

SC/66b/DNA/02

Plans for upgrading the Norwegian Minke
Whale DNA Register (NMDR) in the period
2016 to 2017

Kevin A. Glover, Tore Haug, Nils Oien, Bjorghild B.
Seliussen, Hans J. Skaug



INTERNATIONAL
WHALING COMMISSION

Plans for upgrading the Norwegian Minke Whale DNA Register (NMDR) in the period 2016 to 2017

KEVIN A. GLOVER^{1,*}, TORE HAUG², NILS ØIEN¹, BJØRGHILD B. SELIUSSEN¹, HANS J. SKAUG^{1,3}

¹*Institute of Marine Research, PO box 1870, Nordnes N-5817 Bergen, Norway*

²*Institute of Marine Research, PO box 6404, N-9294, Tromsø, Norway*

³*Department of Mathematics, University of Bergen, N-5008, Bergen, Norway*

*corresponding author: kevin.glover@imr.no

ABSTRACT

The Norwegian Minke Whale DNA Register (NMDR) is at present based on genotyping microsatellites, a single sex marker and sequencing the mtDNA d-loop. Here we present plans to upgrade it to genotyping a suite of carefully selected SNPs which will still keep the register's primary function of traceability of whale products in Norway and the international market.

WHALING, MONITORING, GENETICS, CATHCES, ATLANTIC OCEAN, COMMON MINKE WHALE

The Norwegian Minke whale DNA Register (NMDR) has been in operation since the 1990ies and permits the verification of whale meat for sale in the domestic or international market through individual DNA profiles (Glover *et al.* 2012). The register is based upon individual-whale DNA profiles using genetic data from a combination of microsatellite markers, a sex marker and sequencing a part of the mtDNA D-loop. By matching the genetic profile of a meat sample collected in for example a restaurant or market to the DNA register, validation of legality for the meat on sale is obtained. Likewise, a meat sample not matching the DNA register will be considered as potentially illegal.

The register is in constant operation to provide a tool for the authorities to monitor and potentially enforce regulations in commercial whaling in Norway. It has also been used for a range of scientific purposes including: the identification of minke whale hybrids (Glover *et al.* 2010; Glover *et al.* 2013), investigating population genetic structure (Quintela *et al.* 2014), investigating sibling relationships (Skaug & Øien 2005; Skaug *et al.* 2010), and investigating diets of large marine fish (Leclerc *et al.* 2011).

The individual whale DNA profile for the register is primarily provided by the microsatellite markers genotyped. These are highly polymorphic markers that offer good statistical power for individual-identification, and still form the basis of human DNA registers (criminal registers). However, microsatellites are challenging to genotype accurately (Haaland *et al.* 2011), and they require inter-laboratory calibration in order to permit data sharing between laboratories (for example if a third party would like to cross-validate the Norwegian register). Increasingly, microsatellite markers are being replaced by single nucleotide polymorphisms

(SNPs) for a wide range of routine scientific and management purposes. We propose to gradually transform the NMDR over to SNP genotyping.

The Institute of Marine Research (IMR) in Norway, who is currently charged with conducting the genetic analyses upon which the genetic register is based, aims to start the process to upgrade the NMDR from genotyping microsatellites, a single sex marker and sequencing the mtDNA d-loop, to genotyping a suite of carefully selected SNPs. The register will still provide its primary function of traceability of all whale products in Norway and in the international market. The exact SNPs have not been identified, but when they are these will be made available to the international research community via an open access publication.

REFERENCES

- Glover K.A., Haug T., Øien N., Walløe L., Lindblom L., Seliussen B.B. & Skaug H.J. (2012) The Norwegian minke whale DNA register: a database monitoring commercial harvest and trade of whale products. *Fish and Fisheries* **13**, 313-32.
- Glover K.A., Kanda N., Haug T., Pastene L.A., Øien N., Seliussen B.B., Sørvik A.G.E. & Skaug H.J. (2013) Hybrids between common and Antarctic minke whales are fertile and can back-cross. *Bmc Genetics* **14**.
- Glover K.A., Kanda N., Haug T., Pastene L.A., Øien N., Goto M., Seliussen B.B. & Skaug H.J. (2010) Migration of Antarctic Minke Whales to the Arctic. *Plos One* **5**.
- Haaland Ø.A., Glover K.A., Seliussen B.B. & Skaug H.J. (2011) Genotyping errors in a calibrated DNA -register: implications for identification of individuals. *Bmc Genetics* **12**, 36.
- Leclerc L.M., Lydersen C., Haug T., Glover K.A., Fisk A.T. & Kovacs K.M. (2011) Greenland sharks (*Somniosus microcephalus*) scavenge offal from minke (*Balaenoptera acutorostrata*) whaling operations in Svalbard (Norway). *Polar Research* **In press**.
- Quintela M., Skaug H.J., Øien N., Haug T., Seliussen B.B., Solvang H.K., Pampoulie C., Kanda N., Pastene L.A. & Glover K.A. (2014) Investigating Population Genetic Structure in a Highly Mobile Marine Organism: The Minke Whale *Balaenoptera acutorostrata acutorostrata* in the North East Atlantic. *Plos One* **9**.
- Skaug H.J., Berube M. & Palsbøll P. (2010) Detecting dyads of related individuals in large collections of DNA-profiles by controlling the false discovery rate. *Molecular Ecology Resources* **10**, 693-700.
- Skaug H.J. & Øien N. (2005) Genetic tagging of male North Atlantic minke whales through comparison of maternal and foetal DNA-profiles *Journal of Cetacean Research and Management* **7**, 113-7.