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Economy matters: A study of mislabeling in salmon products from two regions, Alaska and Canada (Northwest of America) and Asturias (Northwest of Spain)

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ABSTRACT

Mislabeling of seafood species has negative economic, social and ecological consequences, from consumer losses due to fraudulent exchange, undermining consumer awareness, to hiding illegal and unreported catches. Salmonids are no exception. They are an important part of the culture and economy of many countries in the northern hemisphere, and identifying possible causes of salmon mislabeling is of great interest, even more so where wild species and species from aquaculture are consumed. Here different types of commercial unrecognizable salmonid products (111 in total) from Asturias in Northwest Spain (Atlantic Ocean), and Alaska and Vancouver Island in Northwest America (Pacific Ocean) were analyzed by DNA Barcoding. The Spanish and Northwest American samples were mislabeled 6% and 23.8% respectively. Species substitutions were respectively wild-farmed and wild-wild, substitute species being cheaper. Economic reasons and social preference of wild over farmed products seem to be the main drivers in the exchanges detected in this study. Enhancing controls over the unrecognizable products to prevent this type of fraud is essential and strongly recommended.

1. Introduction

Fish mislabeling results in a series of varied negative consequences that have been well summarized by Jacquet and Pauly (2008). The economic advantages for the defrauders that obtain profits by selling cheaper species for more expensive fish represent losses in duties and import taxes for governments, as well as inadvertent economic losses for the consumers that buy an unwanted product at expensive prices. At the social level, fraud undermines efforts of sustainable fisheries and aquaculture, and consumer's eco-awareness. For example, if the fish are sustainably caught as it happens for instance for South African hake (Marine Stewardship Council: certified sustainable seafood 2004; as https://www.msc.org/) but are sold abroad under a wrong label (Garcia-Vazquez et al., 2011; Muñoz-Colmenero et al., 2015), the enormous effort of stakeholders for achieving sustainability cannot be recognized by the unaware foreign consumer. Other consequences are ecological. Mislabeling may hide cases of illegal fisheries, for example: the complex case of Pacific rockfish (Logan et al., 2008), endangered angel shark mixed with other sharks (Ardura et al., 2011), mislabeling of cod products in China markets (Xiong et al., 2016), the use of *Gadus chalcogrammus* as substitute of *Merluccius merluccius* (Ferrito et al., 2016), and others.

One case of special importance from a social point of view are salmonids. Wild salmonids are an essential part of traditional cultures in many societies of the northern Hemisphere, both in North America (Finney et al., 2000; Raby et al., 2012) and Europe (Briton, 2014; Valiente et al., 2011) as well as key economic resources especially along the North Pacific American coast. On the other hand, some species such as the Pacific rainbow trout *Oncorhynchus mykiss* and the Atlantic salmon *Salmo salar* are widely cultivated. Wild and farmed salmonids are differently appreciated by consumers worldwide, for example, Verbeke et al. (2007) found that consumers slightly preferred wild over farmed fish on the attributes of taste, health and nutritious value. Consumer's perception about which seafood type conveys the highest quality clearly favors fish and shellfish harvested from the wild, with 53% of consumers preferring wild-caught seafood in the USA (O'Dierno

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Table 1
Examples of mislabeling reported in salmonids. Percent of mislabeling reported, and percent of *Salmo salar* and *Oncorhynchus* (any species) declared in the labels and found from DNA in each study.

		Mislabeling detected	Label species		Real species		
Region	N		*Salmo salar*	*Oncorhynchus* spp.	*Salmo salar*	*Oncorhynchus* spp.	Reference
South Africa	12	8.3%	75%	25%	66.7%	33.3%	Cawthorn et al. (2012)
Northeastern America	9	0	55.6%	44.4%	55.6%	44.4%	Wong and Hanner (2008)
USA	384	7.3%	5%	95%	9.6%	90.4%	Warner et al. (2013)
Washington State	99	20.2%	0	100	11.3%	88.7%	Cline (2012)

et al., 2006). Wild salmon is preferred at least in part due to the general belief that farmed fish contain more mercury than wild fish (average 68.5% European consumers; Pieniak et al., 2013).

The use of DNA is required to identify the species when fish are sold in pieces or processed in any way so that their morphological characteristics cannot be recognized (Muñoz-Colmenero et al., 2015). Several studies applying DNA Barcoding have reported mislabeling in salmonids (e.g.: Pardo et al., 2016; Cawthorn et al., 2012; Cline, 2012; Warner et al., 2013; Wong and Hanner, 2008). In these studies (Table 1) the species substituted with is often farmed salmon for wild salmon (e.g., Atlantic salmon sold instead of king salmon *Oncorhynchus tshawytcha;* Cline, 2012), or trout instead of salmon (e.g. rainbow trout instead of Atlantic salmon; Cawthorn et al., 2012). The substitutions may encompass changes between species from different oceans (Table 1), the *Oncorhynchus* genus being native to the North Pacific and the *Salmo* genus native to the North Atlantic Ocean, although in the case of farmed species hatcheries can be located anywhere in temperate climates.

In this study we have analyzed samples of different salmonid products purchased from public marketplaces on the west coast of North America (Alaska in USA and Vancouver Island in Canada) and in Europe (Principate of Asturias, in the North of Spain, Bay of Biscay). We have performed the sampling in these places due to the high importance of salmonids products, being one of the most common fish type consumed and marketed in those regions (Hanner et al., 2011; Rasmussen et al., 2011; Larios, 1930). In addition, in these places the wild salmon species are very appreciated and with enormous cultural value, with several examples of ancestral traditions related with salmonids (Lynn et al., 2013; Valiente et al., 2011; Blanco et al., 2005). Due to such, we consider those regions as adequate for our study. The main aim of this work was to identify by DNA Barcoding methodology the species contained in salmon processed products, in order to assay the reliability of the labeling of such products in the two regions involved in the study. The expectations were that, in the case of existing mislabeling, any substitute species would be the nonnative and farmed species in each region, exchanging species from *Oncorhynchus* genus by *Salmo* genus and vice versa, which are the most common misidentifications detected in the other works (e.g.: Pardo et al., 2016 and Table 1).

2. Material and methods

2.1. Products analyzed

We obtained samples from local grocery stores in Alaska (USA), Vancouver Island (Canada), and Asturias (North of Spain), choosing one representative city in each target region, in which the salmon products market is high. All products purchased were processed products, being sold as: jerky, candy salmon, slices, loins, etc. (Table 2), and therefore being impossible to recognize the species by their morphological features.

In Alaska and Canada the analyzed products were salmon jerky and candy salmon, which are widely marketed and consumed in those regions. Furthermore, due to the high degree of processing of those samples, they are considered as a good niche for the species exchange, being usually labeled only with the commercial common name, as was the case of the samples analyzed here (Table 2). A total of 31 products sold as salmon jerky were purchased in Anchorage, Alaska, USA from three local marketplaces in the summer of 2013 (Table 2). In Vancouver Island (Victoria, Canada), a total of 13 products were purchased, four salmon jerky and nine candy salmon pieces also from local grocery stores (4).

The samples from Asturias (Northwest Spain) (67) were purchased in six different grocery stores in Oviedo city (Asturias, Bay of Biscay), Spain. These products were more variable because in this region the consumption of processed salmonids products is similar between the different types. The majority of the samples (48) were heavily processed products (canned, smoked, salted, pâte) and the rest of the samples (19) were less processed products (fresh or frozen pieces).

In both regions the sampling was mainly focused on highly processed products since the mislabeling in those products may be higher (Muñoz-Colmenero et al., 2016; Filonzi et al., 2010; Rasmussen and Morrissey, 2008), and they are subject to more permissive laws than the products sold whole and fresh.

For all products and regions the expected species were determined from the information found on the labels and shown in Table 2.

2.2. DNA barcoding

DNA extraction was performed following the protocol developed by Estoup et al. (1996) using Chelex resin. DNA was extracted directly from a ~5 mm^3 piece of fresh or frozen samples. All the other kind of products were previously cleaned with a 2:1:0.8 solution of distilled water, chloroform, and methanol in order to remove potential inhibitors of posterior PCR as oils, salts, etc., not present in frozen and fresh products. A fragment of the Cytochrome oxidase subunit I gene (COI) was amplified using the primers designed by Ward et al. (2005). The PCR conditions were: initial denaturation at 95 °C during 5 min followed by 35 cycles of 20 s at 95 °C, 20 s at 57 °C for annealing and 30 s at 72 °C for elongation. Finally, an extension step of 72 °C for 10 min. PCR was performed in 20 μL of total volume, and the composition was: 2.5 μM Mg^{2+}, reaction buffer of Promega Taq polymerase 1 ×, 0.75 U Promega Taq enzyme (5U/μL), 2.5 mM of each dNTP, 1 μM primers, 2 μL of DNA, and bi-distilled water up to the total volume. PCR products were checked in 2% agarose gel stained with 3 μL ethidium bromide (0.5 μg/μL), purified with Illustra Exostar 1-Step (GE Healthcare Life Sciences), sequenced at the DNA Analysis Facility of the University of Oviedo with the BigDye Terminator Cycle Sequencing Kit v3.1 and analyzed on a 3130xl Genetic Analyzer (Applied Biosystems) Automated Sequencer.

The sequences were manually checked with the BioEdit v 7.0.9.0 Sequence Alignment Editor Software program (Hall, 1999). They were aligned using the Clustal W tool included in BioEdit (Thompson et al., 1994). To assign the species, the nucleotide BLAST tool (nBLAST) located in the GenBank public database from NCBI (http://www.ncbi.nlm.nih.gov/) was employed, with 99% of identity as cut-off. This cut-off is conservative enough to resolve the identification at the species level but keeps 1% for possible intraspecific variability. Those sequences in which mislabeling was found were also checked with the