new and an old (previously considered) sample and into 22 new and 10 old loci. Analyses of genetic differences within pairs of individuals were performed to test for potential temporal structure in whales during the migration. There is no significant 'bump' in the new 22 loci, nor is any 'bump' significant in the 10 old loci among the new individuals. There is however a significant effect of days apart when controlling for estimated age difference. This significant effect is found in several partitions of the data, but its interpretation is unclear.

The Workshop **agreed** the reasons for the correlation between heterozygote deficiency and gene diversity should be examined further. Concerns were raised about the analysis dependent on age because estimating age from length is known to yield very poor age estimates for whales past physical maturity, which occurs at about the age of 50. It was suggested that alternate methods for estimating the age of sampled individuals, such as the work done by Morita and George (2007) [SC/59/AWMP1], be used. The Workshop **agreed** that having age data available as soon as possible would facilitate analyses. It was unclear why days apart only produced a significant 'Oslo bump' signal after controlling for whale ages, but age itself had no significant effect.

In this regard, the Workshop noted that a number of issues related to the ageing of bowhead whales (and also samples sizes of aged animals) had implications for its work. It looked forward to the results of a review paper that was being prepared for the 2007 annual meeting.

mtDNA

SC/J07/AWMP4 presented the results of a mtDNA control region sequencing analysis of the B-C-B bowhead whales based on samples collected in different villages engaged in aboriginal whaling. The total number of sequences available was 380. 68.2% of those come from a single locality (Point Barrow). An additional 24 sequences from the Okhotsk Sea bowhead whale stock and four from the Commander Island were used in the analysis for comparative purposes. As previously reported, the nucleotide diversity was smaller in whales from the Okhotsk Sea stock than in whales from the different localities of the B-C-B stock. The quantification of the temporal and geographical mtDNA differentiation was carried out using the F_{ST} and the chi-square statistics. First temporal (seasonal) differentiation was examined in those localities with larger sample sizes (SLI and Point Barrow). Geographical mtDNA differentiation among four localities (Point Barrow, SLI, Chukotka and Okhotsk Sea), was also examined. No significant levels of heterogeneity were observed for mtDNA among the B-C-B stock whales, except across seasons at St. Lawrence Island. In contrast to a previous mtDNA analysis, no significant levels of heterogeneity were observed in spring and autumn Barrow samples. Significant levels of genetic heterogeneity were detected between the B-C-B stock partitions and whales from the Okhotsk Sea stock. In general, these mtDNA results provide no strong evidence for genetic population structure within the B-C-B stock. Sample sizes for several localities and months, however, remain low and consequently the failure to detect a significant level of heterogeneity in some comparisons could be due to the low statistical power of the analysis. Furthermore samples from Chukotka and SLI obtained in summer months, which are essential to investigate some of the multiple stock hypotheses, are not available because they are difficult to collect since there is no whaling at this time of year. At Barrow, nuclear DNA markers have suggested structure. Thus it is possible that the mtDNA analysis could not identify structure if two stocks mix in similar proportions during the spring and autumn.

It was noted that the linkage between skulls on St. Lawrence Island and actual whales killed over the past 30 years was done by estimating body length of whales from length of the skulls, which is an imprecise approach. The Workshop **agreed** that caution was needed regarding any results that rely on these linkages as was the case for the seasonal comparison made by SC/J07/AWMP4. The generally small sample size from this area was noted. Mention was made that the SNP genotype data generated by SWFSC could be used to identify duplicate individuals among the SLI dataset and that the data were available under the DAA and had been used in to omit a few duplicates in the analysis of SLI strata presented in SC/J07/AWMP8.

SIMULATION STUDIES

SC/J07/AWMP8 summarised a study based on comparisons of mtDNA sequences. The analysis was a repetition of earlier work apart from the age cohort comparison. No level of heterogeneity differences that was statistically significant was detected in any of the temporal or spatial comparisons. The samples used in the analyses were tabulated in SC/J07/AWMP8 and are available electronically.

SC/J07/AWMP5 described the methods that Martien and colleagues plan to use in their genetic modelling of bowhead stock structure hypotheses. The basic model is an

individual-based model implemented in the R package *Rmetasim* (Strand, 2002) and is based on the model presented in Ripley *et al.* (2006). SC/J07/AWMP5 describes the modifications to the Ripley *et al.* model that have been made to realistically simulate historic whaling and two-stocks. Non-linear density dependence is implemented in the same manner as for the TOSSM project (Martien, 2006). The genetic initialisation of the bowhead model has also been modified to mirror the initialisation being used in TOSSM; the coalescent program *SIMCOAL* is used to generate simulated allele and haplotype frequencies with which each *Rmetasim* landscape is initialised. The model has also been modified to allow the simulation of two stocks.

The biggest difference between the model presented in Ripley *et al.* (2006) and that described in SC/J07/AWMP5 is the way in which whaling is modelled. Ripley *et al.* used a highly simplified approach in which the population was instantaneously reduced to $N=300$ or $N=1872$ in the year 1912. In the new model, populations are subjected an annual removal of whales designed to mimic the historical kill from the commercial harvest and Russian and Alaskan subsistence catches from 1848 to 2006. In each year, catches are allocated to stocks based on the catch allocation matrices for the particular stock structure scenario being simulated. For whales from which genetic data are available, an individual from the simulation is chosen that matches the actual sampled individual as closely as possible in terms of age and gender. Thus, the output of the each simulation is a simulated dataset which closely matches the empirical dataset in terms of the age and sex of the samples at each geographic location. These simulated datasets can then be analysed in the same manner that the empirical dataset has been analysed and the results of the analyses can be compared in order to assess the degree to which the stock structure hypotheses are consistent with the empirical genetic data.

Martien noted that it will not be possible to simulate all of the stock structure hypotheses in time for them to be used in the assessment and that the genetic simulations differ from the population dynamic simulations in that their aim was to sufficiently reproduce the genetic signal, which would be most greatly influenced by initial population size, the lowest level of abundance and its duration. The Workshop **agreed** that future analyses should include a figure showing abundance trajectories, but that fitting to recent abundance estimates was not as important as keeping the minimum abundance within the range estimated to have occurred. The Workshop **agreed** that conducting both one and two-stock modelling in the remaining six week period was not feasible and **advised** that efforts should focus on single-stock modelling for the Anchorage meeting.

SC/J07/AWMP6 presented the results of a preliminary study in which the Chukchi Circuit Hypothesis is simulated as in SC/A06/AWMP6 by drawing gene pools for the two putative populations from a Dirichlet distribution and by assigning sampled whales randomly to population by probabilities depending on date of sampling. In SC/J07/AWMP6 these probabilities are estimated roughly from dates of sampling aligned to have equal mid range in each year. A rather extreme genetic distance is required, or the temporal segregation must be substantially sharper than observed in aligned dates of sampling to obtain a simple 'bumpy' temporal pattern in pairwise genetic distances as pronounced as in Jorde *et al.* (2007).

2.3 Review of existing and new non-genetic information on stock structure

2.3.1 Stable isotopes

The nine baleen plates from SLI had cycles in fixed carbon ratios similar to animals taken off Barrow. George noted that a paper would be presented at SC/59 responding to the criticism that these cycles could reflect feeding/fasting cycles rather than feeding that alternated between the Bering and Beaufort (Knoche *et al.*, 2007) [SC/59/BRG13].

2.3.2 Photographic studies

No new analyses were presented. However, a paper will be presented using the data on photo-identification submitted to the DAA that examines links between individuals identified in Bering Strait to other locations.

2.3.3 Telemetry

George described the movement of two tagged individuals. One individual tagged off Barrow in May, spent most of the summer in the Beaufort Sea, moved relatively rapidly to the northern shores of Banks Island, and soon after then moved rapidly west across the Beaufort Sea to feed off northern Chukotka. The second individual was tagged in the autumn at Barrow and was later detected in Chukotka near the first individual.

2.3.4 Historic data

Botkin showed maps of historical catch and effort data presented in Bockstoce *et al.* (2005). The Workshop greatly appreciated the presentation and the ability to see the In Press version of this excellent and detailed paper.

It was noted that the area and date of capture are available for only about 20% of the total pelagic catch, and that these data are assumed to be representative of the remaining catch. In addition, because of the method of operation of the pelagic whalers, it can be assumed that if no whales were taken in an area in which they operated, then few or no whales were there to be taken.

It was noted that presentation of points representing effort on the figures that present the data both by five-year periods and by calendar periods would be very helpful. There was considerable discussion of the decrease in large whales, as indicated by barrels of oil, with time. It was proposed that although the whalers may not have selected for size, the overall harvest could be size selective due to greater availability of larger animals. Large females are among the last to migrate towards the Beaufort Sea if the historical migration behaviour was similar to the current observed migration behaviour. Similarly, smaller individuals migrate into heavy pack ice earlier, making them less available to commercial whalers particularly in the early years prior to the use of steam ships. It was noted that such selectivity may have implications for genetic modelling and that it was not included in the simulations of SC/J07/AWMP5, where 'harvested' individuals were picked at random from the simulated population to represent the historic catches.

Botkin provided data from the 393 individuals with known oil yields including as available biological data (sex, length), harvest date, latitude and longitude for use in further analyses.

2.4 Finalisation of hypotheses to be considered at the Implementation Review and consideration of plausibility

The final set of stock structure hypotheses for which the Bowhead *Implementation Review* will aim to capture broad biological hypotheses that are consistent with the major sources of information, and differ in ways that might affect

the implications of different levels of aboriginal subsistence need. These hypotheses are considered sufficient for the purposes of evaluating whether the Grand Unified Procedure (GUP) is robust to uncertainty regarding stock structure. The Workshop noted that there was insufficient time to discuss the relative plausibility of the final hypotheses; this will have to take place at the next Annual Meeting when the genetic analyses based on the final reference sets (and perhaps other data sets) are available.

The Workshop reviewed the nine hypotheses identified during the first intersessional Workshop (Item 2.1) in light of the new information and analyses (Items 2.2 and 2.3) and **agreed to:**

- (1) combine single stock hypotheses 1-3 to form hypothesis A, noting that there are several plausible reasons for the observed Hardy-Weinberg disequilibria;
- (2) retain hypothesis 4 as hypothesis B, but remove the group of whales that was postulated to migrate from the 'greater' Barrow Canyon area north of Barrow and then follow the Chukchi ice front during summer and feed near the 'Chukchi borderlands' between the Herald and Barrow Canyons (Group 2) from the hypothesis. This group was removed because the lack of sightings and acoustic calls from the area north and east of Barrow in June and July is suggestive of there not being a feeding area in this region. Hypothesis B is supported by the presence of whales in the vicinity of the Chukotka Peninsula in summer. There is no direct evidence for or against site-fidelity at present, owing to lack of data, but the possibility that the whales found at Chukotka are not a separate 'group' cannot be eliminated as implausible;
- (3) replace hypotheses 5 and 6 by a new hypothesis (D) that better explains the information on mixing of putative stocks at Barrow during the spring and autumn migrations. Hypotheses 5 and 6 were constructed to mimic the 'Oslo Bump', but preliminary attempts to replicate an 'Oslo bump' using simulations have been unsuccessful unless the stocks differ greatly genetically (e.g. SC/J07/AWMP6) while these hypotheses are also inconsistent with the results from *STRUCTURE* which suggest that two stocks are found at Barrow in roughly even proportions in spring – it was recognised that further work would be undertaken by the authors of Heide-Jorgensen *et al.* (2007);
- (4) drop hypothesis 7. This hypothesis was dropped because it requires that whales from the Stock 2 do not pass Barrow at the same time as those from Stock 1 during the spring migration but do so during the autumn migration. This is inconsistent with there being no difference in allele numbers and frequencies between the samples collected during spring and autumn;
- (5) drop hypothesis 9. This hypothesis involves whales from Stock 2 not being available to the hunters at SLI. The conservation risk of hypothesis 9 will necessarily be less than for hypothesis 8 (the new hypothesis C);
- (6) introduce a new hypothesis (D). This hypothesis is designed to be consistent with:
 - (a) Hardy-Weinberg disequilibria in both the spring and autumn samples;
 - (b) a possible pulsing structure during the autumn migration at Barrow that could produce the temporal pattern in the genetics of the population that is seen in the data considered by Jorde *et al.* (2007), and also found in analyses in SC/J07/AWMP2 using *STRUCTURE* and the method of Givens and Ozaksoy (2006);

- (c) evidence from the *STRUCTURE* runs of no 'pulses', but the potential presence of two stocks, during the spring migration (SC/J07/AWMP2, SC/J07/AWMP3); and
- (d) traditional knowledge regarding whale migration patterns near SLI.

The following are the final set of stock structure hypotheses. The Workshop **recommended** that the trials for the bowhead *Implementation Review* be based on these hypotheses. The distribution and migration timing of any putative stocks is likely to have changed over time. The descriptions below (see also Fig. 1) refer to distribution patterns and migration routes for the recent period. The relative exposure matrices (see Item 4.2.2) will define how changes over time in distribution and migration are modelled.

Hypothesis A. Single stock – no feeding ground site fidelity. There is one breeding area in the western and central northern Bering Sea, one primary summer feeding area in the Canadian and eastern Alaskan Beaufort Sea, and one primary spring migration route northeast along the Alaskan coast from April to early June and east across the Beaufort Sea. The western autumn migration in September through November bifurcates after passing Barrow, with some whales moving southwest and others west towards the Chukotka coast. The migration is completed when bowhead whales move south along the Chukotka coast through the Bering Strait and into the northern Bering Sea. A single population might deviate from the expectations under panmixia, for instance due to: social or demographic structure; assortative mating; or the effects of a recent bottleneck in a long-lived species.

Hypothesis B. Single stock with feeding ground site fidelity. There is one breeding stock but two summer feeding areas (the eastern Beaufort Sea and the western Russian Chukchi Sea), and fidelity to feeding areas and migratory routes. Most whales migrate as for hypothesis A. The other group of whales migrates north through the Bering Strait in late May-June and summers along the Chukotka coast and further north, with at least a few whales remaining in the northern Gulf of Anadyr throughout the summer. The whales from this group return to the Gulf of Anadyr in the autumn and mix with the first group during the breeding season. Whales from both groups are available to the hunters at St. Lawrence Island in autumn while only whales from the first group are available to these hunters in spring. Whales from both groups are available to hunters at Chukotka in autumn.

Hypothesis C. Two stocks – spatial segregation-St. Lawrence mixed. Identical to hypothesis B, except that each group constitutes a separate breeding stock.

Hypothesis D. Two stocks – mixed migration. There are two breeding areas: one in the western (the W stock) and the other in the central northern Bering Sea (the E stock). In spring, before moving through the Bering Strait, the W whales migrate closer to Gambell (indeed some W whales may winter in the vicinity of St. Lawrence and the south part of Chukotka) whereas the E whale movements see them preferentially available to harvests from SW Cape by hunters from Savoonga (Fig. 2). Once through the Bering Strait, it is primarily W whales that may be found in the vicinity of Chukotka. All the E and most of the W whales then move northeast along the Alaskan coast from April to early June and into feeding areas in the Canadian and eastern Alaskan Beaufort Sea, with the E whales moving further to the east. Both W and E whales are equally

susceptible to harvest from Barrow and other coastal locations during this period, consistent with equal population abundances for a two population hypothesis suggested by the *STRUCTURE* analyses (SC/J07/AWMP2, SC/J07/AWMP3), the absence of an 'Oslo bump', and *STRUCTURE* results showing spring Barrow mixing for whales taken in spring (SC/J07/AWMP2).

The temporal distributions of the western autumn migration in September through November differ somewhat for W and E whales, leading to the 'pulsing' behaviour evident in the genetics data, and for W whales to be more exposed to hunting at Barrow in the autumn than E whales due to their slightly longer availability in the harvesting area during the hunting period. Although equal harvest susceptibility for the two stocks in the autumn Barrow hunt should perhaps be considered the more biologically plausible, the Workshop **agreed** to assume that W whales are more susceptible than E whales to explore a more extreme case, particularly since the case of equal susceptibility might produce aggregate results similar to those for a single-stock scenario.

All whales move to Chukotka and follow the canonical southward migration after passing Barrow. The migration is completed when whales move back through the Bering Strait and into the northern Bering Sea, with W and E whales being equally susceptible to harvest from Gambell, but with a slightly greater propensity for W whales to be harvested at Savoonga because the harvest from Savoonga during autumn is from the village and not the SW Cape (Fig. 2). Inferences about equal or differential susceptibility of W and E whales to harvests from Gambell and Savoonga at different times are informed by the results from some of the *STRUCTURE* analyses (Falush *et al.*, 2003; Pritchard *et al.*, 2000) as well as by traditional knowledge of the areas in the Bering Sea from which whales come or to which they are headed and the possibility that W stock animals may include summer residents near Barrow and winter residents near Chukotka/St. Lawrence Island.

3. ABUNDANCE ESTIMATES AND TRENDS

The abundance estimates obtained by Zeh and Punt (2005) for Barrow will be used by the GUP and when conditioning the operating model (see Item 4.3). The estimate of abundance for Cape Pe'ek (Melnikov and Zeh, 2007) during 2000-2001 will be used as one of the abundance estimates used when conditioning the operating model for stock hypotheses B and C (see Item 4.3). However, this estimate is not used by the GUP when calculating *Strike Limits*; only the estimates of abundance based on counts at Barrow in spring are used when applying the GUP.

4. MODELLING FRAMEWORK FOR THE 2007 IMPLEMENTATION REVIEW

4.1 Use of AWMP-lite

4.1.1 Progress on work agreed at the 2006 Annual Meeting

AWMP-lite is a package that can be used to implement two-stock hypotheses for the B-C-B bowhead whales. The population dynamics are modelled using an age-aggregated model with the carrying capacity for each putative stock estimated by maximising a likelihood function that involves contributions from the abundance data. In contrast, the single-stock common control program (CCP) used during the selection of the Strike Limit Algorithm, *SLA*, for B-C-B bowhead whales is age- and sex-structured. Unlike the CCP,

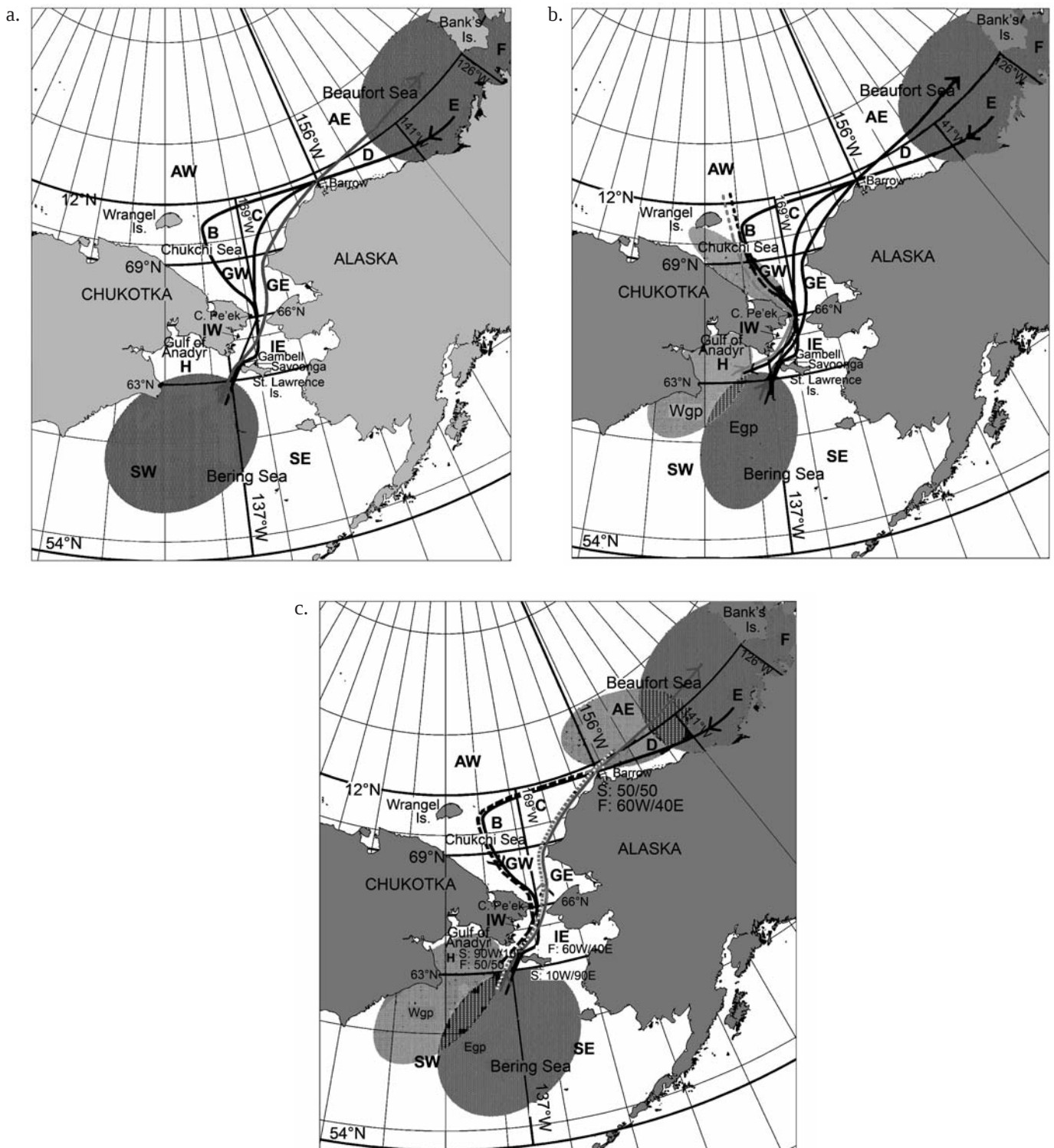


Fig. 1. The stock structure hypothesis.

- a. Hypothesis A.
b. Hypothesis B and C.
c. Hypothesis D.

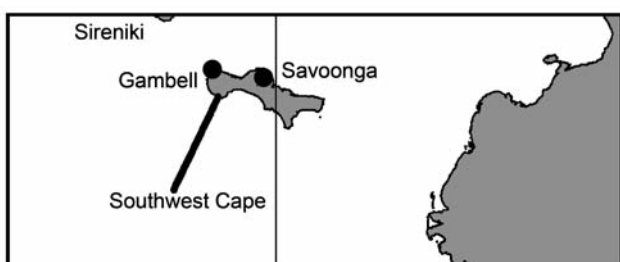


Fig. 2. Map of St. Lawrence Island.

AWMP-lite does not account for uncertainty in the values for the parameters of the operating model. At its 2006 Annual Meeting, the Scientific Committee agreed that AWMP-lite could be used for an initial screening of trials with catch=need.

SC/J07/AWMP1 provides the specifications for an extension to the version of AWMP-lite presented to the 2006 Annual Meeting that is able to use the GUP to specify *Strike Limits*. The data available for the GUP are catches and estimates of abundance. The estimates of abundance are

generated by AWMP-lite using the same algorithm as in the common control program (IWC, 2003). SC/J07/AWMP1 presents the results for two single-stock trials implemented using the CCP and AWMP-lite, and concludes that these results are sufficiently similar that AWMP-lite should be adequate to form the basis for an evaluation of GUP for multi-stock scenarios.

4.1.2 Use of AWMP-Lite for the 2007 Implementation Review

The Workshop **agreed** that AWMP-lite could be used to evaluate the implications of using the GUP to set Strike Limits for the B-C-B whales and **recommended** that Allison validate the latest version of AWMP-lite. The current version of AWMP-lite does not include all of the features needed to implement the *Evaluation Trials* for the B-C-B bowhead whales. The Workshop therefore **recommended** that Allison modify AWMP-lite to implement the trials (see Items 4.3 and 4.4). It also **recommended** that Allison and Punt provide comparison figures for each of the single-stock trials (see Table 1), contrasting the outcomes from AWMP-lite and the CCP, to the next workshop.

The Workshop noted that AWMP-lite does not capture the same amount of variability as the CCP because it does not place priors on the carrying capacity and the biological parameters of the population dynamics model. It **recommended** that the performance of the GUP should be evaluated for the multi-stock trials by comparing this performance with that of the GUP for the 'equivalent' (e.g. same specifications for Maximum Sustainable Yield Rate (*MSYR*) and how the abundance data are generated) single-stock trials. Comparison of the results for catch=0 and catch=need may also prove useful in this regard.

4.2 Catch data and mixing matrices

4.2.1 Progress on work agreed at the 2006 Annual Meeting

A catch matrix specifies the proportion of the annual catch during a given season [spring-summer (March-August) and autumn-winter (September-February)] that is taken from each area considered in the operating model. Table 2 lists the catch mixing matrices for the 13 areas selected during the 2006 Annual Meeting for the two seasons. Separate catch matrices are presented for five blocks of years rather than annually because the spatial split of the historical catch would not have changed much over each of these periods. The full details of how these matrices were constructed will be reviewed and a final decision taken at the forthcoming Workshop in March 2007.

4.2.2 Matrices to be used for the 2007 Implementation Review

There was not sufficient time during the Workshop to set up the relative exposure mixing matrices. For each stock hypothesis (see Item 2.4), the relative exposure matrices define the proportions of each stock in each area and time period that are subject to catching. The first stage of the task is to produce matrices showing the presence or absence of each stock in each area according to the hypothesis and how this may change over time. The entries in the relative exposure matrices will then be constructed taking into account the magnitude and timing of the catch and effort in the area, together with knowledge of the current distribution of stock(s). The task will be completed by an intersessional group comprising Donovan, Allison and George. They will circulate their proposal for comment.

Table 1

The *Evaluation Trials* for the B-C-B Seas stock of bowhead whales. The survey frequency is 10 years unless indicated otherwise; all trials are based on a deterministic model; no age data are generated; differences from the base-case are shown in bold. The footnotes provide the rationale for eliminating some of the trials when conducting multi-stock trials.

Trial no.	Description	Note	<i>MSYR</i> ₁₊	<i>MSYL</i> ₁₊	Final need	Historical survey bias	Future survey bias	Survey CV (true, est)	Other
BE01	Base case		2.5%	0.6	134	1	1	0.25, 0.25	
BE02	Constant need		2.5%	0.6	67	1	1	0.25, 0.25	
BE03	Future +ve bias	3	2.5%	0.6	134	+	1→1.5 in yr 25	0.25, 0.25	
BE04	Future -ve bias	2	2.5%	0.6	134	+	1→.67 in yr 25	0.25, 0.25	
BE04a	Future -ve bias	1, 2	2.5%	0.6	134	+	1→.67 in yr 25	0.25, 0.25	5yr surveys
BE05	Underestimated CVs	4	2.5%	0.6	134	+	+	0.25, 0.10	
BE07	<i>MSYL</i> ₁₊ = 0.8	5	2.5%	0.8	134	+	+	0.25, 0.25	
BE08	5-yr surveys	1	2.5%	0.6	134	+	+	0.25, 0.25	5yr surveys
BE09	<i>MSYR</i> ₁₊ = 1%		1%	0.6	134	0.67 → 1	1	0.25, 0.25	
BE09	<i>MSYR</i> ₁₊ = 1%	1	1%	0.6	134	0.67 → 1	+	0.25, 0.25	5yr surveys
BE10	<i>MSYR</i> ₁₊ = 4%		4%	0.8	134	1	1	0.25, 0.25	
BE10a	<i>MSYR</i> ₁₊ = 4%	1	4%	0.8	134	+	+	0.25, 0.25	5yr surveys
BE11	Bad data		2.5%	0.6	134	1	1→1.5 in yr 25	0.25, 0.10	
BE12	Difficult 1%		1%	0.6	134	1 → 1.5	1.5	0.25, 0.10	
BE12a	Difficult 1%	1	1%	0.6	134	1→1.5	1.5	0.25, 0.10	5yr surveys
BE13	Difficult 1%; constant need		1%	0.6	67	1 → 1.5	1.5	0.25, 0.10	
BE14	Need increases to 201		2.5%	0.6	201	1	1	0.25, 0.25	
BE16	<i>MSYR</i> ₁₊ = 1%; 201 need		1%	0.6	201	0.67 → 1	1	0.25, 0.25	
BE20	<i>MSYR</i> ₁₊ = 4%; 201 need		4%	0.8	201	1	1	0.25, 0.25	
BE21	Integrated	6	U[1.4%]	U[.4-.8]	134	+	+	0.25, 0.25	
BE22	20yr time lag (see i below)	7	2.5%	0.6	134	+	+	0.25, 0.25	20yr lag
BE23	Strategic surveys; (see ii)	7	2.5%	0.6	201	+	+	0.25, 0.25	Strategic surveys
BE24	Inertia Model (see iii below)	7	0.6% *	0.6	134	+	+	0.25, 0.25	Inertia model

1 = Surveys at more frequent intervals than every 10th years are unlikely. 2 = Negatively biased estimates of abundance lead to less risk. 3 = The impact of over-estimated CVs will be explored adequately in trial BE03. 4 = The impact of under-estimated CVs will be explored adequately in trials BE11, BE12 and BE13. 5 = The impact of different *MSYL*s is explored in trials BE10 and BE20. 6 = The integrated trial is dropped because the operating model is deterministic; the impact of an integrated trial can be examined by combining the results for trials BE01, BE09 and BE10. 7 = The impact of this factor was found to be minor for single-stock *Evaluation Trials*.

Table 2
The catch mixing matrices for the 13 selected areas for the two seasons.

Year and season	AW	AE	B	C	D	EF	GW	GE	H	IW	IE	SW	SE	Total
1848-68														
Sp-Su (Mar.-Aug.)	8	0	689	1,057	12	0	2,553	368	1,699	927	479	2,000	22	9,814
Fa-Wi (Sep.-Feb.)	4	0	770	599	0	0	496	87	10	35	0	6	10	2,017
1869-88														
Sp-Su (Mar.-Aug.)	26	0	147	856	73	0	176	145	199	120	112	292	0	2,146
Fa-Wi (Sep.-Feb.)	155	0	890	1,362	138	2	43	19	0	40	0	0	0	2,649
1889-1919														
Sp-Su (Mar.-Aug.)	6	0	0	552	62	997	22	311	37	25	245	49	10	2,316
Fa-Wi (Sep.-Feb.)	151	0	415	219	22	414	11	0	0	37	0	0	0	1,269
1920-89														
Sp-Su (Mar.-Aug.)	0	0	0	937	0	0	0	431	0	0	167	0	0	1,535
Fa-Wi (Sep.-Feb.)	0	0	0	108	61	1	20	0	0	64	0	0	0	254
1990-2005														
Sp-Su (Mar.-Aug.)	0	0	0	302	2	0	0	87	0	0	78	0	0	469
Fa-Wi (Sep.-Feb.)	0	0	0	193	95	2	3	0	0	9	22	0	0	324

4.3 Parameter values and conditioning

The Workshop confirmed its agreement during the first intersessional Meeting that there is no evidence to suggest that in two stock hypotheses, the two stocks have different biological parameters. As a result, all of the trials in which there are two stocks are based on the assumption that *MSYR* and Maximum Sustainable Yield Level (*MSYL*) are the same for both stocks. The Workshop **agreed** not to include permanent movement of individuals among stocks in the trials in which there are two stocks, noting that this will make the trials more difficult because if there is inter-change among two putative stocks, the effect of differential depletion of one of the stocks will be reduced through the effects of permanent movement from the other stock.

The values for the entries in relative exposure matrices will be set as outlined in Item 4.2.2. These values may need to be modified slightly if it proves to be impossible to achieve conditioning.

The 'free' parameters of the operating model are the carrying capacities of each stock. The values for these parameters for each trial are selected based on fitting to the following data:

- (1) the time-series of abundance estimates for Barrow (Zeh and Punt, 2005) [Stock hypotheses A, B, C and D];
- (2) the estimate of abundance for Pe'ek in 2002 [Stock hypotheses B and C];
- (3) the split of the two stocks in spring at Barrow in 2000 [50:50] (area C). This constraint reflects the observation from the *STRUCTURE* runs of no 'pulses', but the potential presence of two stocks of roughly equal size, during the spring migration (SC/J07/AWMP2) [Stock hypothesis D].

The diagnostic statistics that will be used to evaluate the extent to which it is possible to condition the trials are:

- (1) the rate of increase of the bowhead whales predicted to pass Barrow in spring;
- (2) the time-trajectories of abundance by stock with the time-series of abundance estimates superimposed;
- (3) the lowest size of the smallest stock;
- (4) the size of the total population when the commercial fishery collapsed (1914).

Additional diagnostic and plausibility statistics will be developed intersessionally and implemented in the version of AWMP-lite to be presented at the next intersessional workshop.

4.4 Trial structure

Trials are only conducted for stock hypotheses A, C and D because stock hypothesis B is implemented by assuming that each group is a single stock, which will lead to the highest risk. The trials for each stock structure hypothesis (Table 2) are based on the *Evaluation Trials* developed for the Bowhead whale *Implementation* (IWC, 2003). The trials focus on the impacts of three factors: (1) *MSYR*, (2) final need, and (3) data quality (survey bias and the difference between the true and estimated CVs). For the trials in which there is a historical survey bias, the bias will mimic the assumption on which the Bowhead *Evaluation Trials* are based, i.e. the bias starts in 1978 and ends in 2002. Trials for stock hypothesis C will be conducted using three estimates of abundance for Pe'ek for 2002 to be advised by Zeh (and finalised by the intersessional Steering Group) to capture the uncertainty associated with this estimate.

Each trial will consist of 100 simulations of a 100-year projection period. Trials will be run for catch=0, catch=need and catch=GUP.

The performance statistics which will be used to evaluate the performance of the GUP are listed below (N_t^i is number of animals of stock i at the start of year t , K^i is the carrying capacity of stock i , and $\tilde{N}_t^i$ is number of animals of stock i at the start of year t in the absence of exploitation from 2003 onwards. For the multi-stock trials, all risk- and recovery-related performance statistics are reported by stock. The statistic identification numbers are set to that for those Bowhead trials. Statistics marked in bold face are considered the more important.

Risk

- D1.** Final depletion: N_T^i / K^i
D2. Lowest depletion: $\min(N_t^i / K^i) : t = 0, 1, \dots, T$
D6. Plots for simulations 1 and 2 of $\{N_t^i : t = 0, 1, \dots, T\}$
D7. Plots of $\{N_{t[x]}^i : t = 0, 1, \dots, T\}$ where $N_{t[x]}^i$ is the x^{th} percentile of the distribution of N_t^i . Results are presented for $x = 5$ and $x = 50$
D8. Rescaled final population: $N_T^i / \tilde{N}_T^i$
D9. Minimum population level $\min(N_t^i) : t = 0, 1, \dots, T$
D10. Relative increase N_T^i / N_0^i

Need

- N1.** Total need satisfaction: $\sum_{t=0}^{T-1} C_t / \sum_{t=0}^{T-1} Q_t$ where C_t is the catch limit and Q_t the level of need in year t

- N2. Length of shortautumn = (negative of the greatest number of consecutive years in which $C_t < Q_t$)/ T
- N4. Fraction of years in which $C_t = Q_t$
- N5. Proportion of block need satisfaction: where $\Gamma/(T - h + 1)$ where Γ is the number of blocks of h years in which the total catch equals the total need; h is 5 for these trials
- N7. Plot of $\{V_{t[x]} : t = 0, 1, T-1\}$ where $V_{t[x]}$ is the x^{th} percentile of the distribution of $V_t = C_t / Q_t$
- N8. Plots of V_t for simulations 1 and 2.

N9. Average need satisfaction: $\frac{1}{T} \sum_{t=0}^{T-1} \frac{C_t}{Q_t}$

N10. AAV (Average Annual Variation):

$$\sum_{i=-1}^{T-2} |C_{i+1} - C_i| / \sum_{i=-1}^{T-2} C_i$$

N11. Anti-curvature: $\frac{1}{T-1} \sum_{i=0}^{T-2} \left| \frac{C_i - M_i}{\max(10, M_i)} \right|$ where

$$M_i = (C_{i+1} + C_{i-1}) / 2$$

N12. Mean downstep (or modified AAV):

$$\sum_{i=-1}^{T-2} |\min(C_{i+1} - C_i, 0)| / \sum_{i=-1}^{T-2} C_i$$

Recovery

- R1. Relative recovery: $N_{t_r}^i / \tilde{N}_{t_r}^i$ where $\tilde{t}_r^i$ is the first year in which $\tilde{N}_{t_r}^i$ passes through *MSYL*. If $\tilde{N}_{t_r}^i$ never reaches *MSYL*, the statistic is $N_{t_r}^i / \tilde{N}_{t_r}^i$. If $P_o^i > \text{MSYL}$ the statistic is $\min(1, N_{t_r}^i / \text{MSYL})$.
- R3. Time frequency in recovered state = (the number of years for which $N_t^i > 0.9 \text{ MSYL}$, given that $t \geq t_r^i$)/ $(T - t_r^i + 1)$ where t_r^i is the first year in which the population i reaches *MSYL* (or T otherwise).
- R4. Relative time to recovery:

$$RTR^i = \begin{cases} 1 & \text{if } N_0^i \geq \text{MSYL} \\ (T - t_r^i) / T & \text{if } N_0^i < \text{MSYL} \text{ and } N_{t_r}^i \geq \text{MSYL} \\ \min(t | \tilde{N}_t^i \geq N_{t_r}^i) / T & \text{if } N_0^i < \text{MSYL} \text{ and } N_{t_r}^i < \text{MSYL} \end{cases}$$

5. WORK PLAN

5.1 Need for and draft agenda for a March intersessional Workshop and/or pre-meeting meeting

It was **agreed** that there is a need for both a third intersessional Workshop and a pre-meeting meeting. The primary purpose of the third intersessional Workshop will be to progress the modelling work and in particular to review the results of conditioning.

5.2 Tasks and timetable of work (including validation of software)

The Workshop **agreed** that high priority should be given to completing the matrices discussed under Item 4.2. An intersessional group was assigned this task comprising Donovan, Allison and George. They will circulate their proposal for comment. This work is of high priority.

The Workshop also **agreed** to the following modifications to AWMP-lite:

- (1) allow for historical time-trajectories of survey bias;
- (2) Finalise the abundance estimates used by the GUP;
- (3) Implement conditioning for two-stock hypotheses;
- (4) Code the performance measures.

In terms of genetic analyses, the Workshop **agreed** that unless there are exceptional circumstances, the stock structure hypotheses given under Item 2.4 would be used in the *Implementation Review*. Thus, the focus of any further genetic analyses should be to assist in assessing the plausibility of the hypotheses. This information will be valuable to the AWMP Standing Working Group (SWG) in its review of the modelling results. The Workshop also **agreed** that after the Annual Meeting, it will be valuable to develop guidelines for the use of genetic data in *Implementations* and *Implementation Reviews*, based *inter alia* on the valuable experience gained during this review.

5.3 Logistics of the process at the Annual Meeting (allocation of work to the AWMP and bowhead, right and gray whales (BRG) sub-committees)

It was **agreed** that a similar process to last year would be undertaken i.e. there will be a joint meeting of the AWMP and BRG sub-committees (under the auspices of the BRG sub-committee). The primary discussions of any new stock structure analyses will occur in that session (or sessions) and the implications will be taken into account by the AWMP SWG in its review of the results of the model runs and plausibility.

6. ADOPTION OF REPORT

The Chair thanked NMML and in particular, Jeff Breiwick, for hosting the Workshop in an efficient and friendly manner and Dan Botkin and John Bockstoe for their cooperation with respect to historical catches. He also thanked Punt and Allison for their work on AWMP-lite and the rapporteurs. The participants thanked the Chair for his usual excellent job.

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Annex A

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Japan

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Secretariat

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Annex B

Agenda

1. Introductory items
 - 1.1 Convenor's opening remarks
 - 1.2 Election of Chair
 - 1.3 Appointment of rapporteurs
 - 1.4 Adoption of Agenda
 - 1.5 Documents available
2. Stock structure hypotheses
 - 2.1 Short summary of the nine hypotheses agreed at the 2006 intersessional Workshop
 - 2.2 Review of new and existing genetic information
 - 2.2.1 Summary of new data available
 - 2.2.2 Results of new data available
 - 2.2.2.1 Microsatellite
 - 2.2.2.2 mtDNA
 - 2.2.3 Results of new analyses
 - 2.3 Review of existing and new non-genetic information on stock structure
 - 2.3.1 Stable isotopes
 - 2.3.2 Photographic studies
 - 2.3.3 Telemetry
 - 2.3.4 Historic data
 - 2.4 Finalisation of hypotheses to be considered at the *Implementation Review* and consideration of plausibility
3. Abundance estimates and trends
4. Modelling framework for the 2007 *Implementation Review*
 - 4.1 Use of AWMP-lite
 - 4.1.1 Progress on work agreed at the 2006 Annual Meeting
 - 4.1.2 Use of AWMP-lite for the 2007 *Implementation Review*
 - 4.2 Catch data and mixing matrices
 - 4.2.1 Progress on work agreed at the 2006 Annual Meeting
 - 4.2.2 Matrices to be used for the 2007 *Implementation Review*
 - 4.3 Parameter values and conditioning
 - 4.4 Trial structure
5. Work plan
 - 5.1 Need for and draft agenda for a March intersessional Workshop and/or pre-meeting meeting
 - 5.2 Tasks and timetable of work (including validation of software)
 - 5.3 Logistics of the process at the Annual Meeting (allocation of work to the AWMP and bowhead, right and gray whales (BRG) sub-committees)
6. Adoption of report

Annex C

List of Documents

- SC/J07/AWMP
1. PUNT, A.E. AWMP-LITE (Version 5.0).
 2. GIVENS, G., HUEBINGER, R.M., BICKHAM, J.W. AND GEORGE, J.C. Patterns of genetic differentiation in bowhead whales (*Balaena mysticetus*) from the western Arctic.
 3. KITAKADO, T., GOTO, M., KANDA, N. AND PASTENE, L.A. Stock structure analyses for B-C-B stock bowhead whales using microsatellite DNA data.
 4. PASTENE, L.A., GOTO, M., NAOHISA, K. AND KITAKADO, T. Further mitochondrial DNA analyses on stock structure in the B-C-B stock of bowhead whale.
 5. MARTIN, K., ARCHER, E. AND TAYLOR, B. Genesis of simulated genetic data and sampling to emulate empirical bowhead whale samples.
 6. SCHWEDER, T. AND YANGKANG, W. On the Chukchi Circuit Hypothesis.
 7. JORDE, P.E. AND SCHWEDER, T. Brief analysis of stock structure for BCB bowhead whales using microsatellite DNA data.
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Annex D

Some Requested Additional Results

Geof Givens and Ryan Huebinger

1. Heterozygote deficiency p-values split by new/old loci plus 'missingness' by locus

Table 1

Locus	p-value	F_{IS}	Missing
bmy1	.3391	-.000	1
bmy2	.2364	+.023	1
bmy7	.6985	-.050	0
bmy8	.3081	+.025	1
bmy10	.2026	+.016	2
bmy11	.6969	-.005	3
bmy12	.2191	-.024	0
bmy14	.0137	+.052	0
bmy16	.7904	-.017	0
bmy18	.0412	+.034	1
bmy19	.6099	+.001	3
bmy26	.3820	+.006	5
bmy33	.5629	+.012	0
bmy36	.5999	-.004	0
bmy41	.0092	+.006	0
bmy42	.0376	+.080	0
bmy49	.4016	-.000	0
bmy53	.3418	-.005	0
bmy54	.0012	+.068	0
bmy55	.0883	+.029	0
bmy57	.0000	+.019	3
bmy48	.6040	-.006	5

Overall $p \leq 0.000021$ @ $F_{IS} = +.0101$; Overall w/o bmy57 $p = 0.0014$

ev1	.3806	-.031	11
ev104	.2814	+.016	8
gata28	.2952	+.018	4
tv7	.0010	+.096	7
tv11	.0832	+.110	7
tv13	.4298	-.024	3
tv14	.0261	+.051	1
tv16	.5794	-.011	0
tv17	.2323	+.021	21
tv19	.0043	+.058	24
tv20	.5226	+.002	8

Overall @ $p = 0.00044$ @ $F_{IS} = +.0275$

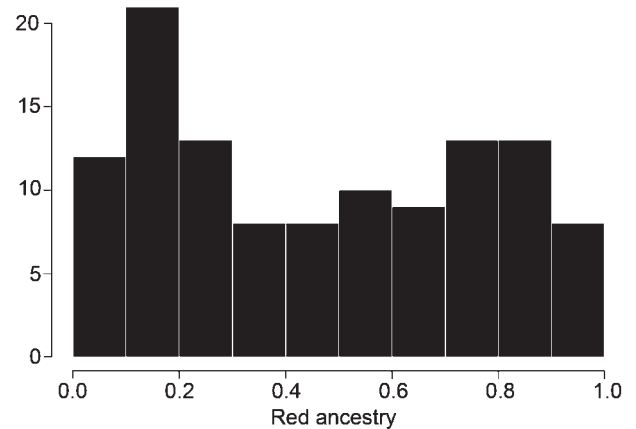
2. Heterozygote deficiency split by red/yellow

Red: $p = 0.000029$ (6/22 new loci) @ or $p = 0.000018$ (9/33 all loci)

Yellow: $p = 0.24$ (1/22 new loci) or $p = 0.0070$ (4/33 all loci)

Since the Red/Yellow ancestry clusters were estimated using only the new loci, the new loci results are the most relevant here.

3. Histogram of red/yellow ancestries



4. The red/yellow F_{st} estimate for the corrected dataset

In the original paper pertained to the uncorrected dataset. For the corrected dataset, the estimate is $F_{st} = 0.006$ (0.003, 0.008) and the same caveat about substantial positive bias applies.

5. Bottleneck results for several different model parameterisations

Table 2

	50S 10V	50S 50V	70S 30V (orig)	90S 50V	90S 10V
Spring	0.01043	0.00025	0.00574	0.19402	0.62488
Autumn	0.01506	0.00005	0.01794	0.23139	0.90651

P -values tabled.

