

Fingerprinting Shark-Fin Soup

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Biologists have a new tool to help them determine which shark species and how many of each are being consumed by Asia's appetite for shark-fin soup.

Increased market demand, poor data on global shark populations, and sharks' inability to reproduce quickly have international conservation organizations concerned about the impacts of increased "finning" on offshore populations (see Canadian Wildlife Oceans 2000, page 38). Physical similarities among the six commonly fished open-ocean sharks - blue, dusky, silky, shortfin and longfin mako, and porbeagle - make it almost impossible to determine visually the origin of fresh tissues or dried fins for fisheries records. Identification can be made by using DNA analysis but authorities haven't implemented genetic testing because it is seen as too slow, expensive, and technically complicated for use in routine large-scale fisheries and trade monitoring. But Mahmood Shivji, of Nova Southeastern University's Guy Harvey Research Institute in Florida, and his colleagues have found a solution: a new all-in-one DNA analysis procedure that is quicker and easier.

"Existing methods for species identification involve a two-to-three-step process. Our method requires only one step," explains Shivji. "And our species-specific primers can be combined so that we can distinguish all six species with a single reaction as opposed to testing for a single species with each test."

To date, the new DNA analysis is ready for use in laboratories, but Shivji and his colleagues are investigating ways to take the test into the field. They are also determined to expand the test to differentiate more of the approximately 35 shark species traded in global markets. With 6 down, that leaves only 29 to go!