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Title: Seventeen years analysing mislabelling from DNA barcodes: towards hake sustainability

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10   ABSTRACT
11   Mislabelling is a common threat to fisheries sustainability. Over the last decades, molecular
12   tools have been established as the main resource to detect mislabelling. This study focuses
13   on these efforts in the genus *Merluccius.* A meta-analysis approach is taken in order to
14   detect trends on mislabelling directions for the last 17 years. A total of 1291 DNA-identified
15   hake products from 45 different studies were compiled. An increase in number of
16   publications using DNA forensics to detect mislabelling in hake can be seen along the
17   studied time period. However, representation of different hake species varies, i.e. Pacific
18   hakes are underrepresented. Different risk of mislabelling has been identified depending on
19   the regions: Highest risk of mislabelling was found in African hake species (only 20.53% of
20   African hake were correctly labelled). Furthermore, a high amount of hake products with
21   incomplete labels (e.g. not reporting the species) were unevenly distributed. Directionality
22   in mislabelling was detected for all cases between sympatric species. Differences in
23   mislabelling rates were found for different regions (Africa, Europe, Pacific America and
24   South America). While a decrease in mislabelling was reported between 2011 and 2014, this
25   has not being sustained over time, as more recent data show an increase in mislabelling
26   rates. Altogether, rigorous monitoring of product authenticity is called for, with special
27   attention to the more vulnerable species.

28   *Keywords*: Mislabelling, Fraud, Hake, *Merluccius*, DNA-authentication, meta-analysis.

29

30   **1. Introduction**
31   Mislabelling and food fraud are high-profile issues that have been reported and covered
32   both in the media and by the academic community. It is a common concern affecting
33   different types of food products (Di Pinto et al., 2015; Stamatis et al., 2015). The seafood
34   sector is one of the most affected: instances of fraud have been widely reported (e.g.

35 (Bénard-Capelle et al., 2015; Galal-Khallaf, Ardura, et al., 2016; Guardone et al., 2017; Helyar
36 et al., 2014; Khaksar et al., 2015). Regulations of different countries demands products to be
37 correctly labelled. For instance, EU regulation (EU 1379/2013) requires fish labels to
38 individually identify each commercial seafood product to the species level. Labels under this
39 regulation must include a scientific name and a commercial designation according to a
40 standardized list with approved names in the official languages of the territories.
41 Information regarding production method and region and date of capture are also required.
42 However, these regulations are not always followed.

43 Illegal, unreported and unregulated fishing (IUU) constitutes about one-fifth of the
44 global catch (Flothmann et al., 2010). IUU products reach the market despite considerable
45 efforts made against them, for example, using eco-labels (Yokessa & Marette, 2019).
46 Evidences of commercial mislabelling hiding covered exploitation of substitute species
47 suggest that this practice happens worldwide (e.g. Ardura et al., 2010; Helyar et al., 2014;
48 Machado-Schiaffino, Martinez, & Garcia-Vazquez, 2008; Muñoz-Colmenero et al., 2017; Von
49 Der Heyden et al., 2010). If the product of IUU fishing is sold fraudulently mislabelled as
50 another species, it is impossible to determine the real catch, thus, hindering sustainable
51 management of the resource (Galal-Khallaf et al., 2016; Marko et al., 2011). Substitutions
52 from one species to another are frequent all along the supply chain (Helyar et al., 2014;
53 Muñoz-Colmenero et al., 2016). Hence, mislabelling is accumulative, and it is carried along
54 from the point where it takes place onwards, up to the final consumer's plate (Gordoa et al.,
55 2017). This is a serious threat for the sustainability of fishing resources, which has been
56 reported for different case studies; e.g. the high level of mislabelling in red snapper
57 (*Lutjanus campechanus*) inflates stock estimates, further damaging the already depleted
58 stocks (Marko et al., 2004; Spencer & Bruno, 2019).

59 Mislabelling is also a problem for the consumer when they buy a substitute species
60 instead of the desired one. Furthermore, inadequate labelling raises health concerns, as
61 potential allergens or unnoticed toxic species may pass unreported (Giusti et al., 2018;
62 Guardone et al., 2017; Muñoz-Colmenero et al., 2013; Sheth et al., 2010; Triantafyllidis et
63 al., 2010), as well as potential contaminants, which may be more frequent in certain areas
64 (Filonzi et al., 2010; Garcia-Vazquez et al., 2011). The economy and consumer's preferences
65 are often behind fish fraud, since substitutes are generally less appreciated species (Muñoz-
66 Colmenero et al., 2017). Moreover, mislabelling covering exploitation of vulnerable species
67 undermines consumer's awareness and conservation efforts (Cawthorn et al., 2011;
68 Christiansen et al., 2018; Garcia-Vazquez et al., 2012; Marko et al., 2011). Thus, it has not
69 only ecological but also social consequences (Crona et al., 2016; Lam & Pauly, 2010; Levin et
70 al., 2014; López de la Lama et al., 2018; Mariani et al., 2014).

71 DNA authentication of seafood products is key to detect mislabelling. It allows for
72 species identification even in processed products where species recognition by other
73 methods, such as morphological identification, would be impossible. Furthermore, DNA-

74 based identification methods require less taxonomic expertise and are easy and quick to
75 apply. While other authentication methods exist, i.e. protein based, or immunological
76 methods, the use of molecular tools has therefore been established as the main tool to
77 detect the mislabelling, allowing for a growing identification of fraud and the raise of
78 awareness against it. This may have an effect on mislabelling rates, that seem to decrease
79 over time, as suggested by Mariani et al. (2014) for cod. However, no standardized
80 procedure or routine genetic controls have been implemented. This has been pointed out
81 by experts (Barcaccia et al., 2016; Clark, 2015; Griffiths et al., 2014; Mariani et al., 2015;
82 Pérez et al., 2018), as well as advised by FAO (2018). Although not routinely applied, there is
83 abundant literature for the development of genetic markers and application of molecular
84 techniques for detecting mislabelling, with different methods and markers being developed
85 constantly (Böhme et al., 2019; Haynes et al., 2019).

86   In this review, we will focus on the genus *Merluccius* (Rafinesque, 1810), as it is of great
87 interest due to its high economic value. Hake is one of the most consumed fish in Europe,
88 especially in Spain, where most of the landings have been reported (Eurostat, 2020). The
89 family Merlucciidae -to which hakes (*Merluccius*) belong- is among the five taxa in which
90 mislabelling risk has been studied the most (Luque & Donlan, 2019). This genus comprises
91 12 species distributed along the Atlantic and the West and Southern part of the Pacific
92 Ocean. Total amount of hake landings pass the million tonnes per year. Currently, North
93 Pacific Hake (*M. productus*), Argentine Hake (*M. hubbsi*) and Cape hakes (*M. capensis* and
94 *M. paradoxus*) are the most caught species (FAO, 2020a), and many of the *Merluccius*
95 species have stocks under high fishing pressure (FAO, 2020b). Declines in their stocks have
96 occurred since the 1990s (Pitcher & Alheit, 1995). As they are sensitive to overfishing
97 pressure (H Arancibia & Neira, 2008), determining IUUs affecting them can play a significant
98 role on undermining stocks assessment and management decisions. Many of the hake
99 species overlap their range of distribution with at least another congeneric species (see the
100 geographic pattern of distribution in Fig. 2, as described in Pitcher & Alheit, (1995)), being
101 generally caught in mixed-stock fisheries. Due to this and their similar morphology,
102 accidental mislabelling occurs between sympatric species, e.g. *M. albidus* and *M. bilinearis*,
103 or *M. capensis* and *M. paradoxus* (Garcia-Vazquez et al., 2009, 2011; Machado-Schiaffino et
104 al., 2008; Muñoz-Colmenero et al., 2015)). However, fraud has been reported in several
105 species from different regions (Barendse et al., 2019; Cawthorn et al., 2015; Delpiani et al.,
106 2020; Muñoz-Colmenero et al., 2015; Pérez et al., 2018), as substitutions occur as well
107 between allopatric *Merluccius* species. First studies developing molecular markers in hake
108 oriented to detecting mislabelling are from the beginning of the 2000s (e.g. Castillo et al.,
109 2003; Perez & Garcia-Vazquez, 2004), and allowed for studies focusing in fraud at market
110 level, which have continued since.

111   Using a meta-analyses approach, the aim of this review is to depict a global picture
112 of labelling issues discovered from DNA-based authentication in hakes, to assess the
113 directionality of the mislabelling, and to identify which species are the most underreported

114 thus at risk of undetected overexploitation. Research gaps in the knowledge of commercial
115 fraud in the different species of hake and the evolution of mislabelling rates in the last
116 seventeen years have also been assessed.

117

2. Material and methods

119 *2.1 Data search and compilation*

120   In order to carry out a meta-analysis through relevant literature, key words were
121 employed to standardize the search and optimize the results. Google Scholar and Web of
122 Science were the engines employed for the literature search. We aimed at research articles
123 reporting molecular identification of mislabelling in *Merluccius* hake species. The key words
124 used were "Mislabelling", "Hake", "*Merluccius*", "IUU", "Molecular Markers", "Gadoids" and
125 "Fish fraud identification". Publications not including samples of the *Merluccius* genus were
126 not considered. In addition, articles which had been referenced in the reviewed literature
127 were also added.

128   The following data from each of the research articles analysed were compiled:
129 species reported on the label (both common name and scientific name); species assigned by
130 molecular tools; genetic marker employed; country of purchase of the product; sampling
131 year; reference article. Products were classed in one of these three categories: correctly
132 labelled, mislabelled, or incompletely labelled (for example not stating the scientific species
133 name or not reaching species level). All compiled data of labels and substitute species can
134 be found in an online repository (Blanco Fernandez et al., 2020).

135

136 *2.2 Data analysis*

137   Data from the different papers were combined in order to focus on different aspects
138 of problematic mislabelling cases. First, we analysed the commercial products by genetically
139 ascertained species. Samples were classified attending to the type of substitute species
140 assigned by DNA-based techniques. Substitute species were classified into the following
141 categories: "Different genus" i.e. not *Merluccius*, "Allopatric" i.e. *Merluccius* species with no
142 overlapping geographical distribution, and "Sympatric" i.e. *Merluccius* species exhibiting the
143 same or at least overlapping distribution. Since hakes of the genus *Merluccius* can be
144 morphologically similar, sympatric substitutions could be due to an accidental mistake in
145 sorting onboard, if the species are caught in mixed fisheries, or at landings. In contrast,
146 substitutions by an allopatric or a non-*Merluccius* species are more probably deliberate.
147 Results were analysed by region of origin of the species (Europe, Africa, South Atlantic
148 America, North Atlantic America and Pacific America).

149   To test the risk of mislabelling in each species, only the subset of data corresponding
150 to complete labels – to a species level- was employed. Rates on mislabelling along time

were analysed according to the year of sample collection. Samples were grouped in four time intervals comprehending similar time spans (2002-2006, 2007-2010, 2011-2014 and 2015-2019), and analysed by regions. In the case of those articles that did not state the year, we assumed samples to have been collected the year before publication. Time intervals were optimized to include as many studies as possible. For this analysis, three studies carried out along a span of several years without individual sample dating were excluded: Borrell et al., (2016); Shehata et al., (2018); Stamatis et al., (2015).

2.3 Statistics

The substitution status identified from DNA (number of samples containing: the same genus and distribution as sympatric; same genus and different distribution as allopatric; a different genus; mixed or ambiguous species; no substitutes) was compared between species using principal component analysis (PCA) with correlation option. The relative contribution of each type of substitutions (no substitution or correct, sympatric, allopatric, mixture, other genus – no *Merluccius*) to the variance of the metadata set was assessed from loadings. Components 1 and 2 were plotted to visualize the relationships among variables and how different hake species were distributed according to their mislabelling. The different substitutions were plotted as diagonals with length proportional to the respective weight in the analysis.

Contingency chi square tests were performed for every regional group of species to test for differences among periods in the proportion of mislabelled (versus correctly labelled) samples i.e. if there was a temporal change in mislabelling in any region. Statistics was performed with PAST free software (Hammer et al., 2001).

3. Results

3.1 Data overview

Using the key words indicated above we retrieved 45 articles spanning 2003-2020. In these articles, 1291 commercial hake samples were analysed and provided 1452 individuals or pieces genetically ascertained. Samples were originated from a total of 22 countries, although not evenly distributed, as most of the samples came from Spain (n=660), followed by Italy (n=156), South Africa (n=91) and Portugal (n=73). The interest in hake mislabelling is reflected in a significant increase of publications over time (linear trend y=0.0058x with r=0.52, 18 d.f., p=0.026), and of commercial products analysed (y=0.0065x + 0.0066 with r=0.67, 18 d.f., p=0.002), with a valley in 2013-2014 and further sustained growth (Fig. 1). The search was done in July 2020, thus the real figure of 2020 could be higher.

Samples were identified at species level using either individual or a combination of different molecular markers: the mitochondrial 16SrDNA (used in 1.8% of products), Cytochrome b (49.1%), cytochrome oxidase subunit 1 or COI (63.5%), and Control Region (5.3%); and/or the nuclear ITS1 (3.6%) and 5SrDNA (25.1%). Of all samples identified from DNA, 1097 were labelled down to a *Merluccius* species level, while the rest were incomplete (i.e. "Hake" or "*Merluccius* spp") or incorrectly labelled as a different genus. Most samples with species labels corresponded to *M. merluccius* (European hake) (n=207), *M. bilinearis* (Silver hake) (n= 172; 171 from a single study (Garcia-Vazquez et al. 2009)), and *M. hubbsi* (Argentine hake) (n=172). South African *M. paradoxus* (Deep water Cape hake) and *M. capensis* (Shallow water Cape hake) samples were abundant as well, although many were ambiguously labelled with both scientific names together. The Pacific hakes *M. productus* (North Pacific hake) and *M. gayi* (South Pacific hake) were underrepresented with only 55 and 39 samples, respectively.

3.2 Incomplete labels

Considering all the compiled data, only 761 out of 1291 hake products were completely labelled down to a single species level (either correct or incorrect from DNA analyses). Products with no clear specification of the fish group (n=28) or simply labelled as "fish" (n=4) were identified as several *Merluccius* species (*M. productus*, *M. bilinearis*, *M. paradoxus*, *M. merluccius*, *M. hubbsi*, *M. gayi*). A total of 307 products exhibited labels at a genus level, stated either as *Merluccius* spp. or as generic, common or vernacular names (i.e. "Merluza", "Bakalairos" (Triantafyllidis et al., 2010), or "European Hake"). Species contributing to incomplete labels were principally *M. paradoxus* (31.57%), *M. hubbsi* (17.74%), M. *productus* (7.37%) and *M. capensis* (6.45%). Other samples were ambiguously labelled as mixes of different species: particularly, Cape hakes *M. paradoxus* and *M. capensis* were labelled as *M. capensis*/*M. paradoxus* in 182 products. From those, 88 products were genetically identified as one of the two species. This group was highly skewed towards *M. paradoxus*, which accounted for 87.5% of the samples identified from DNA.

3.3 Mislabelling risk by species

The different DNA-ascertained hakes found in this study had different risks of being used as a substitute species (Table 1). For this analysis, we considered only those products identified as a single *Merluccius* species by DNA analysis (n=1079 products), excluding those containing mixes of species (see Table 2).

In general, mislabelling risk varied among species (Fig. 2). Higher risk of being employed as a substitute was found for African species (only 22.52% of the products containing African species were correctly labelled) and American Pacific ones (45.07%

correctly labelled) than for species native to other regions (Table 1). For example, more than 83% of the European *M. merluccius* were not substitutes of any other species. In contrast, the highest risk of a species to be a substitute was found for *M. paradoxus*, for which only 9.2% of the products were correctly labelled (226 out of 249 products were incorrectly labelled, the majority as mixtures of species or ambiguously labelled as *M. capensis/M. paradoxus*).

Merluccius angustimanus (Panama hake), *M. polli* (Benguela hake) and *M. albidus* (offshore silver hake) were not reported on any label. However, both *M. albidus* and *M. polli* were found from DNA assignations as substitutes of sympatric species (20 products in total, 10 of each species; note the small sample sizes). *M. albidus* was a substitute of *M. bilinearis* and *M. polli* of *M. senegalensis. M. angustimanus* appeared in two products labelled as *Gadus* sp. (Cod). Since *M. angustimanus* and *M. albidus* were not found as substitutes of allopatric species (Table 1), we could infer that the particular mislabelling found in Panama and offshore silver hakes is probably accidental.

In the case of sympatric species (see Fig. 2), the risk of substitution was asymmetrical; in other words, directional mislabelling was found. In the pair of North American hakes *M. albidus/M. bilinearis*, *M. albidus* was the substitute. In the triplet *M. merluccius/M. senegalensis/M. polli*, *M. polli* was the substitute species. In the *M. capensis/M. paradoxus* pair, the latter species was the main substitute. In sympatric South American hakes, *M. hubbsi* was the main substitute of *M. australis* but not the other way around (Fig. 2). On the other hand, substitution of allopatric species occurred for most species, up to 23.1% in the case of *Merluccius australis* (Table 1).

Merluccius species also appeared as substitutes of other fish in a few samples (N=16; Table 1). *M. merluccius, M. paradoxus, M. hubbsi, M. gayi, M. productus* and *M. angustimanus* were sold as substitutes of cod (as seen above), *G. chalcogrammus* (Alaska Pollock), *Pleuronectes platessa* (European plaice), *Sarda* (Tuna) and *Solea solea* (Common sole). Reciprocally, 40 products labelled as hakes contained substitutes belonging to other genera of Gadiformes (*Gadus chalcogrammus*, *Gadus morhua*, *Macruronus magellanicus*, *M. novaezelandiae*, *Coryphaenoides acrolepis*, *Phycis phycis*, *Pollachius virens,* and *Urophycis tenuis*), also Scombriformes (*Thunnus* sp.*, Katsuwonus pelamis*), Perciformes (*Dissostichus eleginoides*), Pleuronectiformes (*Limanda aspera*) and Siluriformes (*Pangasianodon hypophthalmus*).

The situation of each species regarding its use as a substitute of other species –which can endanger its conservation- can be seen in the PCA plot (Fig. 3). PC1 and PC2 explained more than 80% of the total variance (Table 3). Allopatric substitutions and mix/ambiguous labels had higher weights in PC1 and correct labels and non-*Merluccius* substitutions in PC2, indicating greater differences among species for these types of mislabelling than for sympatric substitutions. In Fig. 3, it is possible to observe that the European *M. merluccius* is

in quadrant I close to the diagonal representing correct labelling, while the Argentinean *M. hubbsi* is in the same quadrant but in the middle of non-*Merluccius* and allopatric substitutions. *M. paradoxus*, together with *M. capensis* in quadrant IV, is clearly weighting for sympatric substitutions and mix/ambiguous labelling. Quadrant II contains *M. bilinearis* and *M. gayi* that are substitutes of other *Merluccius* in none or very few products, being instead used in species mixes or ambiguously labelled products. The species under-represented in the collection of articles analysed are located together in quadrant III of the plot: *M. angustimanus, M. albidus* and *M. polli*. They share the plot with *M. senegalensis, M. productus* and *M. australis*, all of them with intermediate levels of correct labelling and not used in sympatric substitutions (Fig. 3).

3.4 Evolution of mislabelling rate

A total of 1079 samples were included in this analysis after excluding samples that could not be assigned to a time period. As it can be seen in Fig. 4, commercial hake mislabelling seems to be increasing at a global level over the last decade, being that increase statistically significant (Table 3). Mislabelling decreased in 2011-2014 in comparison with the 2007-2010 period (even more in South American hakes), but increased again in 2015-2019 (Fig. 4, Table 3). However, the evolution was not the same for all the species. Significant temporal changes across the studied periods (2002-2006, 2007-2010, 2011-2014 and 2015-2019) were found for species native to all the regions except for Atlantic North American hakes. It should be noted that Atlantic North American and Pacific samples were unequally represented among time periods in this meta-analysis, with some periods in blank (Table 3).

In the specific case of African species, the recent increase (2015-2019) of incorrect labelling (Table 3) included an increase of products not labelled down to species level, principally of the most exploited African hakes, *M*. *capensis* and *M*. *paradoxus*. However, even when the 98 products labelled as mixed cape hakes are taken out of the analysis, the increase in mislabelling rates is still significant (Chi-square = 25.909, $p \ll 0.001$).

In the case of South American and European species, the changes of mislabelling along the timeline were parallel with the mentioned valley for the period 2011-2014. Mislabelling was higher in South American hakes, with more than 40% found in 2007-2010, while in European *M. merluccius* it was near 20% (Table 3).

4. Discussion

In this study we have detected several facts of importance regarding the accuracy of labelling in commercial hake. The first evidence is that, after a period of apparent and significant reduction of mislabelling in the period 2011-2014, it is increasing again in the last

years. This is a call of attention that indicates the need for a more strict control of marketed hake. The decrease of mislabelling by 2014 could perhaps be explained from a significant number of articles followed by press releases between 2008 and 2012 that revealed high level of fraud in hake markets in the previous years (e.g. Triantafyllidis et al. 2010, Garcia-Vazquez et al. 2011, Cawthorn et al. 2012 and others). Mariani et al. (2014) found that media attention on the results of forensic analysis of marketed cod was followed by significant improvement in cod labelling, and our results in hake would concur with theirs. In addition, the appearance of strict EU legislation about seafood labelling in 2013 could also contribute to explain the decrease of mislabelling around that date.

Mislabelling being a discrepancy between a commercial product and its label, indeed, depends on the information that must be displayed on the label. However, labelling related laws are heterogeneous, and vary from one country to another. The European Union has common legal frames for seafood labelling with strict label requirements. European Regulation (EU) 1379/2013 requires labels to provide the scientific name of the species as well as a commercial denomination (common name). However, despite common regulation, there is a lack of harmonization and standardization across the EU and each country may implement control measures differently (Griffiths et al., 2014). In the U.S., Food and Drug Administration (FDA) establishes the obligation of identity labelling in food commodities (Code of Federal Regulations CFR Title 21 Subchapter B Part 101 – Food Labelling, and Part 123 Fish and Fishery Products), with a common name that must appear in the list of recognized species with their scientific names. On the other hand, regulation is scarce in some regions. For instance, many regulations do not require adding the species name but only a list of accepted species that fall under a wider term (i.e. "Hake" for all *Merluccius* species; (Hofherr et al., 2016)). An important source of uncertainty found in this study comes from incompletely labelled products. While regulations vary widely between countries, allowing for common names in the labels that may include several species, incomplete labels are present in countries (e.g. Italy and Spain) where the scientific name of the species is required by current regulations.

Within the *Merluccius* genus, we found that some North Atlantic species (European and Silver hakes) are relatively rare as substitute species, while African species and North Pacific hake have much higher risk of appearing as substitutes of other species or be ambiguously labelled. Reasons for high risk of mislabelling are varied: accidental misclassification of species that are fished together; deliberate fraud for purposes of catching over quota; obtaining higher economic benefit when the label species is more expensive than the substitute; exploiting protected species, and more (e.g. Donlan & Luque, 2019; Muñoz-Colmenero et al., 2015). In the market, European hake is generally more expensive than the African species (Muñoz-Colmenero et al. 2015), thus its lower use as a substitute can be easily explained by economic reasons. *M. bilinearis* has been sold occasionally as a substitute of the more expensive *M. merluccius* (Sánchez et al., 2009), but given its smaller size (commonly 37 cm in average versus 45 cm of *M. merluccius*, 50 of *M. capensis* or 80 of

341 *M. australis*; Cohen et al. 1990) it is not the best substitute of larger and more appreciated
342 species.

343   Since most samples were purchased in Europe, the conclusions of this meta-analysis
344 should not be taken as universal. Mislabelling may differ greatly in other regions that have
345 been less studied, thus mislabelling in the species marketed there may be overlooked. This
346 would be the case for Pacific hake species that are underrepresented in this meta-analysis in
347 comparison to catch reports. For example, *M. productus* catch was 299270 tonnes between
348 2014 and 2017 (FAO, 2020a). Only 47 products of this species are represented in this review;
349 in contrast, for the same period we found 172 samples of *M. merluccius* analysed
350 forensically while the catch of this species was 104180 tonnes, less than one half of *M.*
351 *productus* catch. Increased efforts in DNA analysis of Pacific species would be
352 recommended.

353   The prevalent use of incomplete labels hinders sustainability of affected fisheries
354 (Cawthorn et al., 2012). This is well documented for Cape hakes, which are usually managed
355 as a single stock (FAO, 2011; Wilhelm et al., 2015). Typically, *M. paradoxus* has been
356 described as the predominant landings in the eastern and south coast, and *M. capensis* in
357 the west coast of South Africa (FAO, 2011). However, this is not supported by the data, as
358 there is an unbalance in the occurrence of both species in products identified from DNA that
359 could not be explained from the reported catches. Managing two species together without
360 accounting for their differences in biology and ecology may lead to an overestimation of the
361 available stock (Kathena et al., 2016). This is likely to occur for all overlapping species and
362 has been reported for other taxa where species that are morphologically similar are caught
363 together (Crego-prieto et al., 2010; Iglésias et al., 2010). In particular, special focus should
364 be put on hakes whose distributions largely overlap, like silver hakes in the west North
365 Atlantic and all the African hakes. Moreover, there was no record of products labelled as *M.*
366 *polli*, *M. angustimanus* or *M. albidus* although we found those species from DNA analyses.
367 Special efforts should be made to cover these species.

368   In our meta-analysis we focused on hake products marketed for human consumption.
369 However, the presence of hakes in products destined to other uses may go unnoticed. For
370 example, forensic studies on fish meals are scarce, although the content of the pellets is
371 frequently not disclosed and may hide the use of overexploited or endangered species (A
372 Ardura et al., 2012; Galal-Khallaf, Osman, et al., 2016; Martín et al., 2010; Pegels et al.,
373 2013; Prado et al., 2012; Vlachavas et al., 2019). Thus, we would encourage the analysis of
374 fishmeal pellets DNA using specific primers to detect hake species. On the other hand, other
375 types of products may contain hake, like those based on gelatin (e.g. candies and other
376 foodstuffs); Muñoz-Colmenero et al. (2016) found traces of different hakes in marshmallows
377 and jelly gummies. Expanding forensic analysis of these and other commodities would also
378 be recommended for detection of commercial niches where hake is actually employed,
379 declared or not.

380   Correct fisheries management is essential for the sustainability of the stocks. This
381   includes detecting IUUs, as can be done from forensic analysis of commercial products
382   (Ogden, 2008). Signs of improvement reported for some hake fisheries by 2014 (e.g. *M.*
383   *merluccius* and *M. hubbsi*; (Antelo et al., 2012; Lorenzo & Defeo, 2015), coinciding with
384   lower mislabelling detected in our analysis, do not seem to be maintained for the later years
385   (2015-2019). Precisely in these years mislabelling increased again in Africa, Europe and
386   South Atlantic America (Fig. 4). Indeed, this is just an observation and cause-effect cannot
387   be inferred from it, but a continuous monitoring of the label accuracy is called for in order
388   to avoid irreparable declines in stock resources. The conservation status of *Merluccius*
389   species is diverse, as their fisheries are. *M. senegalensis* is considered as endangered species
390   (Iwamoto, 2015c), while *M. merluccius* is vulnerable (Di Natale et al., 2011), and *M.*
391   *bilinearis* is near threatened (Carpenter, 2015). In the case of *M. gayi,* the data is deficient
392   (Iwamoto, T., Eschmeyer, W., Alvarado, J., Bussing, 2010a) to evaluate its status. The status
393   of *M. australis*, *M. hubbsi* and *M. paradoxus* are not evaluated yet, and the rest are of
394   species are considered of least concern (*M. angustimanus* (Iwamoto et al., 2010), *M.*
395   *productus* (Iwamoto, T., Eschmeyer, W., Alvarado, J., Bussing, 2010b), *M. capensis*
396   (Iwamoto, 2015a), *M. polli* (Iwamoto, 2015b) and *M. albidus* (McEachran & Polanco
397   Fernandez, A Russell, 2015). At least the species catalogued as endangered, vulnerable and
398   near threatened, i.e. *M. senegalensis*, *M. merluccius* and *M. bilinearis*, should be targets of
399   specific campaigns for forensic control of mislabelling.

400

5. Conclusions

402   After a decline in mislabelling rates from 2011 to 2014, our data shows a new rise in
403   recent years. All *Merluccius* species are not equally affected by mislabelling; species from
404   Africa and from the Pacific seem to be used as substitutes more frequently. Furthermore,
405   special attention must be given to incomplete labelling, which is a great source of
406   uncertainty, masking mislabelling between sympatric species and hindering correct
407   management of stocks. Notoriously, this is reflected for Cape hakes, where DNA
408   identifications found deep Cape hake to be the predominant species in commercial
409   products, despite this not being reflected in catches reports. More research is needed for
410   other species, particularly; Pacific hakes appear underrepresented, as well as species with
411   lower commercial interest, i.e. *M. polli*. Ensuring the correct labelling of products helps the
412   detection of IUUs, hence stricter labels and monitoring should be implemented with special
413   attention to threatened species. There is an urgent need for an international harmonization
414   in seafood labelling, in order to have a better control of mislabelling to ensure consumer
415   rights and fisheries sustainability worldwide.

CRediT authorship contribution statement

Carmen Blanco-Fernandez: Conceptualization, Methodology, Data curation, Formal analysis, Writing - original draft. **Eva Garcia-Vazquez**: Conceptualization, Formal analysis, Writing - review & editing, Supervision, Funding acquisition. **Gonzalo Machado-Schiaffino**: Conceptualization, Methodology, Writing - review & editing, Supervision, Funding acquisition.

Declaration of competing interest

The authors declare that there is no conflict of interest.

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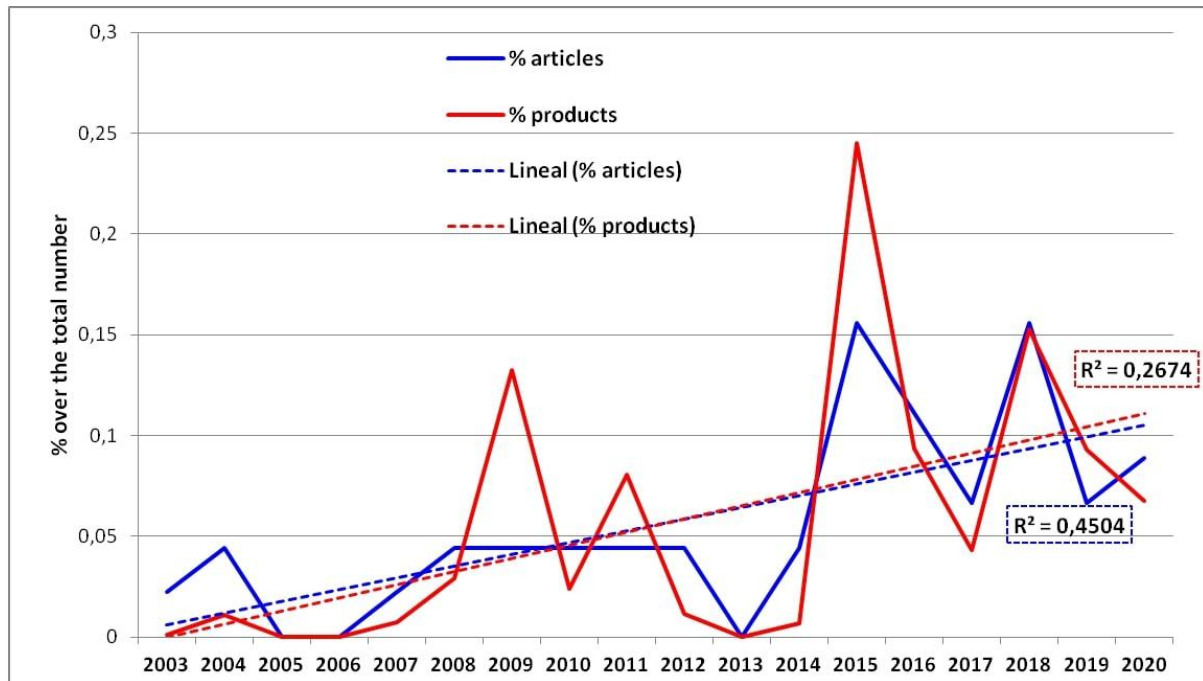720   https://doi.org/10.1561/101.00000107

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Figures

Fig. 1. Evolution of publications about hake mislabelling in the two last decades, presented as the proportion of the total number of articles published and products analysed between 2003 and 2020 by year.
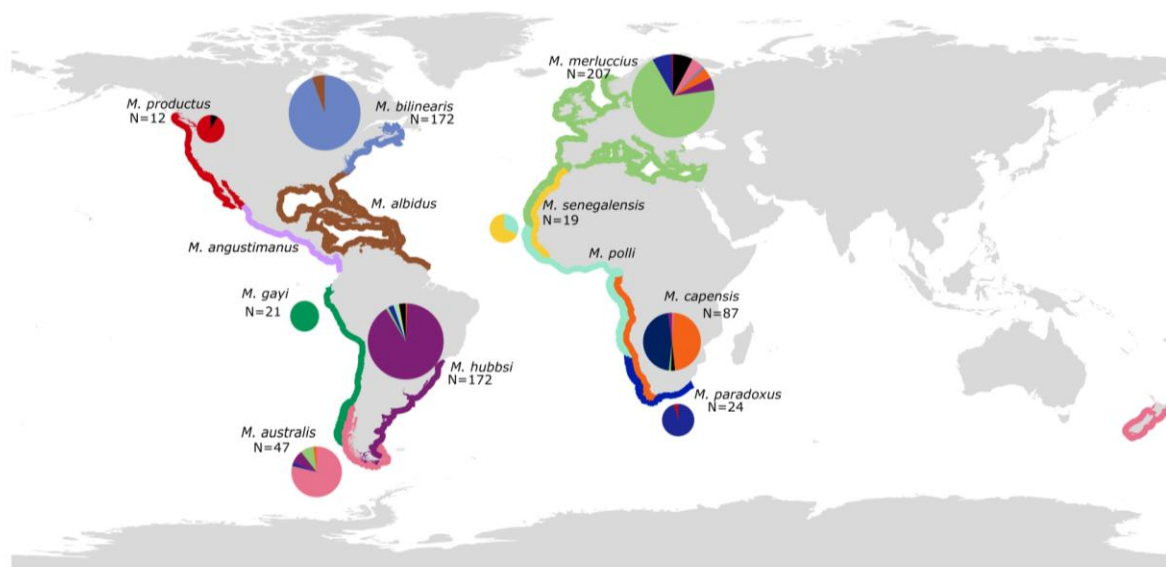

Fig. 2. Meta-analysis of mislabelling in individual commercial hake samples (total N = 761) identified from DNA. Pie charts represent the proportion of each DNA-authenticated species marketed under the same species name. Colour codes of DNA-identified species: *Merluccius*

albidus (brown), *M. angustimanus* (light purple), *M. australis* (pink), *M. bilinearis* (light blue), *M. capensis* (orange), *M. gayi* dark (green), *M. hubbsi (*dark purple), *M. merluccius* (light green), *M. paradoxus* (dark blue), *M. polli* (blue green), *M. productus* (red). The distribution of each species is shaded with the same colour codes.

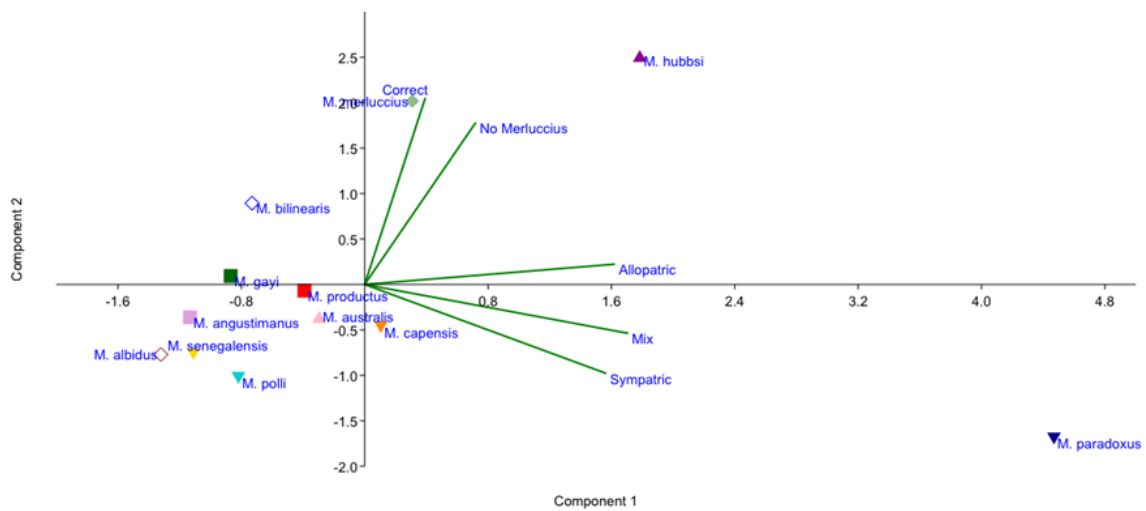**Fig. 3.** PCA scatter plot showing the different *Merluccius* species in relation to the five types of substitution considered (no substitution or correct labelling, substitutes of sympatric, or allopatric species, substitutes of species of another genus or no *Merluccius*, ambiguously labelled as a species mixture or "mix"). Diagonals are proportional to the relative weight of each type of substitution in the analysis.
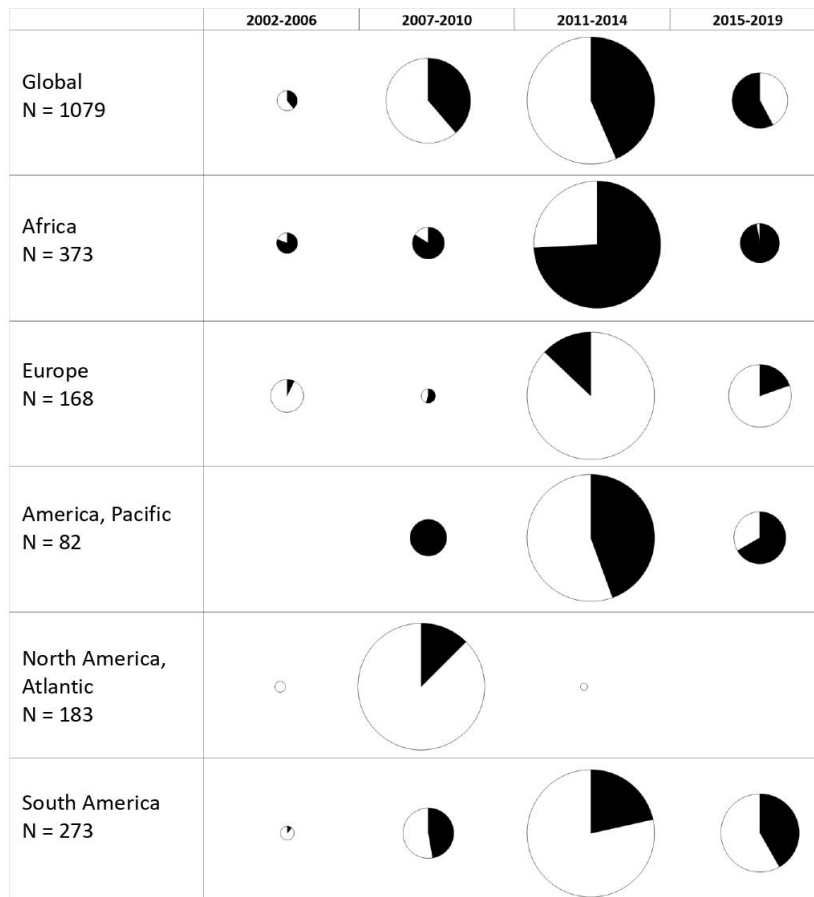
Fig. 4. Evolution of mislabelling by geographic region over the last 17 years. White represents correct labels and black is mislabelling. Pie sizes are proportional to the sample sizes. Mislabelling includes incomplete labels and labels indicating different species.

–Table 1. Hake mislabelling by species, presented as % of mislabelling in samples ascertained from DNA. Categories for each species (as determined by DNA analyses) include different types of labelling: hake samples which were mislabelled outside of *Merluccius* genus, samples mislabelled as an allopatric *Merluccius* species, samples mislabelled as a sympatric species, samples with a label which does not indicate species, and correctly labelled samples. N corresponds to the total amount of sample products which have been identified by DNA as each *Merluccius* species. Species' regional distribution is provided: Africa, Europe, Atlantic North America, Pacific North America and South America; as well as the total mislabelling per region counting all species of the region (in bold). Allopatric *Merluccius*: no overlapping distribution, versus a sympatric *Merluccius* species. Raw data can be found in the repository table (Blanco Fernandez et al., 2020).

DNA identified species	Incorrect labelling				Correctly labelled	N (sample size)
	A different genus (%)	Other *Merluccius* (no overlapping distribution)	Other overlapping *Merluccius* species	Label does not contain a single species name		
Africa	**0.53**	**9.60**	**12.27**	**57.07**	**20.53**	**375**
M. senegalensis	0.00	4.17	0.00	41.67	54.17	24
M. polli	0.00	30.00	60.00	10.00	0.00	10
M. capensis	0.00	12.64	0.00	45.98	47.13	92
M. paradoxus	0.80	8.43	16.06	65.46	9.24	249
Europe	**2.91**	**4.65**	**0.00**	**9.30**	**83.14**	**172**
M. merluccius	2.91	4.65	0.00	9.30	83.14	172
America, Pacific	**9.76**	**3.66**	**0.00**	**47.56**	**39.02**	**82**
M. angustimanus	100.00	0.00	0.00	0.00	0.00	2
M. productos	6.38	6.38	0.00	63.83	23.40	47
M. gayi	9.09	0.00	0.00	27.27	63.64	33
North America, Atlantic	**0.00**	**1.09**	**5.46**	**4.92**	**88.52**	**183**
M. albidus	0.00	0.00	100.00	0.00	0.00	10
M. bilinearis	0.00	1.16	0.00	5.20	93.64	173
South America, Atlantic	**2.46**	**9.82**	**1.40**	**18.60**	**67.72**	**285**
M. australis	0.00	23.08	0.00	5.77	71.15	52
M. hubbsi	3.00	6.87	1.72	21.46	66.95	233

Table 2. Principal component (PC1, PC2 and PC3) Eigenvalue, % of the total variance and loadings. The substitution types most contributing to each component are marked in bold.

	PC 1	PC 2	PC 3
Eigenvalue	2.7	1.52	0.49
% variance	54.1	30.5	9.9
No *Merluccius*	0.244	**0.604**	**-0.754**
Allopatric	**0.551**	0.076	0.252
Sympatric	0.532	-0.332	-0.022
Mix	**0.58**	-0.183	-0.041
Correct	0.133	**0.697**	**0.605**

Table 3. Evolution of mislabelling by geographic region over the last 17 years. Mislabelling is given in percentage (%) over the total number of samples analysed each period (N), and includes incomplete labels and labels indicating different species. Contingency Chi-square value and its associated p is given. Significant p-values are in italics.

		2002-2006	2007-2010	2011-2014	2015-2019	Chi square	*p*-value
Africa	N	47	62	192	72	23.38	*3.37E-05*
	%	80.85	83.87	70.83	97.22		
Europe	N	28	9	85	46	13.09	*0.004*
	%	7.14	55.56	12.94	19.57		
America (Pacific)	N	0	16	45	21	15.69	*0.0004*
	%	-	100	44.44	66.67		
North America (Atlantic)	N	14	168	1	0	2.12	*0.35*
	%	0	12.5	0	-		
South America	N	18	55	121	79	19.16	*0.0002*
	%	11.11	47.27	21.49	41.77		
GLOBAL	N	107	310	444	218	21.19	*9.60E-05*
	%	39.25	38.71	43.47	57.80		