Misdescription incidents in seafood sector

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ABSTRACT

Seafood consumption has increased worldwide in the last 50 years considering both wild catches and aquaculture production. According to the Food and Agriculture Organization (FAO), the majority of world fisheries is at maximum exploitation levels or over-exploited. Illegal, unreported and unregulated fishing is contributing to overfishing, as well as intentional or unintentional mislabeling of fish catches or their geographical origin. DNA identification methods can contribute to monitor mislabeling, mainly when dealing with processed seafood or morphologically similar species. It cannot be ignored that seafood mislabeling can also have food safety implications, due to the presence of toxic substances directly related to certain species or to the catch area. In this context, a review has been conducted analyzing scientific reports related to seafood mislabeling incidents published in the last five years to try to identify the level of real mislabeling, as well as, the more relevant gaps in this area. A total of 51 peer-reviewed papers including 4500 samples analyzed globally by DNA methodologies have been taken into account. The average percentage of reported misdescription is 30%. In general, incidents in restaurants and takeaways are much more common than in supermarkets and retailers. Therefore, specific studies should be conducted to confirm it because only 10% of analyzed samples were obtained from restaurants. In addition, we have observed a remarkable absence of appropriate sampling plans prior to sample collection.

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1. Introduction

Seafood is the most traded food commodity in the world. Its production has been steadily growing over the last decades, with notable progress in aquaculture over the past two decades, accounting for 42% of global seafood production in 2012 (FAO., 2014). According to the Food and Agriculture Organization (FAO), the world seafood production is close to 158 million tons, with 91.3 million tons of captures (inland and marine) and 66.6 million tons of total aquaculture (inland and marine). Furthermore, it was estimated that in 2012, 50% of the world's fisheries were at maximum exploitation levels and approximately 25% were over-exploited (FAO., 2014). Additionally, IUU (illegal, unreported and unregulated) fishing can lead to inadvertent overfishing, thus contributing to inaccurate estimates of exploitation rates. This might also include possible endangered marine stocks.

Mislabeling and erroneous identification of fish catches, or their geographical origin, is one of the factors involved in underreported exploitation of stocks and could threaten the sustainability of fisheries, therefore contributing to the depletion of fishery resources, or even the eventual extinction of the overexploited species (Agnew et al., 2009).

There is also a potential public health implications since mislabeled species may be toxic like some oilfish species (Cabrero, Hernández, Tango, Hillera, & Marcos, 2015) and puffer fish (Armani, Guardone, La Castellana et al., 2015).

Morphological characteristics are lost when fish are sold filleted while some others, such as color, might be unstable after freezing. Therefore, there is a need to apply currently available DNA analysis methods when visual methods are not good enough for species identification. PCR sequencing is indeed the most commonly used method in fish identification (Griffiths et al., 2014).

In the European Union the identification of seafood is mandatory, as stated in the Council Regulation (EC) No 1379/2013 of 11 December 2013 on the common organization of the markets in fishery and aquaculture products, amending Council Regulations (EC) No 1184/2006 and (EC) No 1224/2009 and repealing Council Regulation (EC) No 104/2000. These regulations require that seafood labels indicate the complete scientific name of the species (i.e. genus and species, Latin binomial nomenclature) without in-

ducing errors and in order to ensure a high level of protection for human health.

It has been repeatedly recognized that the use of common names or commercial designations to describe various fish types can hamper consumer choice, since this groups together species for sale that have markedly different prices. In this global chaos, the utilization of recognizable both locally and internationally names in seafood product labeling must be officially taken into consideration to ensure traceability in the seafood chain (Armani, Castigliego, & Guidi, 2012). However, "intentional" misdescription should be always considered as fraud or economically motivated adulteration (Spink & Moyer, 2011). For this reason, it is highly unlikely that mislabeling occurs by accident through misidentification by industry workers who handle these species on a daily basis (Miller, Jesse, & Mariani, 2012).

The purpose of the present review is to identify the levels of fraud as well as the more relevant gaps in research described in seafood mislabeling assessment articles published in peer-reviewed journals over the last five years.

2. Approach

Seafood misdescription incidents have been selected by performing a comprehensive analysis of the period 2010 to 2015. In total, 51 peer-reviewed journal articles have been selected. The databases used for the article selection were Science Direct, Web of Science, Google searches and PubMed. Keywords used for this search included: "fish", "seafood", "fraud", "authentication", "misdescription", "substitution", "mislabeling", "adulteration" and their combinations. Primary articles identified were also reviewed for relevant secondary cited references.

3. Origin of samples and sampling plan

The number of samples analyzed in this work was 4500. Studies vary in size, ranging from 5 to 386 samples and they have been conducted across all continents. Europe has the highest number of samples reported, comprising 60% of the total, followed by North America (14%) and Africa (13%). In terms of countries, United Kingdom (20%) has the highest number of sample studies on seafood mislabeling, followed by Spain (16%) and Italy (13%) (Fig. 1). The vast majority of studies (90%) focused their sampling efforts at the retail end of the supply chain, mainly supermarkets and fishmongers. Few studies (10%) used samples from hotels, restaurants and catering (HORECA) (Armani, D'Amico et al., 2012; Armani, Guardone, Castigliego, et al., 2015; Armani et al., 2013; Carvalho, Palhares, Drummond, & Frigo, 2014; Cawthorn, Duncan, Kastern, Francis, & Hoffman, 2015; Cline, 2012; Hanner,
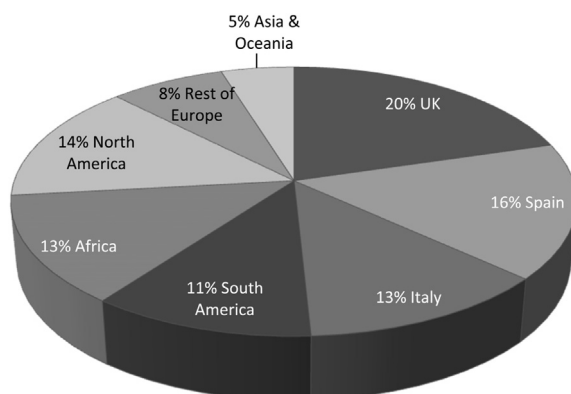
Becker, Ivanova, & Steinke, 2011; Heyden, Barendse, Seebregts, & Matthee, 2010; Khaksar et al., 2015). Most of these studies determined that HORECA mislabeling is significantly higher than that of supermarkets and retailers (Cline, 2012; Hanner et al., 2011; Khaksar et al., 2015). For instance, a higher rate of misdescription was recently identified in restaurants (14.8%) compared with retailers (2.2%) from the San Francisco Bay area in USA (Khaksar et al., 2015). Conversely, the misdescription rates reported in other studies described similar misrepresentation rates between restaurants and retailers (Armani, Guardone, Castigliego, et al., 2015; Cawthorn et al., 2015). In addition, some studies addressed other considerations such as the spatial distribution of sampling efforts among different areas representing varied demographic (Miller, Jesse, et al., 2012) or geographical characteristics (Cawthorn et al., 2015; Cawthorn, Steinman, & Witthuhn, 2012). Seasonal concerns were also addressed in some surveys (Carvalho et al., 2014; Hanner et al., 2011). Regarding the sampling plan, the estimation of the number of seafood samples required to conclude any percentage of fraud or misdescription in a given market, country or region was only specified in two references (Cawthorn et al., 2015; Changizi, Farahmand, Soltani, Darvish, & Elmdoost, 2013). Other authors indicated that the sampling plan was assessed "randomly" (Armani, Guardone, Castigliego, et al., 2015; Barbuto et al., 2010; Carvalho et al., 2014; E. Garcia-Vazquez et al., 2011; Pappalardo & Ferrito, 2015) but the majority of studies did not provide any information regarding the organization of the sampling plan. Finally, it must be highlighted that the name of the commercial products companies were not disclosed in any of the references included in this review to protect the confidentiality of the data.

4. Analytical methodologies

In recent years, DNA-based techniques have been widely used in species identification, including the assessment of mislabeling. DNA shows numerous advantages such as high stability and relative ease of isolation, even from highly processed foods. DNA-based methods show high sensitivity, specificity and reliability of results. In this sense, PCR-sequencing is the method most commonly employed (Griffiths et al., 2014).

Mitochondrial DNA (mtDNA) is a common target for species identification since mitochondrial sequences help to differentiate between closely relates species (Meyer, 1993). Most of the methodologies are based on mitochondrial DNA markers since they have a high number of copies per cell, facilitating the amplification. In general, Genbank and other public databases contain more sequences of mitochondrial genes than nuclear genes of fish. However, in the case of some tuna species, there is a problem of mitochondrial introgression that cannot be solved by mitochondrial markers and requires nuclear markers such as internal transcribed spacer 1 (*ITS1*) (Chow, Nakagawa, Suzuki, Takeyama, & Matsunaga, 2006). This region has been used in the genetic identification of other species suffering mitochondrial introgression events such as Arctic char and Brook trout, flounder and plaice (Gross, Gum, Reiter, & Kühn, 2004; Kijewska, Burzyński, & Wenne, 2009).

The most widely used identification technique by far is PCR-FINS (Forensically informative nucleotide sequencing); based on PCR amplification followed by direct sequencing of specific mitochondrial DNA markers like cytochrome *b* (*CytB*) (Armani, Castigliego, Tinacci, Gianfaldoni, & Guidi, 2011; Cutarelli et al., 2013; Espiñeira & Vieites, 2012a; Huang et al., 2014; Melo Palmeira et al., 2013) 16S rDNA (Melo Palmeira et al., 2013) and cytochrome *c* oxidase I gene (*COI*) (Hanner et al., 2011). The DNA barcoding method, based on the sequencing of a standardized region of the *COI*, has become a useful tool for ensuring the rapid and accurate identification of species. It is currently being used to differentiate animal taxa, including the authentication of fish and fish-derived products

Fig. 1. Representative pie chart showing the main fish surveys by regions.