

Annex N

Report of the Working Group on DNA Testing

Members: Pastene (Chair), Baker, Cipriano, Goto, LeDuc, Nakatsuka, Natoli, Palsbøll, Perrin, Pomilla, Skaug.

1. ELECTION OF CHAIR

Pastene convened and chaired the Group.

2. ADOPTION OF AGENDA

The agenda is given as Appendix 1. Items 5, 6 and 7 of the agenda are in response to requirements placed on the Scientific Committee by IWC Resolution 1999-8 (IWC, 2000), which called for annual reports on progress in the following areas:

- (1) Genetic methods for species, stocks and individual identification.
- (2) Collection and archiving of tissue samples from catches and bycatch.
- (3) Status of and conditions for access to reference databases of DNA sequences or microsatellite profiles derived from directed catches, bycatch, frozen stockpiles and products impounded or seized because of suspected infractions.

3. APPOINTMENT OF RAPPORTEURS

Perrin acted as rapporteur.

4. REVIEW OF DOCUMENTS

Relevant information was contained in SC/56/BRG34, SC/56/SD 3 and SD4 and SC/56/ProgRepNorway.

5. PROGRESS ON GENETIC METHODS FOR SPECIES, STOCK AND INDIVIDUAL IDENTIFICATION

SC/56/SD4 reported on the public sequence archive GenBank (National Center for Biotechnology Information: www.ncbi.nlm.gov/). The archive contains 2,723 sequences. Currently, sequence data is missing or limited for many cetacean species, and it appears that more sequence information is privately held than is publicly available. For example, four putative species have no sequence data available; another 17 lack even a single control-region sequence (the main locus used for forensic identification); 20 lack a cytochrome *b* sequence; 34 species are represented by only one control-region sequence or cytochrome *b* sequence. Antarctic minke whales and dwarf minke whales, central in the controversy over whaling under scientific permit by Japan in the Southern Ocean, are not represented by a single control region or cytochrome *b* sequence. Archiving of sequence data is encouraged by many scientific journals through editorial policies that require authors to provide GenBank accession numbers with each manuscript submitted.

It was noted that the taxonomy employed by GenBank may not always be current and that therefore care should be taken to ensure that any sequences extracted from the archive are indeed of the species of interest.

The Working Group recommends that members of the Scientific Committee be urged to deposit sequences to be used in a published report in GenBank and include the GenBank accession numbers in the publication, whether or not this is required by the journal. At present the Journal of Cetacean Research and Management does not require deposit of sequences used in submitted papers; it is recommended that this be made part of the editorial policy of the journal. It is further recommended that similar practices be established for public archiving of non-sequence genetic data, such as microsatellite loci, primers, alleles, and profiles, where feasible. Such data are not presently accepted by GenBank, and some research may be necessary to identify a suitable archive. One potential provisional venue is the websites maintained by most major journals for supplementary data and information accompanying published papers.

SC/56/BRG34 reported research on quality of DNA samples from tissues collected in the Arctic. Tissue samples for genetic analyses of bowhead whales came from subsistence hunts in Alaska and Russia. Samples from near Barrow were collected by biologists, while those from more remote villages were provided by the hunters. To test the relative reliability of the different sources, DNA was quantified from 20 bowhead whale samples from remote villages, and from 20 random samples from the North Slope of Alaska (Barrow). The two sources were compared in several measures of data quality. Although the differences were not significant, perhaps due to low sample sizes, there were trends of lower DNA concentrations in samples coming from outside the North Slope, correlated with lower PCR success rate and higher homozygosity, possibly due to allelic dropout. These results, which could bias analyses of population structure, may be the result of differential handling of samples from the remote villages. They emphasize the importance of the chain of sample collection and treatment to good results in the laboratory. The conclusion after discussion was that some of the problems encountered in Alaska and similar situations may be alleviated by consistent use of an appropriate preservative and refrigeration of the samples.

6. PROGRESS ON COLLECTION AND ARCHIVING OF SAMPLES FROM CATCHES AND BYCATCHES

The status of the Norwegian minke whale DNA-register was reported in SC/56/ProgRepNorway, covering the years 1997-2002. This is the first year that these statistics have been included in the national progress report. The Working Group welcomed this response to the Commission's call for such reporting. It was noted that progress has been made toward achieving a fully diagnostic register; no samples were missing for the 625 whales landed in 2002. The number of missing samples in earlier years ranged from 3 to 11. No samples were reported from stranded whales.

No information on collection and archiving of samples in Japan was available to the Working Group. It was noted that provision of a progress report on collection and archiving of samples would assist the Working Group in meeting its terms of reference as assigned by the Commission.

7. REFERENCE DATABASES AND STANDARDS FOR A DIAGNOSTIC REGISTER OF DNA PROFILES

SC/56/SD3 reported on a study where DNA-profiles from 288 mother-fetus pairs were compared for consistency. The aim was to check the quality of the 10 microsatellite profiles contained in the Norwegian minke whale DNA-register. The 288 mothers, as part of the DNA-register, had previously been analysed, and the fetuses were analysed in a blind experiment using the same laboratory and protocol as used for the DNA-register. Several inconsistencies between mother and offspring were found. In a second stage of the study the laboratory was informed about which females were the mothers of which fetuses, and this information was used to resolve the inconsistency. This second stage involved complete re-analysis of several individuals. Table 4 of SC/56/SD3 reported all errors found in the mother profiles as a result of this process. The causes of errors were not given. This information will be used to estimate error rates for the DNA-register, with the goal of improving the matching criterion used in the operation of the DNA-register.

No new information was available on the register maintained by Japan. Again, it was emphasized that progress reports on development of the databases and standards for the register would aid the Working Group in fulfilling its remit as assigned by the Commission.

8. WORK PLAN

The terms of reference for the Working Group for the next year will remain the same, unless the Commission requests other information in the interim.

9. ADOPTION OF REPORT

The report was adopted by consensus.

Appendix 1

AGENDA

1. Election of Chair
2. Adoption of agenda
3. Appointment of rapporteurs
4. Review of documents
5. Progress on genetic methods for species, stock and individual identification
6. Progress on collection and archiving of samples from catches and bycatches
7. Reference databases and standards for a diagnostic register of DNA profiles
8. Work plan
9. Adoption of report