

CONVENTION ON INTERNATIONAL TRADE IN ENDANGERED SPECIES
OF WILD FAUNA AND FLORA



Fourteenth meeting of the Conference of the Parties
The Hague (Netherlands), 3-15 June 2007

Additional Information on
Identification Aid for Shark Specimens or Shark Meat

The attached information document has been submitted by Germany.

Porbeagle (*Lamna nasus*) and Spiny Dogfish (*Squalus acanthias*)

Additional Information on Identification Aid for Shark Specimens or Shark Meat

In addition to the information presented in document CoP14 Prop. 15 and CoP14 Prop. 16 the following information is available on the identification of parts and especially meat of the two shark species mentioned above.

1) Morphological Identification of fins

An identification guide for shark fins is in preparation by Pascal P. DEYNAT, Museum National d'Histoire naturelle, Paris, in cooperation with WWF. It is planned to finish it in the course of 2007. [person. comm. to German Scientific Authority, March 2007).

2) DNA tests

A very simple, rapid and highly accurate PCR primer based test for porbeagle has been developed by SHIVJI et al. 2002 (see amendment proposal)¹.

A COI gene sequence test is already available for spiny dogfish, developed by Robert WARD, CSIRO Marine and Atmospheric Research, Hobart, Tasmania/Australia (available in the internet)². An additional, primer based one - comparable to the one for the porbeagle - could be easily developed, probably within half year, depending on the availability of samples from shark species needed.

Both tests can be carried out by any laboratory used to practise normal DNA techniques.

3) Turn around time of the DNA tests

Primer based genetic tests are quicker and less expensive than COI gene sequence tests. A single test may be carried out in 3-4 hours only, based on COI gene sequence it may take approximately 8-12 hours. The turn around time relies as well, of course, on the number and quality of samples to be tested.

The big advantage of the primer based test becomes evident when a high number of samples have to be tested at the same time. Once the specific primers have been developed (as done with regard to the porbeagle) it is possible to run up to 1000 samples (or even more) per day which is not the case using the gene sequence test.

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¹ SHIVJI, M., CLARKE, S., PANK, M., NATANSON, L., KOHLER, N. & STANHOPE, M. (2002): Rapid molecular genetic identification of pelagic shark body parts for conservation and trade monitoring. -- *Conserv. Biol.*, 16(4): 1036-1047.

² www.barcodinglife.org