Should we trust the names of fish sold to us? An in-depth analysis of adulteration throughout the Belgian fisheries industry

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As the fisheries industry continues to aggrandise and consumers press to receive reliable and accurate product information, more rigid regulation of labelling and control mechanisms of food products throughout the fisheries industry are needed. The removal of certain deterministic traits such as fins or the head causes a major problem for accurate identification of species in fish products. In addition, fish in prepared meals or fish soup are impossible to identify using traditional methods. DNA barcoding forms a solution for these processed food products and has already shown to be successful at revealing adulteration of several fishes. This method involves amplifying and sequencing a small biomarker fragment of DNA from the samples and comparing the sequence to a reference database with sequences of known species. These databases, however, are prone to mistakes due to a lack of curators and additionally the species names used in this database are not always compendious. In this study, a reference database with COI (Cytochrome oxidase 1) and Cytb (Cytochrome b) mitochondrial genes was created to serve as a reliable platform for barcode sequences of European seafood species. This database contains voucher specimens collected across various European seas (and rivers) which are photographed and morphologically identified to species level by taxonomic experts. This ensures sequences are linked to the correct species. Thus far the database contains 81 COI sequences and 77 Cytb sequences from 24 fishes spanning 11 families, which are regularly consumed in Europe or frequently used as adulterants. Phylogenetic trees and the distribution of intra- and interspecific P-distances show these genes' strengths as barcoding sequences. COI displays a clear barcoding gap and indicates that using a threshold of 2 to 5.2% divergence will give a 100% correct species identification. Cytb displays some overlap between species, but still indicates that a threshold of 4.5 to 4.6% divergence will give an error rate of 0,18% which is well within a 95% confidence interval. Most adulteration studies have focused on the end point of the food chain. Our approach is to assess more precisely where and how adulteration takes place along the whole food chain. For this, we will thoroughly map out all steps in the fish processing chain. Once we have a clear overview of the different steps we will sample a selected number of fishes at various points along the supply chain. *Gadus morhua* and *Solea solea* are consistently among the most preferred fishes for consumption by Belgian consumers and are consistently among the most landed fish. Both fishes are also expensive, making them prone to adulteration. In addition, there is a substantial amount of imported fish in Belgium, especially of round fish, which are suspects to be adulterants of cod. The application of DNA barcoding will unveil the prevalence of fishery product adulteration in the Belgian market and the factors influencing adulteration (such as times transferred, type of supplier, distance from ocean, price or processing type) of fish products in the Belgian market.

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