## Test to Monitor Fin Trade

by Jeff Hecht New Scientist - August 3, 2002



When a shark has been unceremoniously turned into a soup dish, identifying which species it was isn't easy. But a new genetic fingerprinting technique could now allow conservationists and fisheries managers to assess which of the 400 shark species are most threatened by the booming trade in their fins.

Shark-fin soup has become an expensive delicacy in South-East Asia, costing up to \$90 a bowl in Hong Kong, for example. Since the shark flesh doesn't keep well, fishermen usually just hack the fins off the animals and toss the bodies back into the ocean. But sharks are slow to mature and only produce a few offspring at a time, so they are vulnerable to overfishing.

Monitoring the shark -fin trade is all but impossible, as once a fin has been cut off, it can be extremely difficult to work out precisely which species it was taken from. Conventional genetic

analysis can do this, but the process is too costly and time-consuming to be used widely in the field. First, small amounts of DNA from the fin must be copied repeatedly, or amplified, using the polymerase chain reaction (PCR). The genetic material is then chopped up, and a large number of fragments are analysed using an electrophoresis gel that separates the sections according to size. The DNA profile is then compared with the profiles of various species to look for a match.

Now Mahmood Shivji of Nova Southeastern University in Dania Beach, Florida, has developed a faster identification process. Shivji has designed a range of "primers" - short pieces of DNA that are complementary to a particular sequence of DNA. Each primer is specific to the DNA of a single shark species.

The primers are added to the shark fin material and put through the PCR. This amplifies only the DNA bound to the primer for the species in question. Putting the fragments through the gel allows the researchers to instantly identify which species is present, because each species-specific primer chain is a different length. Shivji says this is quicker than comparing whole DNA profiles, and further refinements could lead to portable equipment that gives results within hours.

He has already used the technique to identify six species of shark commonly caught off North America from both fresh and dried fins (*Conservation Biology*, vol 16, p 1036).

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