

Research proposal associated with variant 2 for North Atlantic fin whales under RMP *Implementation Simulation Trials* stock structure hypothesis IV.

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ABSTRACT

This paper presents a proposal for a research programme on fin whales associated with RMP variant 2 under the IST stock structure Hypothesis IV. The suggested programme follows the PRO_FORMA agreed by the SC in 2007 and incorporates research techniques suggested by the SC in this respect, i.e. genetic tagging, identification of close relatives and satellite tracking. A power analysis of the required sample size is included.

STOCK STRUCTURE, CPUE, GENETIC TAGGING, BIOPSY SAMPLING, SATELLITE TAGGING

Background

In 2003, Iceland proposed that the SC started the process of a RMP implementation for North Atlantic fin whales (Vikingsson et al. 2003). Subsequently a pre-implementation was conducted during 2005-2006 (International Whaling Commission, 2006, 2007) according to a general scheme agreed by the SC in 2002 (International Whaling Commission, 2003). As a part of the pre-implementation assessment, a joint NAMMCO/IWC scientific workshop on the catch history, stock structure and abundance of North Atlantic fin whales was held in 2006 (International Whaling Commission, 2006; IWC and NAMMCO, 2006). The RMP implementation process was then formally initiated in 2007 following the 2-year time table agreed by the SC in 2004 (IWC 2005).

During the pre-implementation and the 1st intersessional workshop detailed discussions focused on the stock structure of fin whales in the North Atlantic. These resulted in seven stock structure hypotheses carried forward into the assessment process in the spirit of being inclusive.

At the 1st Annual Meeting the SC agreed unanimously that five of these (I, II, III, V, VI) should be assigned 'high' plausibility and hypothesis VII 'medium' plausibility (International Whaling Commission, 2009a, Hypothesis IV was accepted in spite of objections at the 2008 annual meeting (International Whaling Commission, 2009b, Gunnlaugsson et al 2010). These included specific points regarding lack of fit to certain features in the available data and certain data that were not included in the IST model. These points are addressed in SC/64/RMP3 and the trend in time detected in the Discovery Markings, which contradicts the hypothesis. More generally the assumption that set this hypothesis apart from other hypotheses is the lack of response in foraging behaviour to changes in density. The history of the stock indicates that it recovered quickly in depleted areas. There are no references or data to support the permanently fixed proportional site fidelity in whale foraging behaviour. If the C2 breeding component did get exterminated then hypothesis IV predicts that 5% of breeding stocks C1 and C3 would continue to visit the area, but there would be no density response within the area such that it would ever come close to the original density. Such behaviour would have grave consequences for the species in case of anticipated environmental changes. We have called for a biological realization of how this hypothesis is supposed to function has been called for without a response. That, in it self should have disqualified the hypothesis.

The SC has thus already chosen to ignore observations that contradict this hypothesis. In addition the SC has rejected that the decline in catch per boat in the early modern whaling period should be fitted in the IST model. If this CPUE trend were accepted a 1% MSYR (of mature stock) would be rejected. It is worth recalling that historical CPUE series were the sole basis for most of the conservation actions recommended by the SC in the past. The SC however did not consider contemporary updates of CPUE series to be reliable enough as a basis for the setting of quotas. Although we consider that presently available data should be sufficient to refute assignment of "high plausibility" to stock structure hypothesis IV, we will still consider here the possibilities of more rigid testing of the hypothesis with further research. Not considered here is meta research that would reduce the plausibility of the 1% MSYR case in general. Problems with sustainability only occur in case of assumed 1% MSYR (of the mature stock), a value for which there has been no agreement and is not consistently used in other work of the SC.

At the 2nd intersessional workshop the following six management variants were considered (SC/61/Rep3) (see Fig. 1):

- V1 Sub-area WI is a Small Area;
- V2 Sub-area (WI+EG) is a Small Area. The entire Catch Limit is taken in the WI sub-area;
- V3 Sub-area (WI+EG+EI/F) is a Small Area. All of the catch is taken in the WI sub-area;
- V4 Sub-area WI is a Small Area. Catch limits will be set based on survey estimates for the WI sub-area north of 60°N (both historic and future surveys). Note: trial NF15 is not applicable for this variant. The same proportions are used in setting future abundance estimates as for trial NF15 (see item F). The catch series is unchanged as all historic catches in the WI sub-area were taken north of 60°N;
- V5 Sub-areas WI and EG are taken to be Small Areas and sub-area WI+EG is taken to be a Combination area. The catch limits set for the EG Small Area are not taken;
- V6 Sub-areas WI, EI/F and EG are taken to be Small Areas and sub-area WI+EI/F+EG is taken to be a Combination area. The catch limits set for the EG & EI/F Small Areas are not taken.

Based on IST performance, all variants except V2 were classified as ‘acceptable without research’ (IWC 2010). Performance of V2 was ‘acceptable’ in all but one of the 27 ‘high’ weight trials, the exception (NF-10-2) being ranked as ‘borderline’ Three ‘medium’ weight trials were classified as ‘unacceptable’. All the four trials mentioned above are based on stock structure hypothesis IV. Variant 2 was preferred by the government of Iceland as the variant showing the best catch-related performance¹. The Scientific Committee has thus agreed that RMP variant 2 could be accepted if accompanied with a research programme that it considered likely to resolve uncertainties around stock structure, in particular Hypothesis IV (International Whaling Commission, 2010).

The process of designating the variant as ‘acceptable with research’ involves two steps:

- 1) To determine whether performance is acceptable if the variant is replaced by an ‘acceptable’ variant after an initial 10 year period.
- 2) To demonstrate to the SC’s satisfaction that a research programme has a good chance of being able to clarify the situation with respect to stock structure, and in particular to confirm or deny that stock structure hypothesis IV is implausible.

The SC has agreed that the requirements for stage 1 of the process have been met (International Whaling Commission, 2010).

At the last SC meeting (International Whaling Commission, 2011) analyses were presented on the time trend in the Discovery marking data (Gunnlaugsson, 2011a). The SC agreed that while the results were suggestive that hypothesis IV can be rejected, it recommended further analysis in the context of the *Implementation Simulation Trials* to be presented before a decision would be taken on whether research was needed for implementing NA fin whales variant 2 for the RMP on fin whales in the central North Atlantic. Such analysis is provided in SC/64/RMP3. If needed the SC agreed to review a revised research proposal at the 2012 meeting.

As mentioned above the SC has agreed that the requirements for the first stage of the process have been met (IWC 2010). The latter stage of this process is to demonstrate to the SC’s satisfaction that a research programme has a good chance of being able to clarify the situation. This paper is prepared on this request from the SC in line with the PRO-FORMA for research programmes associated with the “variant with research” option, as agreed by the SC in 2007 (IWC 2008, Appendix 5 to Annex D: 115). Introductions to this proposal were presented at earlier meetings (Gunnlaugsson and Víkingsson, 2009; Gunnlaugsson et al., 2010). and requested statistical analyses were provided in 2011 (Elvarsson, 2011). The SC (2011) agreed that the results presented in 2010 (Gunnlaugsson et al. 2010) and 2011 (Elvarsson, 2011) in combination provide an adequate basis to justify sample sizes. No specific revisions to the proposed research as given there were requested by the SC. The research proposed concentrates on evaluating the assumptions of Hypothesis IV with management variant 2. The objective is to show that with proposed research there is a good chance of disproving the hypothesis or show that it should be modified such that performance becomes acceptable. Rejection must be shown to be unlikely if in fact the hypothesis is true.

A requested power analyses of the effect of different hypotheses on the ratio of recoveries from genetic tagging in different small areas is given in a separate paper to this meeting (SC/64/RMP1).

Gunnlaugsson, (2011b, in press) gives formulas for probabilities of relatives alive between samples collected at different times, both from catches and biopsies. Also presented are programs written to calculate parent-offspring (PO) and half-sibling/grand-parentage (HS) LOD score distributions with assumptions of no, PO or HS relatedness (Skaug, 2001), from allele frequencies at a single locus, and the convolution of many loci (available at <http://www.hafro.is/~thg/skaug/fin/>). With these an optimal matching criterion can be approximated to minimize false positive and determine appropriate sample size.

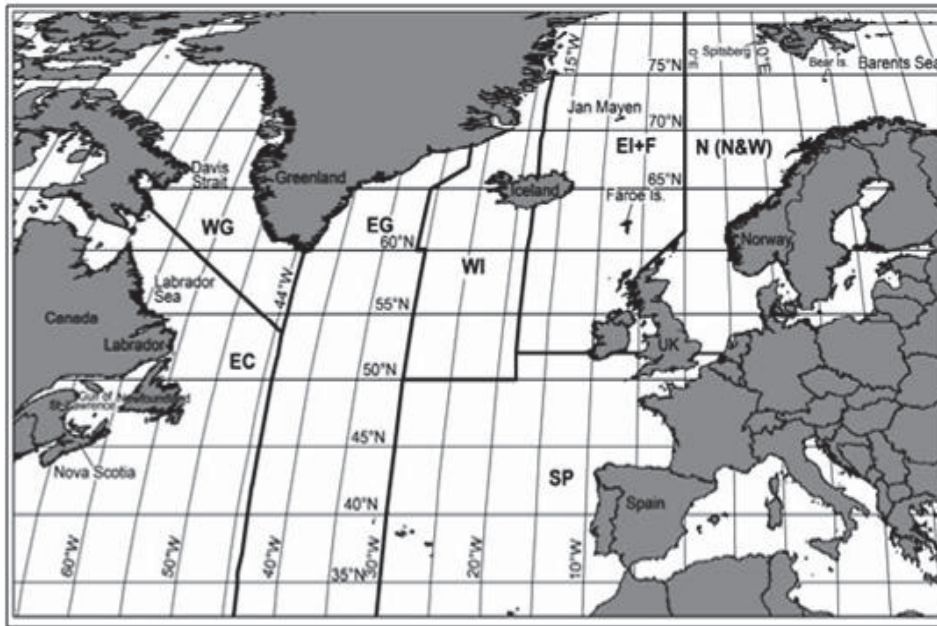


Figure 1. Map of the North Atlantic showing the fin whale *Small Areas*.

Basic features of hypothesis IV.

Hypothesis IV differs from the others hypotheses in that it assumes that there is no interchange between the three sub-stocks in the central North Atlantic at the breeding areas (Figure 2). The hypothesis assumes that 90% the fin whales feeding west of Iceland (WI small area) originate from an isolated breeding sub-stock (C2) while 5% come from each of separate breeding sub-stocks (C1 and C3) that feed mainly on each side of the WI area. Similarly 5% of the C2 breeding sub-stock goes to each side to feed. According to the hypothesis the visiting whales have no memory next year of where they were the year before and do not change their foraging behaviour in response to changes in density of whales and/or prey in any one feeding area, but will go back to their native feeding area 95% of the time next year. With variant 2 the sub-areas WI+EG constitute the Small Area to which the CLA is applied, while all of the catch is taken in the WI sub-area. As variant 2 gives the highest catches (although considerably lower than the average for this entire operation) this is the variant preferred by the government of Iceland.

The breeding area of fin whales in the North Atlantic is unknown and the hypothesis does not suggest where the three breeding areas are but the whales must be breeding in the deep waters in the open ocean with no geographic barriers. The breeding areas would however need to be non overlapping or else the whales would be expected to interbreed. In light of the numerous cases of hybrids between fin and blue whales, it is uncertain how animals would, with no genetic difference, avoid interbreeding. If the animals inter-breed there will be no genetic stock to preserve and the 5%/90%/5% behaviour can not be genetically transmitted/sustained. At the 2nd Intersessional meeting objections were however raised to this and it was stated that the 5%/90%/5% behaviour could be learned as the calves would follow their mothers to the feeding grounds. The calves are likely to follow their mothers only once but would have to learn different rules depending on which breeding grounds they came from. Such learning of proportions by animals is unheard of and should not be taken seriously by the SC. To address this satellite tagging or individual identification to the breeding grounds would be required.

For the hypothesis to hold, at most 5% of the whales from the neighbouring areas can be captured in the WI area in a single year (even if all the whales in WI were caught). This is how the hypothesis has been implemented in trials and should be tested. Different implementations of the hypothesis may be possible but would then call for trials to be rerun and should then be brought up under an implementation review. With tagging it would be impossible to disprove the hypothesis if it did allow the animals to be moving during the season back and forth as long as they did spend only 5% of the time in the wrong area, then more than 5% of the C1 and C3 breeding stocks could be captured in one season off WI. Such “visiting” behaviour would also be even less comprehensible as the density of whales falls in one area, and the “visiting” whales still spend only 5% of their time in that area having detected higher food availability (lower density) there. The mixing has since been estimated 8% and significantly different from 5%, while 22% mixing would be needed for variant 2 to be acceptable under hypothesis IV (Elvarsson, 2011).

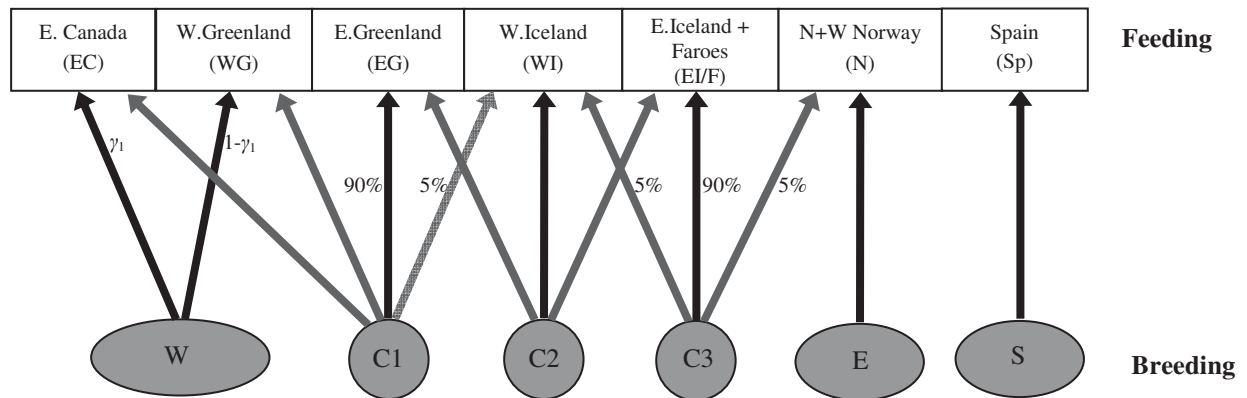


Figure 2. Hypothesis (IV). 4 breeding stocks but without interchange between the C sub-stocks

Research options

In 2006, the SC identified the following methods as having potential to distinguish among competing stock structure hypotheses (International Whaling Commission, 2007):

- 1) New genetic methods based on analysis of close relatives.
- 2) Satellite tracking
- 3) Photo identification

General considerations on methodology:

Method 1) Hypervariable genetic markers enable the unique identification of individuals. Such tagging by biopsy collection for direct re-identification (mark-recapture) by matching of genetic samples and a new method based on identification of close relatives (Skaug, 2001); (Skaug et al., 2010) is particularly promising. The present annual catch limits issued by Icelandic authorities are 154 fin whales. It is assumed that this will be the catch through out the 10 year research period. This catch level is about 2/3 of the average catches during the 1948-1985 commercial whaling period for which biological parameters have been estimated. At least 565 genetic samples exist from the whaling pre 1990 and 7, 125 and 148 from 2006, 2009 and 2010 respectively. Problems have been encountered in work with some of the old samples, but we it is assumed that most of the samples could be worked up within the research time-frame. A preliminary analysis of 358 of these samples (Skaug and Daníelsdóttir, 2006) using 15 micro-satellite DNA loci did detect 11 parent-offspring pairs (expected 80% detection) where of likely 1 or 2 were false positives (FP). In optimized analysis with this number of loci the detection could be 95% of PO pairs with even fewer FPs expected. This number of loci is too small for a reliable sample of type 2 (T2) relatedness (half-sibling and grandparentage). The number of loci would have to be tripled for 65% detection of T2 relatedness and then 17% FPs are expected. Full-siblings have been assumed a minor proportion. Alternative genetic methods could also be implemented such as Single nucleotide Polymorphism (SNPs), which will imply the genome sequencing of few individuals and an additional development cost, but a lower running cost. In particular, this should be considered, as microsatellite loci in marine mammals are not that highly variable.

In relatedness studies the expected number of related pairs depends on the probability of the related animal being alive at the time of the re-sampling. This probability is highest if the sampling is spaced in time to a certain extent depending on the type of relatedness. If the time difference is one year the probability of a parent or grand parent alive in the earlier sample with offspring in the latter sample becomes multiplied up by $1/S$ (S annual survival) and multiplied down by S in the reverse case, but $1/S+S \geq 2$ for all S , so the probability of a parent alive is highest when the time difference of samples is equal to the age at recruitment to the sampling (R), as animals are most likely sampled at that age and parents were certainly alive (available) in the year when the animal was conceived (mating season taken as start of year). In the case when the earlier sample is from the catches, there can be no direct matches and all samples (whales caught) prior to the birth of the later sampled animals are excluded as parents, so PO probability becomes lower than in biopsy samples when the distance in time exceeds the minimum age of the later sampled animals. The implication is that not only will biopsies sampled at the start of the program be more likely to be matched directly in the catches, but also PO pairs will then be more likely. If biopsy samples are collected prior to a 10 year sampling period (from a closed population) the ratio of direct matches to relatedness matches changes from 2.8 in the first year to 5.5 in the last year ($S=0.93$) mainly due to fewer direct matches alive in the end. Over the period of 25-30 years there are still expected around two closely related individuals alive, so matches to the early samples should also turn out to be significant.

To detect dispersal the observations of direct recaptures need to be spaced in time, to allow for dispersal to accumulate during the period between the samples. In case of relatedness the dispersal starts when the matched animals departed. Here it is assumed that fathers depart their offspring after conception and mothers soon after weaning. Most related pairs will therefore have dispersed for a considerable period in addition to the time difference of the samples. For PO relatedness the minimum is the recruitment age of the offspring and for siblings it is the sum of the recruitment ages. For grand parentage relatedness the minimum is the sum of the recruitment age and sexual maturation age of the parent. Relatedness between the areas should therefore already be similar to that within the areas from the very start. Biopsy sampling in the EG area is therefore seen as most likely to provide significant data.

Method 2) Success with satellite tagging of balaenopterid whales has in general been rather low and this method is here seen as a secondary option. However, efforts to track fin whales via satellite have been relatively few on a global scale. Out of four satellite tagging attempts in Icelandic waters one provided useful data (45 days; Watkins et al., 1996). Due to these limitations, this method is not expected to provide significant sample sizes unless definite technical improvements are made. However, each successful tracking over considerable time provides a large amount of data informative for stock structure questions.

Method 3 and other options) Available photo-id catalogues in the North Atlantic and the Mediterranean Sea have been summarized (Robbins et al., 2007). The SC subsequently recommended that an effort be undertaken to match the small holdings in the eastern North Atlantic to catalogues in the western North Atlantic. To our knowledge this has not been undertaken yet. Although such studies have the potential to invalidate the hypothesis by detecting interchange between areas where there should be none, given the relatively small size of the catalogues compared to estimated abundance of fin whales in the North Atlantic (50,000+) and that no catalogue exists for the main area of interest here, this option is not considered further. Considerable collection/availability of genetic samples from remote areas for genetic recapture or relatedness is similarly not considered a realistic possibility.

The assumption of Hypothesis IV of separate breeding stocks (C1, C2 and C3) was not based on any observations, to the contrary, previous genetic studies performed with microsatellite loci and mtDNA did not reveal any genetic structure among samples collected at several different feeding grounds over a period of 20 years (Pampoulie et al., 2008). Further genetic studies along these lines are therefore of little interest, but might have some potential if samples were obtained from the breeding grounds, which is unrealistic in the near future.

Additional abundance estimates that are anticipated from continued surveys as required under the RMP, or from other methods such as genetics, may lead to somewhat better performance of the trials, in particular if higher or more precise estimates are obtained, but such an outcome is uncertain and the effect likely too small.

(1) RESEARCH OBJECTIVES

Genetic “mark-recapture” and relatedness studies

Comparison of interchange across area boundaries from relatedness studies

Parent offspring related pairs detected are expected to outnumber direct recoveries and with a larger set of loci the detected T2 related pairs should then be double the PO pairs. SC/64/RMP1 analyzes the ratio of relatedness recoveries from the genetic tagging (biopsies) in the EG area and within the catches in the WI area. It is found

that the proposed biopsy sampling of 100 whales in the EG area which should result in matches (direct plus relatedness recoveries) equivalent to up to 500 markings, has a good chance of rejecting hypothesis IV in favour of hypothesis III. To this data the relatedness of the biopsies to the earlier (pre 1990) sampling could be added. Expected relatedness within the biopsies could be included, although small.

Detection of mixing over time from recaptures and relatedness studies

According to hypothesis IV mixing does not change over time as the mixing in the WI area is assumed constant and markings in the other areas should remain equally available over time at the level of mixing. Discovery markings are without replacement and therefore a slightly decreasing rate of returns with time is expected in the WI area, where in total 47 out of 191 got recovered, compared to the EG area from where 9 out of 89 marks placed got recovered in the WI area. The mark returns by area however show greater differences over time, with 5 out of the 9 from the EG returned 5 years or later but only 4 out of the 47 (thereof 37 between season) from the WI area. Trials based on hypothesis IV fit the mark recoveries poorly and differ in that inherently they can not explain why marks placed on the grounds (WI) recover soon after marking (mean 2.7 years excluding same season recoveries) while marks placed in the EG area have recovered later (mean 4.8 although here including 1 same season recovery). The external recoveries are expected to increase with time and peak after at about 10 years when $S=0.93$ and dispersion is 7%. Due to the short time that elapsed from the placing of most of the Discovery marks till the cessation of whaling the data is limited. However a significant trend has been found (Gunnlaugsson, Th. 2011a; SC/64/RMP3) and these results are already considered sufficient to reject hypothesis IV. According to the results of SC/64/RMP1 the ability to reject hypothesis IV in favour of III based on the research data is weak. Hypothesis III assumes dispersal between the stocks (on the breeding grounds) and instantaneous full mixing on the feeding grounds, whereas the most likely model is a single breeding stock with a certain affinity to location, that is most likely to visit the same feeding spot the next year, which is the approach in SC/64/RMP3. The proposed 100 biopsy samples from EG at the start of the research period should double the Discovery-marking dataset of direct recoveries between the areas. Although related pairs will be dispersed for considerable time they should also show some signs of dispersal over time, incompatible with hypothesis IV.

Satellite tagging

Satellite tagging to reveal mixing between the areas

Satellite tagging early in the season could reveal animals moving across area boundaries within the season, and proportional time spent in each area. Two instances of such movements have been observed. One is a radio tagging experiment in 1980 (Watkins et al., 1984) where a whale was followed from west off Iceland to East Greenland in the course of a week. One Discovery mark placed at coastal East Greenland (of a total of 65 there) was found in the catch in Iceland a week later in 1986. As same season recoveries are generally not included in mark-recapture analysis, neither of these observations have been included in the IST model data and may not easily be incorporated there. The likelihood of such events needs to be integrated with the likelihood of the model outcome. Mixing that exceeds 5% invalidates the hypothesis, and a binomial test with a proposed sample size of 50 animals (25 animals both in the East Greenland and in the West Iceland area) would detect a difference between 5% and 20% with >80% power (Clopper and Pearson, 1934).

Satellite tagging to reveal overlap of WI and EG animals on the breeding grounds

Satellite tagging (in particular if conducted late in the season) on the feeding grounds may survive long enough for detection of breeding grounds. A fin whale was tracked in 1994 for 45 days, when contact was lost on 24. September, had not started autumn migration (Watkins et al., 1996). The discovery of breeding grounds would then open up a range of research opportunities including genetic sampling and satellite tagging on breeding grounds. Hypothesis IV is invalidated if overlap of the feeding ground animals is observed on the breeding grounds that exceeds what would be expected according to the hypothesis.

(2) METHODS – DATA COLLECTION

The primary target is to collect in total 100 biopsies in the EG *small area*. These will be collected using ‘Larsen guns’ (Palsbøll, 2008) and crossbows. A secondary target is to satellite tag 25 animals in each of the two small areas EG and WI. Satellite transmitters will be instrumented using the ARTS system (Heide-Jørgensen et al., 2001); (Vikingsson and Heide-Jørgensen, 2006). To take advantage of rapid technological developments the choice of satellite transmitter will not be made until close to the start of the programme.

Biopsies might be directed at recruited animals for immediate availability in the catches and for easier modelling.

If catches turn out to be lower than assumed here, then other effort such as biopsy sampling may need to be scaled up accordingly.

(3) METHODS - ANALYTICAL

An efficient two step relatedness study (Skaug et al., 2010) for T2 (half-sibling/grand-parentage) relatedness would need at least double the presently analysed number of loci to detect 35% of the HS pairs. With an anticipated total sample size of around 2,000 these would come along with around a hundred false positive (FP) pairs in the first step that would then need to be further screened at additional markers in a second step. This would be realistic today. We anticipate that within a time-frame of 10 years more than half the HS pairs could be detected with a tolerable FP error rate (1%).

Mother-foetus pairs do more accurately genetically mark the parental line in the population (Pampoulie et al., 2012) and should be integrated with the other pairs, although such samples will likely be few.

Direct genetic identification matches will be added to the Discovery marking data as fitted in the trial model and relatedness data will be incorporated in a similar way in the models.

Methods to integrate different pieces of information (satellite tagging) that cannot be fitted in the IST model will be identified.

(4) TIMELINE – INCLUDING ASSESSMENT OF FEASIBILITY

(a) Annual data collection – feasibility

Year 1. Feasibility study - Collect around 20 biopsies in EG small area and satellite tag 10 animals.

Year 2. Collect remaining biopsies in EG small area to fill 100 with effort allocation based on the feasibility study.

Year 2-10. Additional satellite tagging. Based on the feasibility study in year 1, 25 animals will be tagged in each of the two areas (EG+WI).

Years 1-10. Collect samples from catches.

(b) Annual laboratory work – data validation.

Years 1-6. Identify new markers for relatedness studies (but SNP alternative. Present markers are sufficient for direct matches and only a few additional markers are needed for good PO detection. Alternately sequence individuals and isolate useful SNPs

Years 6-10. Genetic work on samples in two stages with final aim equivalent of triple the number of present loci. Alternately routine SNP runs.

(c) Annual analysis and completion targets.

Years 1-6 Programming and development of models.

Years 7-10 Statistical analyses of samples and model runs.

Work on the IST model amendments and modified hypotheses will need to be in cooperation with the Secretariat Computing. The work will take note of any best practice guidelines or requirements established by the Committee.

(a) Data availability: Data will be made available to SC members as specified under the DAA.

(b) Reports to the SC: Progress will be reported to the SC annually.

This proposal is designed to meet the requirements of the SC and provide general useful information on the stock dynamics in the North Atlantic. Another approach to reject hypothesis IV would be to collect biopsies on the whaling grounds. The direct relatedness recoveries from these would not be suspect of tag mortality, tag loss or tag shedding, so if they confirmed the results of the Discovery-markings, where the marked animals vanished from the catches in a few years, then hypothesis IV would have to be rejected. Settling the Discovery-marking dispute is also of global significance. This would however not provide any information on where the animals dispersed to, they might as well have dispersed north or south as to the EG feeding area. There would be little gain in the biopsy relatedness.

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