

defrauds consumers but could also adversely affect estimates of stock size if it influences the reporting of catch data that are used in fisheries management.

The red snapper, or *L. campechanus*, is found in offshore waters around coral reefs and rocky outcroppings² and is one of the most economically important fisheries in the Gulf of Mexico, with greater total landings and commanding higher prices than any other snapper species^{3,4}. In 1996, the Gulf of Mexico Fishery Management Council and the United States Department of Commerce declared that *L. campechanus* was grossly overfished and called for strict management measures to restore stocks to sustainable levels.

Tight restrictions may create an economic incentive for seafood substitution, whereby less valuable species are mislabelled and sold under the names of more expensive ones. Substitutions among closely related fish species are difficult to detect, because most distinguishing features are lost during processing. Although the name 'red snapper' is applied to other species in different countries, only *L. campechanus* can legally be labelled as red snapper in the United States¹.

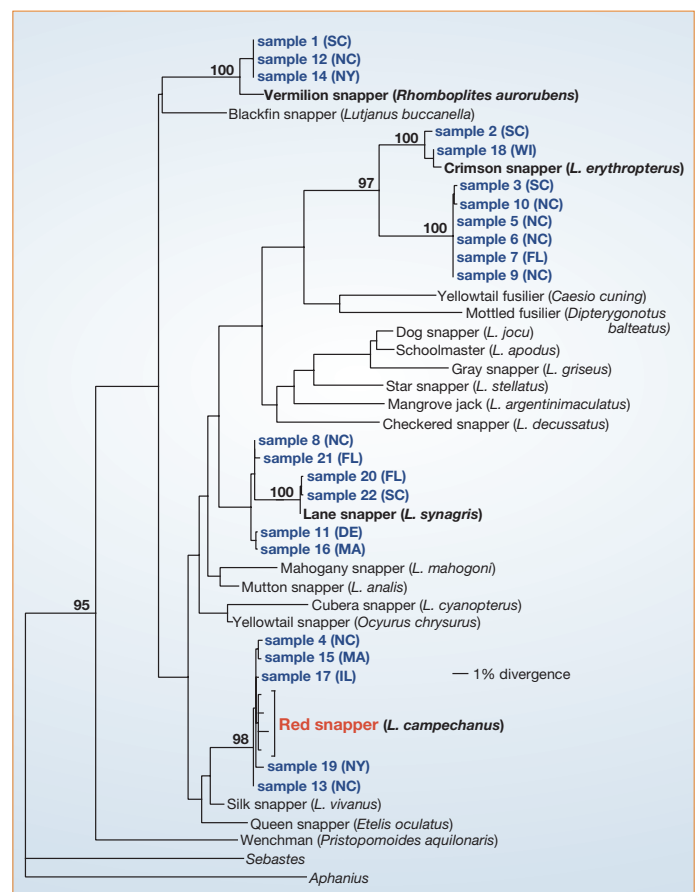
To investigate the extent of possible mislabelling in the United States, we did a molecular phylogenetic analysis of fish purchased from nine vendors in eight states (Fig. 1). We compared DNA sequences from retail samples with those deposited in GenBank, which contains sequences from all snappers for which landing data are recorded by the US National Marine Fisheries Service (NMFS).

Our results show that mislabelling is a large-scale phenomenon: 77% of fish sold as red snapper (17/22) were in fact other species (Fig. 1). This estimate has a margin of error of 17%, meaning that between 60% and 94% of fish sold as red snapper in the United States are mislabelled. Among the sequences from fish that are not *L. campechanus*, five are grouped very closely with those from other Atlantic species. Of these, sequences from two are nearly identical to those from the lane snapper, differing only by single-nucleotide substitutions (Fig. 1). The three other putative Atlantic snappers in our sample are grouped with vermilion snapper, with only about 2% sequence divergence.

Surprisingly, more than half of our analysed sequences are either grouped closely with species from other regions of the world or represent species too rare to have yet been included in molecular phylogenetic surveys⁵. For example, two fish can be definitively identified as crimson snappers, a species from the Indo-West Pacific. And sequences from several other fish form clades that do not seem to be closely related to any reference sequences. These fish represent species that are either not caught in US waters or not yet individually managed by the NMFS.

Mislabelling of fish can occur at different points in the commercial process: for

Figure 1 Maximum-likelihood tree (GTR + I + G model) of cytochrome-*b* DNA sequences from retail 'red snapper' (GenBank accession numbers: AY294187-205; AV651957-59) and reference sequences (AF23-9677-78, 80-82; AF240-750; AF381270; AF031516; AF299290; U26949, 51-58, 61-62). Numbers at nodes are bootstrap percentages (1,000 replicates) from an unweighted parsimony search. Sequences of 953 base pairs were obtained using the polymerase chain reaction and the primers CB12F (5'-TGGCAAGCTAC-GCAAAC-3') and CB13R (5'-TATTCGGCCGATT-CAGGT-AA-3') followed by automated sequencing on an ABI 377. Phylogenetic analyses were completed using PAUP* 4.0 software¹³. State abbreviations: DE, Delaware; FL, Florida; IL, Illinois; MA, Massachusetts; NY, New York; NC, North Carolina; SC, South Carolina; WI, Wisconsin.



example, retail mislabelling probably explains the presence of crimson snapper in our sample, because these fish occur in an entirely different part of the world from *L. campechanus*. Fish substitutions may occur on the boat or at the dock, because species that are morphologically similar to *L. campechanus* are caught together, as is the case for most reef fisheries⁶. The implications for resource management are important: substitutions made before commercial landing data are submitted to the regulatory agencies will cause inflation of catch estimates for the most desirable species and simultaneous underreporting of catches for less desirable, and potentially unmanaged, species. Although it is widely acknowledged that intentional misreporting and unintentional misidentification of species can both bias fishery-dependent data⁷⁻¹¹, the contribution of this effect cannot be evaluated unless fish are sampled before the collection of catch data.

The remarkable extent of product mislabelling in the case of *L. campechanus* threatens to distort the status of fish stocks as perceived by consumers, which contributes to the false impression that the supply of fish is keeping up with demand¹².

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