A meta-review of DNA-based identification methods and mislabeling analysis of Eastern South Pacific seafood

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Abstract

The Eastern South Pacific Ocean is a nutrient-rich and highly diverse region that plays a pivotal

role in the global seafood trade. Despite its importance, the seafood industry in this region is

hindered by complex supply chains and insufficient regulation frameworks, which facilitate

illegal practices, including mislabeling. DNA-based methods have emerged as essential tools

for seafood authentication, helping to mitigate mislabeling and supporting conservation

strategies. This study provides the first comprehensive review of DNA-based methods used

globally to identify seafood species from the Eastern South Pacific Ocean. Historical and

current techniques were systematically examined, with a focus on emerging technologies that

offer promising applications in the field. Nearly three decades of research have enabled the

successful identification of over 200 commercially valuable species using more than ten

distinct DNA-based methods. Fish and mollusks constituted the most extensively studied

seafood groups, with DNA sequencing emerging as the predominant technique. Furthermore,

a global mislabeling meta-analysis, encompassing 1,806 seafood products from the Eastern

South Pacific Ocean, revealed an estimated mislabeling rate of 24.8% (95% CI [22.9-26.9]).

Notably, a substantial proportion of mislabeled and substituted products corresponds to highly

threatened shark species. This raises serious conservation concerns, particularly given that

nations bordering the Eastern South Pacific Ocean are major players in the global shark trade.

Overall, the findings of this review underscore the urgent need to integrate advanced DNA-

based techniques into existing regulatory frameworks. They also establish a solid foundation

for developing targeted policies and encouraging collaborative efforts among nations in this

region.

Keywords: Molecular identification, seafood fraud, meta-analysis, South America

1. Introduction

Fish and seafood products have become some of the most traded commodities around the world, with an estimated annual production value of US$ 472 billion (Hellberg, 2024; Lawrence et al., 2022; FAO, 2024). During 2022, seafood contributed an estimated 20.7 kg per capita and provided about 15% of the world´s animal protein supply (FAO, 2024). A significant portion of this production comes from the coastal and oceanic fisheries of the eastern South Pacific Ocean (hereafter referred to as ESPO). In 2021, landings from the ESPO reached 10 million tons, accounting for 12.5% of global landings (FAO, 2024). Marine ecosystems in the ESPO are characterized by nutrient-rich waters and highly productive coastal upwelling zones. These factors make the ESPO one of the most productive marine systems in the world, exhibiting extremely high primary productivity that supports a rich and diverse array of marine life (Gonzalez et al., 2019; Serratosa et al., 2020).

Despite management efforts, several fisheries in developing countries, including those bordering the ESPO region, suffer from weak regulatory systems, wildlife trafficking, and high levels of illegal, unreported, and unregulated (IUU) fishing (Marín et al., 2018; De la Puente et al., 2020; Gozzer-Wuest et al., 2023). These issues create opportunities for deceptive practices such as mislabeling and species substitution throughout the supply chain (Lawrence et al., 2022). Seafood mislabeling not only undermines conservation and sustainability initiatives, but it also poses risks to consumers' health, economic well-being, trust, and even religious beliefs (Marín et al., 2013; Silva & Hellberg, 2021; Neo et al., 2022).

In this context, accurate species identification of commercially important marine resources is a crucial step toward effective management and prevention of dishonest practices. Although some seafood species are easily recognized, many marine organisms undergo various adaptive evolutionary processes that complicate their morphological differentiation. These processes include convergent phenotypic evolution, interspecific conservatism, phenotypic plasticity,

hybridization, and morphological variation within species (Pérez-Jiménez et al., 2005; Hanner

et al., 2011; Mynhardt et al., 2014; Pliego-Cárdenas et al., 2016; Neves et al., 2021; Marín et

al., 2022). Furthermore, most processed and cooked seafood products lack distinctive

morphological features, making them unsuitable for identification through conventional

taxonomic methods. To address this issue, several alternative molecular identification methods

have been developed, which are independent of morphological characters and have proven to

be effective for identifying both fresh and processed seafood species (Ali et al., 2012; Lago et

al., 2014).

Recent advances in molecular biology have led to the development of various accurate and

sensitive methods that can of identify organisms at the species level, even from highly

processed samples or minuscule amounts of tissue. Consequently, a range of analytical

techniques based on proteins and DNA have been employed to authenticate seafood products

(Ali et al., 2012; Lago et al., 2014; Silva & Hellberg, 2021). However, the heat-labile nature

of most proteins limits the applicability of protein-based techniques to fresh or lightly

processed seafood samples (Teletchea, 2009; Silva & Hellberg, 2021; Aditi et al., 2024). In

contrast, DNA is more resistant to heat degradation, making it suitable for analyzing highly

processed seafood products, such as canned or cooked items. This advantage allows DNA

techniques to overcome the limitations associated with protein-based methods (Teletchea,

2009). Furthermore, DNA can be PCR-amplified from very small amounts of starting material,

which can be collected from virtually any organic substrate, including fins, blood, mucus, and

bones (Teletchea, 2009; Silva & Hellberg, 2021; Aditi et al., 2024).

Although some comprehensive reviews have discussed DNA-based techniques for global

seafood authentication and mislabeling (Teletchea, 2009; Ali et al., 2012; Lago et al., 2014;

Pardo et al., 2016; Luque & Donlan, 2019; Silva & Hellberg, 2021; Aditi et al., 2024), most of

the reviewed studies from South American countries are primarily focused on research

conducted in Brazil, which examines species from the western South Atlantic Ocean. In

contrast, reviewed studies addressing seafood species from the ESPO region remain

underrepresented. There is a noticeable lack of reviews on DNA detection of seafood diversity

and mislabeling rates in articles from ESPO nations, despite the region´s rich marine

biodiversity, significant wild-capture and mariculture production, and the wide variety of

seafood products that these nations offer commercially around the globe.

This review provides a comprehensive overview of both past and present DNA-based methods

used to identify commercially important species from the ESPO region. It offers a summary of

the techniques, DNA markers, and oligonucleotide primers found in the reviewed literature.

This review also intends to examine the ESPO's species diversity that has been identified using

DNA methods, presenting the most current database of commercially significant species

accompanied by molecular identification records. Furthermore, I performed an analysis of their

current conservation statuses based on information from the International Union for

Conservation of Nature (IUCN). Lastly, a systematic meta-review of seafood mislabeling was

conducted based on data sourced from the surveyed articles, which feature samples collected

from both domestic and international markets where ESPO species are sold.

2. Materials and methods

2.1 Data collection and inclusion criteria

This study is based on an exhaustive analysis of peer-reviewed papers published between mid-

December 1998 and early July 2025. The Level 1 screening focused on articles that report the

development and application of DNA-based tools for identifying commercial marine samples

from fisheries and mariculture within the ESPO region. Samples were collected throughout the

seafood supply chain, including fish landings, farms, curing facilities, wholesale fish markets,

manufacturers, fishmongers, local markets, supermarkets, ethnic markets, restaurants, and

exporters in ESPO's countries and international markets. Articles that originated outside the ESPO's countries were included only if they analyzed products that contained declared species from the ESPO region, specifically those identified as imported commodities. Relevant research articles were sourced from multiple databases, including Google Scholar, Direct, PubMed, ResearchScience, SciELO, and Scopus, using the following search terms (in both English and Spanish): "canned" OR "crab" OR "crustaceans" OR "fish" OR "fish market" OR "gastropods" OR "DNA barcoding" OR "DNA meta-barcoding" OR "DNA-based techniques" OR "DNA-sequencing" OR "High-throughput sequencing" OR "mislabeling" OR "molecular identification" OR "molecular markers" OR "mollusks" OR "polymerase chain reaction (PCR)" OR "protected marine species" OR "qPCR" OR "seafood authentication" OR "seafood fraud" OR "seafood supply chain" OR "sharks" OR "shellfish" OR "species identification" OR "species-specific primers" OR "Eastern South Pacific" OR "South America" OR "Chile" OR "Colombia" OR "Ecuador" OR "Peru". Cited references from the identified articles were also reviewed to find related papers not identified in the initial search.

The most targeted studies focused on developing molecular markers and applying DNA-based identification tools for seafood authentication and detecting mislabeling. However, studies that utilized DNA-based methods for identifying new range expansions, species occurrences, phylogenetic relationships, or population genetics were considered only if the specimens analyzed had commercial origins or were captured by fishermen, indicating the type of retail venue and location where the samples were obtained. Studies based on self-collected samples from wild populations and environmental DNA (eDNA) were excluded. However, articles validating novel DNA-based methods (e.g. assessing the performance of novel primers) using self-collected samples from natural populations were included if the target species had economic significance. Unpublished studies, preprints, abstracts, or any research that had not undergone a peer-review process were disregarded. Additionally, this review included studies

that analyzed samples from protected or endangered species of commercial value in local or

international markets (whether these samples were commercially obtained or seized by

authorities) whose trade is banned or regulated. Lastly, this review also examined articles that

reported on the molecular authentication of fish feed claimed to contain commercially valuable

species from the ESPO.

2.2 DNA-based methods, molecular markers, and primers

For practical purposes, DNA-based methods used for seafood authentication of ESPO's species

were categorized into three distinct groups. The first category consists of methods that rely on

the amplification of DNA by an enzymatic reaction. The results from these methods are based

on the visualization of a specific size fragment or band pattern in a gel matrix, a positive

colorimetric reaction, or a fluorescence signal pattern displayed digitally. This category

includes the following methods: 1) PCR-RFLP (Restriction Fragment Length Polymorphism),

2) PCR-RAPD (Random Amplified Polymorphic DNA), 3) PCR-SSCP (Single Strand

Conformation Polymorphism), 4) PCR-SSP (Species Specific Primers), 5) qPCR-SSP, 6)

Multiplex PCR and qPCR, 7) qPCR High-Resolution Melting (HRM), and 8) PCR-

Microarrays, and 9) Loop-Mediated Isothermal Amplification (LAMP). The second category

encompasses methods that depend on DNA sequencing technologies. This category further

divides into two subcategories: a) sequences generated through a PCR step followed by the

Sanger Sequencing technique, which includes: 10) FINS (Forensically Informative Nucleotide

Sequencing) and DNA Barcoding; and b) sequences generated by high-throughput NGS (Next

Generation Sequencing) technologies, specifically 11) HTS NGS-metabarcoding. The third

category includes seafood species identification based on 12) mass spectrometry analysis. The

genetic markers discussed in the reviewed articles were organized into three levels based on 1)

genome origin: mitochondrial, nuclear, and random markers (like those targeted by RAPD

primers), 2) target organisms, and 3) DNA-based methods. Similarly, all oligonucleotide

primers reported in the analyzed articles were classified into two levels according to 1) target

molecular marker (e.g., mitochondrial COI gene, nuclear rhodopsin gene) and 2) targeted

animal groups.

2.3 Commercial species diversity and conservation statuses

The species composition of commercially traded seafood from the ESPO region was assessed,

considering both domestic and international markets. This assessment was based on the species

identification results reported in the reviewed articles. This review focused exclusively on

seafood species from the ESPO region, which includes marine species (such as sharks and

tuna) and diadromous fish (like eel, herring, salmon, and trout). Strict freshwater species (such

as tilapia) were not included in the analysis. Only species that are native to the ESPO region

were considered; however, introduced or naturalized species of commercial value were also

taken into account. Species identified in reviewed studies collected from domestic ESPO

markets, which have a confirmed distribution range outside the ESPO (likely sourced from

imported commodities), were excluded from the assessment. Distribution ranges were verified

using several databases: The Ocean Biodiversity Information System OBIS (https://obis.org),

FishBase (https://fishbase.org), SeaLifeBase (https://www.sealifebase.org), The Barcode of

Life Data System -BOLD-(https://boldsystems.org), and the World Register of Marine Species

-WoRMS- (https://marinespecies.org). All identified species reported in the analyzed studies

were organized at the taxonomic resolution level based on the current accepted classification

and scientific names provided by the WoRMS database. Additionally, the current conservation

status of all species identified in the papers analyzed in this review were searched in the IUCN

Red List of Threatened Species website (https://www.iucnredlist.org).

2.4 Mislabeling meta-analysis

The mislabeling meta-analysis dataset was constructed using articles that met the Level 1 screening criteria. These articles underwent a second screening based on Level 2 criteria, which required that the study analyzes samples of commercial origin. Following this, a third screening was conducted using the Level 3 criteria, which mandated that detailed information for each analyzed sample be provided either in the main text or as a supplementary file. This information included the label (commercial name), type of product (e.g. fresh, cooked, cured, canned), and sampling venue (e.g. fish landing site, market). Only samples identified at the species level were considered, and classifications above the species level were not included. The samples included in the mislabeling meta-analysis consisted of seafood products that were labeled as containing an ESPO species, such as "Peruvian anchoveta" (*Engraulis ringens*). These products were either identified as the correct species or were found to be substituted with another ESPO species (e.g. *Sardinops sagax*), a non-ESPO species (e.g. "European anchovy", *E. encrasicolus*), or a freshwater species. Additionally, the analysis included cases where ESPO species were used to replace non-native ESPO species from international markets, for example, the Peruvian scallop (*Argopecten purpuratus*) being sold as the European king scallop (*Pecten maximus*).

In an attempt to recover samples that had been identified at a higher taxonomic level due to a lack of reference sequences at the time of publication, a curation update step was implemented. This involved using publicly available DNA sequences cited in the reviewed papers, which were re-analyzed and compared against current reference sequences from the GenBank and BOLD databases.

To prevent the inclusion of samples that might have been classified as mislabeled due to a strict interpretation of expected common names, I carefully checked the label information (commercial designation or common name) and the reported scientific name of each analyzed

sample. This information was compared against common names used in official landing reports,

governmental websites, relevant literature, the FAO ASFIS database, and listed common

names from the FishBase database. For instance, samples from domestic ESPO markets that

were originally reported as mislabeled because they used generic names such as squid

("*calamar*"), flounder ("*lenguado*"), grouper ("*mero*"), shark ("*tiburón*" or "*tollo*") were not

considered mislabeled in this review if the identified species belonged to a seafood group

implied by the declared generic term. This criterion was adopted because generic or umbrella

market names are commonly used in seafood markets in the ESPO region, where no official

lists of commercial designations for seafood species have been established. In fact, several

acceptable market names included in the FDA´s The Seafood List (available at

https://www.hfpappexternal.fda.gov/scripts/fdcc/index.cfm?set=SeafoodList) are examples of

generic seafood names (e.g. abalone, anchovy, grouper, sea bass, shark). In contrast, for

samples purchased within European markets, which have stricter seafood labeling regulations,

products must be labeled with unique commercial designations and the scientific name,

according to Regulation (EU) Nº 1379/2013. Therefore, official market names were verified

using the commercial and scientific name of seafood species listed on the European Union

(EU) website (https://oceans-and-fisheries.ec.europa.eu/fisheries/markets-and-trade/seafood-

markets/commercial-and-scientific-name-species_en). For samples collected in Canada, the

Canadian Food Inspection Agency (CFIA) fish list was consulted from its official website

(https://inspection.canada.ca/en/food-labels/labelling/industry/fish/list).

Cured samples from selected articles were pooled across studies and organized into different

levels including label information, seafood type (e.g. finfish, sharks, bivalves), sampling venue,

and country. The mislabeling rate was calculated using the formula [mn/n*100], where "mn"

is the number of mislabeled samples and "n" is the total number of samples.

2.4.1 Statistical analyses

Confidence intervals of the mislabeling rates were calculated using the "binom.confint" function from the "binom" package implemented in R (R for Mac OS X GUI version 4.2.3) (R core Team, 2022) to generate upper and lower estimates of the predicted mislabeling rates. The Agresti-Coull method was used for calculating 95% confidence intervals (CI) for large sample sizes (n > 40), while the Wilson method was chosen for small sample sizes (n ≤ 40) (Brown et al., 2001). Since these values represent percentages, any negative confidence intervals were reported as zero, and those exceeding 100% were reported as 100% (Bubernick & Faulstick, 1993). Exploratory analyses were conducted to assess the independence of the association between mislabeling rates based on continent, country, distribution channel, and seafood type. Categories with sample sizes of fewer than 25 (n < 25) were excluded from the analyses. The analyses utilized the Chi-square test or Fisher's exact test, depending on whether any cell count was below 5. This approach was taken because Chi-square test relies on approximations that become unreliable with small expected cell counts (Kim, 2017). When a significant association between variables was observed ($p < 0.05$), further pairwise tests were conducted in R to determine which pairwise comparisons were significantly different. p values were adjusted for multiple comparisons using the Bonferroni correction method, and the α-level was set at 0.05 for all analyses. All R scripts used in the analyses are provided in Supplementary File S1 to S5.

3. Results and discussion

3.1 Data collection overview

This review compiled all the DNA-based methods used globally to identify commercially important species in the ESPO region. A total of 75 published articles (see Table 1) met the Level 1 screening criteria outlined in section 2.1 and were selected for analysis. The 75 reviewed articles were published across 43 different peer-review journals, with publication

dates ranging from mid-December 1998 to early July 2025. Notably, there were no relevant articles published between 1999 and 2001. The journals "*Food Control*" and "*Journal of Agricultural and Food Chemistry*" were the most frequent publication venues, with 12 articles (16%) and 6 articles (8%), respectively. English was the predominant language, appearing in 69 articles (92%). Three articles were written in Spanish, and one article each was published in Chinese, German, and Korean. Out of the 75 studies, 30 were conducted entirely in ESPO countries: Chile (14 studies), Peru (12 studies), Colombia (3 studies), and Ecuador (1 study). The remaining 45 studies analyzed seafood samples collected around the world, including those from the ESPO region. These were conducted in Spain (17 studies), Germany (4), Japan (4), Mexico (4), Canada (3), China (2), France (2), Italy (2), and one study was carried out in each of the following countries: Austria, Brazil, Hong Kong, South Korea, Poland, Switzerland, and the United Kingdom. A total of 63 articles reported the authentication of commercial products from the ESPO. The remaining 12 articles validated their molecular assays using reference samples of non-commercial origin, which were obtained from natural populations within the ESPO, collected by researchers, donated by colleagues, or obtained from research facilities. Out of the 63 articles that reported the use of commercial ESPO products, 24 did not meet the Level 3 screening criteria, as they did not provide detailed information about each individual sample. This lack of detail prevented me from using their results in further mislabeling meta-analysis. As a result, only the findings from 39 papers were included in the mislabeling meta-analysis review (section 3.7).

3.2 DNA-based identification methods for seafood species from the ESPO region

3.2.1 PCR-RFLP

This technique involves three main steps: 1) the PCR amplification of a specific DNA fragment using universal or group-specific primer sets; 2) enzymatic digestion with one or more

restriction endonucleases that recognize specific sites; and 3) the separation of the digested DNA fragments in a gel matrix. A successful RFLP assay will result in the amplicon being cut into two or more fragments, generating species-specific band patterns (Lago et al., 2014). The main advantage of this method relies on its simplicity and relatively low cost. However, one potential drawback is that incomplete enzymatic digestion can lead to misleading diagnostic results, which may necessitate longer incubation times to achieve more reliable outcomes, thereby extending the overall duration of the identification procedure. Additionally, prior knowledge of the target DNA sequence is essential to select the adequate enzyme capable of producing distinct fragment patterns between two or more species (Bossier, 1999; Lago et al., 2014).

PCR-RFLP has been widely utilized to authenticate seafood products globally since the early 90´s (Chow & Inoue, 1993; Chow et al., 1993). In the ESPO region, various commercial species targeted for the development of RFLP assays have been documented in 13 studies. These studies include Chilean mollusks like mussels focusing on various markers such as 18S rDNA, ITS, PAPM, COI, and 16S rRNA (Toro, 1998; Toro et al., 2005; Fernández-Tajes et al., 2011; Jilberto et al., 2017; Larraín et al., 2019; Colihueque et al., 2020; Quintrel et al., 2021; Giusti et al., 2022) and keyhole limpets using the mitochondrial cytochrome b (CYTB) gene (Olivares-Paz et al., 2006). Additionally, PCR-RFLP was used to identify different fish species including canned sardines from Peru based on the CYTB gene (Jérôme et al., 2003a), Chilean hake using the CYTB and 5S rDNA genes (Perez & Vazquez-García, 2004), as well as bream, salmon, and trout from Chile (Espiñeira et al., 2009b) and salmon from Chilean restaurants (Prida et al., 2020) using the CYTB gene.

3.2.2 PCR-RAPD

This approach utilizes short oligonucleotides of arbitrarily chosen sequence (10-12 nt) to generate species-specific electrophoretic patterns, known as fingerprinting, based on the random PCR amplification of several anonymous DNA fragments across the genome (Yamashita et al., 2024). The primary advantage of this method is that it requires little prior knowledge of the target DNA sequence. However, despite its speed and simplicity, the reproducibility of PCR-RAPD can be affected by slight changes in the quality and quantity of the target DNA (Bossier, 1999; Yamashita et al., 2024). As a result, the number of studies reporting RAPD-based protocols has declined over time. Nevertheless, intra- and inter-laboratory reproducible RAPD results can be achieved if reactions are performed under strictly identical conditions (Atienzar et al., 2006).

PCR-RAPD has been applied to species of economic significance from the ESPO, such as differentiating the Mediterranean mussel *Mytilus galloprovincialis* from other commercially valuable mussel species, including the Chilean mussel *M. chilensis* collected from a harvested natural population in Puerto Aguirre, Chile (Rego et al., 2002). In another study, Marín et al. (2007) developed a RAPD-based method for identifying the Pacific abalone *Haliotis discus hannai* and the red abalone *H. rufescens*, as well as their potential hybrids, obtained from a Chilean research institute´s hatchery. Based on their RAPD results, the authors reported that the supposed hybrids were actually phenotypic variants of *H. rufescens*.

3.2.3 PCR-SSCP

This method relies on the electrophoretic mobility of single-stranded DNA through a non-denaturing gel. Specific nucleotide mutations present in a single-stranded PCR product alter the molecule´s conformation, causing two DNA strands that differ by a single nucleotide to migrate differently (Gasser et al., 2006; Lago et al., 2014). While this method is relatively

simple, cost-effective, and time-efficient, it has some disadvantages, such as poor

reproducibility and the need for reference samples (Gasser et al., 2006; Silva & Hellberg, 2021).

Two studies have demonstrated the application of the PCR-SSCP method to identify fish and

abalone species of global commercial interest, including samples collected from the ESPO

region. Rehbein et al. (2002) evaluated the utility of PCR-SSCP and RFLP-SCCP assays using

a 464 bp fragment of the CYTB gene to identify various fish species in commercially produced

fishmeal samples. These samples included anchovy, mackerel, sardine, and hake from Peru

and Chile. In another study, Aranceta-Garza et al. (2011) developed a PCR-SSCP technique

based on two PCR products targeting partial fragments of the 18S rDNA and Lysin precursor

genes in three abalone (Haliotidae) species namely *H. corrugata*, *H. fulgens*, and *H. rufescens*,

as well as other gastropod species in raw, frozen, and canned presentations from different

origins (Chile, Mexico, and Peru). By utilizing the PCR-SSCP method for the 18S rDNA gene

fragment, the authors revealed that a canned abalone sample had been substituted with

Concholepas concholepas (Muricidae) from Peru.

3.2.4 PCR-SSP

Species identification using species-specific primers (SSPs) is a rapid, highly accurate, and

sensitive method. It relies on a perfect or near perfect complementarity between the SSP and

the target species' strand, along with the presence of punctual mutations within the primer

hybridization region of non-target species (Marín et al., 2025). Mismatches at the primer's 3'-

terminal of the primer can severely disrupt polymerase activity, leading to the most significant

detrimental effects (Stadhouders et al., 2010; So et al., 2020). Several techniques for species

identification utilize SSPs, including multiplex PCR, qPCR, eDNA monitoring, and more

recently, CRISPR-based methods (Goldberg et al., 2016; Williams et al., 2019; Silva &

Hellberg, 2021). The PCR-SSP technique for species identification can be conducted with basic

molecular laboratory equipment, and the final diagnostic is electrophoretically resolved based

on the presence or absence of a PCR product of a known size. This makes the method both

time-effective and easy-to-interpret. Additionally, modified SSPs can be combined with

isothermal amplification technologies, using nanoparticle-based colorimetric or lateral flow

strip approaches, to enable faster, *in-situ* identification of seafood (Maggioni et al., 2020;

Frigerio et al., 2023, Tiktak et al., 2024). The primary drawback of the SSPs approach is the

need for prior DNA sequence information from both target and non-target species.

In the ESPO region, the PCR-SSP method has been mentioned in four articles for identifying

shark species through fin samples collected in Chile (Hernández et al., 2008, 2010), as well as

from artisanal landings in Colombia (Caballero et al., 2012), and a market in Ecuador

(Manzanillas-Castro & Acosta-López et al., 2022). Additionally, the PCR-SSP method was

used to differentiate the Peruvian anchoveta, *E. ringens* (Chairi & Rebordinos, 2014), and the

Peruvian scallop, *A. purpuratus* (Marín et al., 2013, 2017, 2025). Furthermore, this method

was proven effective for the accurate identification of a squid and nine fish species of

commercial value in the Peruvian seafood sector (Marín et al., 2025).

3.2.5 qPCR-SSP

This method is a faster and more sensitive variant of endpoint PCR-SSP that relies on the real-

time detection of a fluorescent signal, which is proportional to the concentration of the DNA

product (Silva et al., 2021). Fluorescent chemistries can be derived from non-specific dsDNA-

binding dyes (e.g. SYBR Green I) or sequence-specific hydrolysis probes (e.g. TaqMan)

(Tajadini et al., 2014). The former technology is relatively inexpensive and easy to use, while

the latter offers better specificity because the fluorescent signal is emitted only from specific

amplifications (Tajadini et al., 2014). The qPCR-SSP method generally targets relatively short

DNA fragments (less than 300bp) and has proven highly effective in identifying seafood

species worldwide (Silva et al., 2021), including fish species of the ESPO region, as reported

in five articles compiled in this review.

Herrero et al. (2011) successfully developed and applied TaqMan qPCR-SSP assays targeting

commercial samples of Atlantic salmon (*Salmo salar*) collected from various countries,

including supermarkets in Chile. In another study, Mora et al. (2018) developed novel qPCR-

SSP assays for authenticating commercial Peruvian weakfish (*Cynoscion analis*) and hake

products (*Merluccius gayi* and *M. peruanus*) based on partial fragments of the ATP6 gene and

the control region, respectively. Additionally, Marín et al. (2025) used a partial fragment of the

mitochondrial 16S rRNA gene to create a novel qPCR-SSP protocol aimed at authenticating

Peruvian scallop samples collected from markets, supermarkets, and restaurants in Peru. qPCR-

SSP protocols have also been developed to monitor the trade of ESPO species used in

traditional Chinese medicine. Marín et al. (2021) developed a qPCR-SSP assay designed to

target a 136 bp fragment of the mitochondrial 16S rRNA gene of the protected Peruvian

seahorse, *Hippocampus ingens*. They assessed its effectiveness using specimens confiscated

by Peruvian authorities, as well as dried and powdered presentations of seahorses. In a separate

study, Cardeñosa et al. (2023) applied a previously established qPCR-SSP protocol (Cardeñosa

et al., 2018) to identify CITES-listed sharks using fins that were seized by Colombian

authorities that were declared as "dried fish bladders".

3.2.6   Multiplex-PCR and qPCR

Multiplex-PCR involves the simultaneous amplification of two or more target loci by including

multiple primer sets in a single PCR reaction (Markoulatos et al., 2002). This method is both

time-saving and cost-effective, allowing for the identification of different species in one run.

The result is the generation of species-specific DNA fragments of varying sizes (Rasmussen &

Morrissey, 2008), which can be resolved on an agarose gel following endpoint PCR or analyzed

through melting curve analyses based on species-specific melt profiles after qPCR (Winder et

al., 2011). Some of the disadvantages of this method include the need for proper primer design,

which is crucial to avoid the formation of primer dimers and non-specific PCR products, which

can deplete the reaction components (Edwards and Gibbs, 1994) and negatively affect

efficiency. Additionally, all primers should be designed to have the same or closely related

annealing temperatures to ensure effective co-amplification of all target loci. Achieving

optimal co-amplification results also requires careful titration of component concentrations,

including primers, $MgCl_2$, and dNTPs (Marín et al., 2025), which can be a time-demanding

process during PCR reaction standardization.

A total of nine studies reviewed herein assessed the effectiveness of multiplex PCR or qPCR

methods for authenticating species from the ESPO region, specifically focusing on sharks

(Hernández et al., 2008, 2010; Caballero et al., 2012; Manzanillas-Castro & Acosta-López,

2022; Cardeñosa et al., 2023), and scallops (Marín et al., 2013, 2017). Additionally, five

commercially important finfish species from the ESPO region were targeted for species

identification using multiplex PCR-SSP assays. These species include the Peruvian anchoveta,

E. ringens, which was identified through a SSP assays based on the nuclear 5S rDNA gene

(Chairi & Rebordinos, 2014). Also, fresh and cooked commercial samples of two congeneric

rock seabass, *Paralabrax callaensis* and *P. humeralis*, were successfully identified using a

PCR-SSP assay that targeted a partial fragment of the mitochondrial 16S rRNA gene (Marín

et al., 2025). In the same study, the authors reported a second multiplex PCR-SSP assay that

targeted a partial region of the mitochondrial COI gene for the simultaneous identification of

commercial cooked fish that share the same market name "*ojo de uva*" in Peruvian markets:

the mocosa ruff *Schedophilus haedrichi*, and the grape-eye seabass *Hemilutjanus*

macrophthalmos (Marín et al., 2025). Conversely, less attention has been given to developing

multiplex PCR assays for identifying commercial invertebrate species from the ESPO region.

Thus far, only the Peruvian scallop, *A. purpuratus*, has been included in two different multiplex

PCR-SSP assays targeting the mitochondrial 16S rRNA gene (Marín et al., 2013, 2017).

3.2.7   qPCR-HRM

High-resolution melting (HRM) is a qPCR-based technique primarily used for genotyping

single-nucleotide polymorphisms (SNPs) and for species identification. This method monitors

the fluorescence signal shift that occurs during the dissociation of the qPCR product from

double-stranded to single-stranded DNA in the presence of a saturating dye as the temperature

increases (Kim et al., 2023). Specialized HRM software utilizes this fluorescence data to create

sequence-specific peak patterns based on the amplicon sequence and temperature of the

melting curves (Warnke et al., 2020). This single-tube reaction method is both time- and cost-

effective, and it has proven successful in authenticating fish and shellfish species globally

(Silva & Hellberg, 2021).

Nevertheless, within the ESPO region, the HRM approach has only been used for the

identification of native, introduced, and hybrid commercial mussel species from Chile,

specifically *M. chilensis*, *M. edulis*, and *M. galloprovincialis*. This identification is based on

the Polyphenolic Adhesive Protein of Mussels (PAPM) (Jilberto et al., 2007; Asorey et al.,

2022), and also on a multilocus approach using SNPs discovered through data mining from

ESTs and RADseq (Quintrel et al., 2021).

3.2.8   PCR-Microarrays

PCR-Microarrays, also known as DNA chips, traditionally consists of a glass microscopy slide

that has oligonucleotide probes attached. These probes are specifically designed to be

complementary to the DNA of target species (Teletchea, 2009). Typically, during the PCR

process, products are labeled with fluorophores. This labelling allows for the detection of target

DNA after hybridization with the species-specific oligonucleotide probes, following the
washing steps (Teletchea, 2009). This method enables the simultaneous identification of
hundreds, or even thousands, of species. Several studies from different countries across Asia,
Europe, and North America have demonstrated its effectiveness for fish identification
(Teletchea, 2009; Silva & Hellberg, 2021).

A recent proof-of-concept study (Kappel et al., 2021) assessed the utility of a DNA microarray
assay using 21 crustacean species-specific probes targeting a segment of the 16S rRNA gene.
This study focused on the giant tiger prawn, *Penaeus (Penaeus) monodon*, and the Pacific
whiteleg shrimp *P. (Litopenaeus) vannamei*. The assay proved successful in identifying
commercial samples of *P. (Litopenaeus) vannamei* from Ecuador. Importantly, all probes
designed to recognize *P. (Litopenaeus) vannamei* sequences displayed no cross-reactivity with
any other crustacean species examined, highlighting the high specificity of the reported
microarray assay.

3.2.9 LAMP

LAMP is a fast, cost-effective, and sensitive method that enables DNA amplification at an
isothermal temperature without the need for a thermal cycler. It typically requires a set of 6
especially designed primers that recognize 8 different regions of the target sequence, resulting
in higher specificity (Sahoo et al., 2016). It utilizes a DNA polymerase with strand
displacement activity, which is crucial for loop-mediated isothermal amplification (Yang et al.,
2024). The main advantages of this technique are its high specificity, sensitivity, and faster
performance compared to traditional PCR. Additionally, it requires basic equipment, making
it suitable for field applications. The main disadvantage is that the primer design is more
complex than in PCR, and the standardization process can be cumbersome and time-consuming
(Silva & Hellberg, 2021).

Tiktak et al. (2024) developed a Lab-on-a-Chip (LOC) systems integrating field-based DNA

extraction and LAMP detection of three CITES-listed shark species: *Alopias pelagicus*, *A.*

supercilious, and *Isurus oxyrinchus*. These systems target a partial region of the mitochondrial

control region in *I. oxyrinchus* and *A. pelagicus*, while the nuclear ITS2 region was used in *A.*

supercilious. The authors reported successful and fast (full analyses lasted less than one hour)

species-level identifications of different shark samples collected from fishing ports and markets

in Ecuador.

3.2.10 FINS and DNA Barcoding

Although both strategies share a similar rationale, the FINS method for species authentication

was first introduced in 1992 by Bartlett and Davidson (1992) to identify tuna species using the

DNA sequence information from the CYTB gene. Later, in 2003, Paul Hebert and colleagues

proposed the concept of DNA barcoding, which focuses on using a partial region of the

mitochondrial COI gene to identify species across all animal phyla, except for the Cnidaria

(Hebert et al., 2003). Both species identification methods consist of three main steps: 1) PCR

amplification of a specific partial DNA fragment from the target sample; 2) Sanger sequencing

of the PCR product; and 3) phylogenetic analysis based on genetic distance (Tamura and Nei,

1993) and Neighbor-Joining methods (Saitou and Nei, 1987), in which the query sequence is

compared to related reference sequences obtained from databases. The final results are

presented in a phylogenetic tree, where the unknown sample clusters with the reference

sequences that exhibit the fewest nucleotide substitutions or genetic distance (Bartlett &

Davidson, 1992; Rasmussen & Morrissey, 2008). A key difference between FINS and DNA

barcoding is that FINS relies on informative sites and phylogenetic relationships derived from

vouchered reference organisms (Li et al., 2011). In contrast, DNA barcoding follows a

standardized procedure that emphasizes the presence of a "barcode gap". This gap indicates

sufficient interspecific genetic distance to allow for species resolution (Bucklin et al., 2011;

Hellberg et al., 2016).

This review indicates that DNA sequencing methods, such as FINS or DNA barcoding, were

the most commonly used method for seafood species identification, appearing in 44 (58.7%)

out of the 75 papers compiled for this study. For instance, DNA barcoding was utilized to

examine mislabeling at different stages of the supply chain in Peru and Chile (Marín et al.,

2018; Biffi et al., 2020; Velez-Zuazo et al., 2021; Dufflocq et al., 2022). Additionally, it was

employed to uncover unreported fish species in landings from both Peru and Chile (Canales-

Aguirre et al., 2018; Marín et al., 2022). Other studies have utilized traditional taxonomic

methods combined with DNA barcoding to describe new distribution ranges, determine species

boundaries, and document rare occurrences in fish samples from Peruvian artisanal fisheries

(Cabanillas-Torpoco et al., 2020; Cañedo-Apolaya et al., 2021; Vera et al., 2023).

Additional economically significant marine species from the ESPO region identified through

DNA sequencing include sharks from landings in Peru (Velez-Zuazo et al., 2015) and

Colombia (Caballero et al., 2012; Villate-Moreno et al., 2022), Myliobatiform rays collected

from artisanal fisheries in Peru and Ecuador (Alfaro-Cordova et al., 2023; Ehemann et al.,

2024a), and a variety of crustaceans (crabs and shrimps) and mollusks (clams, scallops, snails,

squids, and octopus) from the Peruvian fishery sector (Marín et al., 2018). Furthermore, DNA

analysis has been applied to crab meat products in Chilean markets (Haye et al., 2012),

cephalopod species from Ecuador (Pliego-Cárdenas et al., 2016), and non-traditional seafood

products such as cetacean meat sold in Peruvian markets (Tzika et al., 2010; Biffi et al., 2020).

A DNA mini-barcoding approach, which is a variation of the full DNA barcoding, utilizes short

DNA sequences (typically shorter than 200 bp) and has been effective in identifying seafood

species from highly degraded samples, such as processed seafood products (Fernandes et al.,

2021). Marín et al. (2018, 2025) successfully applied this mini-barcoding method, focusing on

short fragments of the mitochondrial COI and 12S rRNA genes, to authenticate various cooked

fish samples sourced from Peruvian restaurants. It is important to note that none of these

samples were amplifiable using different full DNA barcoding markers.

In the addition to the COI marker, numerous studies have reported the utility of DNA sequences

from other mitochondrial gene regions for seafood authentication, such as the 16S rRNA gene.

This genetic marker was utilized by Ardura et al. (2012) and Horreo et al. (2013) to authenticate

fish feed samples from various origins, including the Peruvian anchovy, *E. ringens*, which is

marketed in France, Germany, and Spain. Similar, the same marker was also employed to

authenticate scallop samples collected worldwide, including the Peruvian scallop, *A.*

purpuratus, sourced from seafood markets in Peru, Germany, and Spain (Näumann et al., 2012;

Marín et al., 2015, 2018; Klapper & Schröeder, 2021; Parrondo et al., 2021).

The performance of some nuclear genetic markers has also been assessed in FINS studies

aimed at identifying seafood species. For instance, Espiñeira et al. (2009a) highlighted the

effectiveness of the ribosomal 18S rDNA gene for identifying commercially important marine

bivalves collected from different regions worldwide, including Chile and Peru. Conversely, a

study by Asorey et al. (2022) showed that FINS based on the histone H1C gene were not

effective for distinguishing between the mussels *M. chilensis* and *M. galloprovincialis* sourced

from a growing center in Chile.

3.2.11 HTS NGS-metabarcoding

Next-generation sequencing (NGS) technologies enable the simultaneous sequencing of

hundreds of millions of DNA molecules from multiple samples within a relatively short

timeframe (Fernandes et al., 2021; Silva & Hellberg, 2021). The NGS approach focused on

species identification is known as "NGS metabarcoding". This method utilizes universal

primers to achieve massive amplification of barcode sequences from different species in a

single run (Fernandes et al., 2021). Numerous studies reported successful species identification

of seafood samples (e.g. tuna, cod, bivalves, clupeids, flatfish) using specific HTS techniques

based on Illumina, pyrosequencing, and Ion Torrent platforms (Silva & Hellberg, 2021; Silva

et al., 2021).

Among these NGS technologies, 454 pyrosequencing by Roche was the first commercially

available platform that used real-time detection of pyrophosphate (PPi) molecules released

during DNA sequencing. This process results in light emission from the firefly enzyme

luciferase, which is visualized as specific peaks corresponding to individual nucleotides

(Fernandes et al., 2021; Silva & Hellberg, 2021). This method has the advantage of providing

fast and high accurate performance, and the ability to produce longer reads (Fernandes et al.,

2021). Abbadi et al. (2017) utilized 454-pyrosequencing based on the mitochondrial COI and

16S rRNA genes to successfully identify 15 different bivalve species, including both fresh and

processed samples of the Chilean mussel, *M. chilensis*, sourced from markets in Italy.

Currently, the Illumina platform is the most widely used NGS technology. This method relies

on the PCR amplification and sequencing of DNA clusters that are immobilized on a disposable

flow cell, using reversible fluorescent dideoxy terminators (Fernandes et al., 2021; Silva &

Hellberg, 2021). One of the major advantage of this approach over traditional Sanger

sequencing is its higher throughput per run and lower cost per base (Silva & Hellberg, 2021).

Gense et al. (2021) reported the development of a DNA metabarcoding assay using the MiSeq

and Iseq Illumina platforms, which focused on a fragment of the mitochondrial 16S rRNA gene.

This assay was used to authenticate local and imported oyster, mussel, and scallop seafood

products purchased from different commerce in Austria. The authors accurately identified a

frozen Peruvian scallop (*A. purpuratus)* sample that was correctly labelled as "*purpur*

*kammmusc*hel" (German for "purple scallop), as well as 17 mussel products that claimed to

contain the Chilean mussel, *M. chilensis*. However, these products were identified as two

different mussel species: *M. edulis* and *M. galloprovincialis*.

3.2.12 Mass spectrometry-based SNP genotyping

Mass spectrometry is one of the most commonly used method for protein identification and

quantification (Cerqueira et al., 2024). However, it can also be applied to the analysis of nucleic

acids, including the detection of SNPs and indels (Ellis & Ong, 2017). The process for SNP

detection using mass spectrometry involves coupling it with endpoint PCR. In this method,

targeted SNPs are amplified through standard PCR, followed by a "single base PCR extension"

reaction. This reaction employs mass-modified dideoxynucleotide (ddNTPs) terminators in an

oligonucleotide primer (called the extension primer) that anneals just upstream of the

polymorphic mutation site. Finally, the mass spectrometer detects the distinct mass of the

extended primer within the PCR product, thereby identifying the SNP allele (Gabriel et al.,

2009). Wenne et al. (2022) reported the development of a multi-locus SNP assay using mass

array spectrometry to authenticate mussel samples. This assay is based on a panel of 54 SNPs

from two mussel genes: Me15–16 (a nuclear adhesive protein gene marker) and M7 (an

acrosomal sperm protein called M7 lysin). The purpose of this assay was to assess the species

and geographical origin information declared in the label of mussel products sold in EU

markets. Reference samples from various *Mytilus* species, including farmed *M. chilensis*

collected in the province of Chiloe (Chile), were used in this analysis.

3.3 Molecular markers and primers

A total of 16 genetic markers were used to identify the ESPO species. Half of these markers

originated from the mitochondrial genome, including ATP6, COI, COIII, CYTB, NAD2, 12S

rRNA, 16S rRNA, and the Control Region. The other half came from the nuclear genome and

included M7, M1C, MAC-1, ITS, PAPM, Rhodopsin, 5S rDNA, and 18S rDNA. The

relationships among the molecular markers, target species, and detection methods discussed in

the surveyed articles are presented in the form of a Sankey diagram in Fig. 1.

The mitochondrial COI gene was the most frequently used marker, appearing in 35 articles

(46.7%). It was primary applied in DNA sequencing identification methods, including DNA

barcoding, mini barcoding, FINS, and pyrosequencing, to identify fish, mollusks, crustaceans,

cetaceans, and holothurians. The mitochondrial 16S rRNA gene was the second most

commonly utilized marker, featured in 24 articles (32%). This gene was employed in

sequencing and species-specific primers detection methods targeting crustaceans, fish,

holothurians, and mollusks. The nuclear ITS region and the mitochondrial CYTB gene were

the third and fourth most assessed marker, with 11 articles (14.7%) and 10 articles (13.3%)

respectively. The nuclear ITS region was utilized in species-specific primer and RFLP

detection methods targeting gastropods, mussels, sharks, and salmon. The CYTB gene was

used in DNA sequencing and RFLP methods focused on fish and cetaceans.

Most mitochondrial markers reviewed herein have been used to identify multiple animal groups,

including the COI, 16S rRNA, 12S rRNA, and CYTB genes. In contrast, four mitochondrial

markers were specifically employed to identify individual seafood types: ATP6, NAD2, and

the control region for fish, and the COIII for cephalopods. Among nuclear markers, the ITS

and the 18S rDNA were used to target multiple seafood types, while the H1C, M7, Mac-1, and

PAPM genes were dedicated solely to authenticate mussels. The 5S rDNA was used for fish

identification, and Rhodopsin was designated for cephalopods.

The DNA marker assessed using the highest number of detection methods corresponds to the

mitochondrial 16S rRNA gene. This marker was utilized in ten different methods including

multiplex PCR-SSP, PCR and qPCR-SSP, Direct qPCR-SSP, DNA sequencing (FINS and

barcoding), NGS meta-barcoding, microarray, NGS pyrosequencing, and RFLP. These

findings demonstrate the high utility and effectiveness of this mitochondrial marker for

identifying a wide range of seafood species. This effectiveness is supported by the broadly

targeted region spanned by the universal primers developed by Palumbi (1991), as well as by

the extensive number of available 16S rRNA gene sequences in public databases.

A descriptive analysis of the primers used in the reviewed articles is provided in Supplementary

File S6. This section includes a detailed list of all the primers identified in the articles, along

with their associated molecular markers, targeted species, and original reference sources.

3.4 Species diversity

A total of 204 species from the ESPO were identified by DNA-based methods reported in the

articles reviewed herein. These species were distributed among 142 genera, 82 families, and

44 orders (Table 2, Fig. 2). Fish accounted for the majority of the identified samples (152

species, 74.5%), followed by mollusks (40 species, 19.6%), crustaceans (7 species, 3.4%),

cetaceans (4 species, 2%), and holothurians (1 species, 0.5%). Out of the total species identified,

192 were native to the ESPO, whereas 10 were introduced species. The introduced organisms

included 6 fish species (*Oncorhynchus kisutch*, *O. mykiss*, *O. tshawytscha*, *Salmo salar, S.*

trutta, and *Rachycentron canadum*), two mussel species (*Mytilus edulis* and *M.*

galloprovincialis), and two abalone species (*Haliotis discus hannai* and *H. rufescens*).

3.4.1 Fish

Fish were the most extensively studied seafood group, with samples analyzed in 36 studies. A

total of 152 species were identified, distributed within 59 families and 28 orders. This group

accounting for 74.5% of all identified species. The diversity within the fish group was primarily

dominated by finsfish, which included 104 species (68.4%). This was followed by sharks with

30 species (19.7%), batoids with 17 species (11.2%), and chimaeras with just 1 species (0.7%).

The fish group with the highest number of identified species belongs to the shark *Carcharhinus*,

which has 7 species. This was followed by the finfish genus *Cynoscion*, which has 5 species.

3.4.2 Mollusks

The mollusk group comprised 40 species identified in 32 studies, distributed across 17 families

and 13 orders. This group was evenly represented by gastropods and bivalves, with each group

containing 17 species (42.5% each). Cephalopods were represented by 6 species, accounting

for 15% of the mollusk group. The commercially important Chilean keyhole limpet species

belonging to the genus *Fissurella* accounted for most of the gastropod species (12 out of 17

species).

3.4.3 Crustaceans

This shellfish group was analyzed in seven studies, including seven species from three families

within one order. Six crab species, accounting for 85.7% of the findings, and one shrimp

species, making up 14.3%, were identified in the studies reviewed herein.

3.4.4 Cetaceans

Cetaceans were represented by only four species (2%) in two studies conducted in Peru. The

first study, reported by Tzika et al. (2010), analyzed DNA sequences of the mitochondrial

CYTB gene from meat samples purchased in local markets across various coastal cities in Peru.

This study identified four cetacean species namely: *Delphinus delphis*, *Lagenorhynchus*

obscurus, *Phocoena spinipinnis*, and *Tursiops truncatus*. I should mention that *D. capensis* was

also reported but it was later synonymized with *D. delphis* in 2015 (see Cunha et al., 2015).

The second article, published by Biffi et al. (2020), provided molecular evidence of dolphin

meat sold in a market in Lima, the capital of Peru. Their findings, based on COI sequences,

revealed the illegal trade of a *D. delphis* meat sample labeled as "*muchame*", which is the

market term used in Peru for fresh or cured cetacean meat. These results indicate that illegal

catches and trade of small cetaceans continue to occur in Peru, despite conservation efforts and

a ban against on the capture and commercialization of these species established by the Peruvian

government in Law Nº 26585 on April 9, 1996 (El Peruano, 1996). This situation aligns with

previous findings reported by Campbell et al. (2020).

3.4.5   Holothurians

This animal group included a single species, the burrowing shaggy sea cucumber (*Athyonidium*

chilensis), which accounted for the smallest proportion (0.5%) of the total number of species

analyzed in this review. Only two studies conducted in China (Hu et al., 2019; Xing et al.,

2021) have focused on this commercially valuable group, underscoring the need for more

research from ESPO countries to enhance our understanding of local holothurian diversity.

3.5   Limitations of DNA-based methods in identifying ESPO species

While most DNA-based methods for identifying seafood species are highly sensitive, efficient,

and accurate, several factors can complicate the identification process. These include:

• **Degraded DNA**: highly degraded DNA, often found in canned and cooked seafood due to

physical and chemical alterations, can hinder DNA extraction and further PCR amplification.

DNA mini-barcoding may help analyze degraded DNA, but it can struggle to distinguish

closely related species due to low coverage in gene regions with minimal or no variation.

This limitation often restricts identification to the genus level or higher taxonomic

categories.

• **Non-target DNA amplification**: Universal primers, which are frequently used for seafood

species identification, can mistakenly bind to non-target DNA, including that of parasites

and bacteria associated with the target organism.

• **Lack of a comprehensive database with reference sequences**: a database containing low-

coverage of reference sequences for species diversity can negatively impact seafood

identification. The success of DNA sequencing methods for species identification relies

heavily on a comprehensive DNA sequence database for accurate sequence comparison.

• **Incorrect marker selection**: choosing the right DNA marker is crucial for successful

seafood species identification. For example, slow-evolving markers may fail to distinguish

between closely related or recently diverged species. Additionally, low copy number

markers, such as those from the nuclear genome, can complicate the identification of highly

processed seafood products or when only a small amount of tissue is available.

• **Poor primer design:** effective primer design is essential for successful PCR amplification,

and this requires the use of appropriate bioinformatics tools and experienced researchers.

Primers that are designed based on highly variable regions or on a limited number of

sequences may inadvertently miss detecting crucial mutations within the template strand

that correspond to the complementary region of the primer's 3' end. This oversight can

inhibit PCR amplification in organisms that contains these mutations.

• **Intrinsic biological nature of target seafood species**: the biological complexity of target

seafood species can also complicate identification. Factors such as species complexes,

cryptic taxa, recently diverged species, hybridization, and interspecific conservatism can

hinder accurate interpretation of seafood species identification results.

• **Human error**: another important factor to consider during the identification process is the

human error factor. These errors can occur at any stage, including seafood sampling,

molecular identification analysis (such as DNA extraction, PCR amplification, and

sequencing), and interpretation of the results.

Reviewed papers have highlighted some challenges in the successful identification of certain

seafood species from the ESPO. These challenges primarily stem from a lack of comprehensive

reference sequences and low levels of genetic differentiation among closely related species.

Reviewed studies reported several instances of identifications at the genus level for tunas

(*Thunnus* sp.), smooth-hound sharks (*Mustelus* sp.), rays (*Gymnura* sp. and *Myliobatis* sp.),

silversides (*Odontesthes* sp.), and clams (*Semele* sp.) (Marín et al., 2018; Biffi et al., 2020;

Velez-Zuazo et al., 2021). Furthermore, species complexes have complicated the identification

of butterfly rays (*Gymnura* sp., Ehemann et al., 2024b), octopuses (*Octopus* sp., Marín et al.,

2018), and keyhole limpets (*Fissurella* sp., Olivares-Paz et al., 2006). These findings

underscore the urgent need for developing an extensive database of DNA sequences for

seafood species in the ESPO. To address these issues, researchers should consider exploring

alternative and more robust molecular techniques, like multilocus approaches (Feitosa et al.,

2018), phylomitogenomics (Alfaro et al., 2025), and whole genome sequencing (WGS)

combined with RAD-Seq targeting species-specific SNPs (Jiang et al., 2020).

3.6 IUCN conservation status

According to the International Union for Conservation of Nature´s Red List of Threatened

Species, out of the 204 species analyzed in the studies reviewed, 11 are listed as Critically

Endangered (CR) (5.4%), 11 as Endangered (EN) (5.4%), 22 as Vulnerable (VU) (10.8%), 9

as Near Threatened (NT) (4.4%), 80 as Least Concern (LC) (39.2%), 17 as Data Deficient (DD)

(8.3%), and 54 as Not Evaluated (NE) (26.5%) (see Fig. 2). Threatened categories (CR, EN, or

VU) include a total of 44 species (21.6%), with sharks accounting for the majority at 24 species

(54.6%), followed by 13 batoids (29.5%), 4 finfish (9.1%), 2 gastropods (4.5%), and 1

chimaeroid fish (2.3%) (Fig. 2).

These findings highlight the rapid depletion of several commercial elasmobranch species,

primarily due to intense fishing pressure, overexploitation, and high bycatch rates. Additionally,

the K-strategist nature of these species (low fecundity, long gestation periods, slow growth,

and late sexual maturity) makes them particularly vulnerable to even moderate levels of fishing

pressure (Wheeler et al., 2020). All these characteristics contribute to their sensitivity to

environmental changes and human activities (Marín et al., 2018).

On the other hand, the LC category primarily consists of finfish species, with 71 out of a total

of 80 LC species. This category includes various small to medium-sized fish species, such as

anchovies, herring, mullets, pilchards, and sardines. These species exhibit r-strategist

characteristics, which include high fecundity, early age at first reproduction, and short life

spans, enabling them to withstand high levels of fishing pressure (Crosetti, 2016; Patti et al.,

2020; Owatari et al., 2024).

Of particular concern is that a considerable proportion of the species compiled are categorized

as NE with 54 species (26.5%) falling into this group. This category mainly comprises shellfish

species, including 40 species in total: 17 bivalves, 15 gastropods, 7 crustaceans, and 1

holothurian, along with 13 fish species. These findings indicate an urgent need for population

and demographic studies of commercially important shellfish species from the ESPO region.

The results from such studies would contribute to better assessments and determinations of the

current conservation statuses and population trends, ultimately leading to improved

management and sustainable exploitation of those resources.

3.7 Mislabeling meta-analysis in ESPO seafood species

This study presents the first quantitative meta-analysis focused on seafood mislabeling of ESPO species sold globally. Based on the Level 3 screening criteria, 39 articles were selected, which included a total of 1,806 cured samples purchased throughout the entire supply chain, from harvesting and processing to distribution and retail, across 16 countries. The number of samples for each taxonomic group were: 882 finfish (48.8%), 485 bivalves (26.9%), 337 sharks (18.7%), 39 cephalopods (2.2%), 26 batoids (1.4%), 27 crustaceans (1.5%), 6 gastropods (0.3%), 2 holothurians (0.1%), 1 chimaera fish (0.05%), and 1 cetacean (0.05%).

A re-analysis of seafood samples with publicly available DNA sequences allowed me to upgrade eight seafood samples that were previously identified only to the genus level due to a lack of reference sequences at the time of their publication. Among these upgrades was a canned sardine identified by Jérôme et al. (2003b), which was reclassified from *Sardinops* sp. to *S. sagax* (GenBank AY394046). Furthermore, four samples originally identified as *Mustelus* sp. were upgraded to *Mustelus whitneyi* (Genbank MH194477, MH194478, MH194497, and MH194506). Additionally, two samples identified as *Gymnura* sp. were upgraded to *Gymnura afuerae* (Genbank MH194463 and MH194465), and one sample initially identified as *Semele* sp. was reclassified as *Semele corrugata* (Genbank MH194538) (Marín et al., 2018). This findings highlight the importance of sharing DNA records, which aligns with the data availability policies of several relevant journals. Sharing DNA records not only supports the conclusions of studies but also benefit the research community by allowing re-analysis of published results, facilitating meta-analyses, and reducing costs of further research (Sielemann et al., 2020). In this review, it was noted that out of the 39 articles selected for the meta-analysis, 27 studies focused on DNA sequencing, of which only 11 made their DNA records publicly accessible.

The results of the global mislabeling analysis are shown in Fig. 3. These results indicated that

out of the 1,806 seafood products, 448 were mislabeled. This represents a global mislabeling

rate of 24.8% (95% CI [22.9-26.9]). The mislabeling rate found in this review, which focused

specifically on ESPO seafood species, falls within the range of previous global mislabeling

meta-analyses, which reported rates between 19% and 30% (Pardo et al., 2016; Warner et al.,

2016; Luque & Donlan, 2019). The complete meta-dataset can be found in Supplementary

Table S1. While the findings of the mislabeling meta-analysis are informative, they should be

interpreted with caution due to varying sampling strategies and efforts used across the different

studies reviewed.

3.7.1 Mislabeling per geographic region

Overall, the reviewed samples were collected from five continents, encompassing 16 countries.

The mislabeling results, categorized by continent, indicated that Asia had the highest rate of

mislabeling at 44.4% (4/9, CI [18.9-73.3]), followed by South America at 25.6% (375/1464,

95% CI [23.7-28.2]), Europe at 22.3%, (67/301, 95% CI [17.9-27.3]), and North America at

8.7%, (2/23, 95% CI [2.4-26.8]).

No mislabeling was detected in samples from Africa (0/9, 95% CI [0-30]), although the sample

size for this continent was small and not representative (see panel B in Supplementary Table

S1). Only South America and Europe had sampling sizes exceeding the threshold of n > 25,

consequently only both continents were included in the statistical test of significant association.

The mislabeling rates observed in these two continents did not show a statistically significant

relationship (Chi-square, $p = 0.25$) (Fig. 4).

When mislabeling analyses were organized by country, the highest mislabeling rates of 100%

were found in Colombia (194/194, CI [97.7-100]) and Hong Kong (2/2, 95% CI [34.2-100]).

It should be noted that samples analyzed from Colombia involved 194 shark fins that were

incorrectly labeled as fish bladders. All of these selected fins were confiscated during an

official inspection at an airport, therefore mislabeling rates in these samples were expected to

be high. On the other hand, the sample size from Hong Kong consisted of only two ESPO

samples, which is not representative. Other estimates from countries with small sample sizes

(n < 10) reported mislabeling rates of 0% for China, Ecuador, Egypt, England, and France,

while Mexico, Germany, and South Korea reported mislabeling between 40% and 50%.

Countries with more representative sample sizes include Peru with a mislabeling rate at 16.5%

(125/774, 95% CI [13.7-18.9.3]), Chile at 11.5% (56/487, 95% CI [8.9-14.7]), Spain at 25.4%

(49/193, 95% CI [19.8-31.9]), and Italy at 1.3% (1/76, 95% CI [0-7.8]). A statistical test of

significant association between the mislabeling rates detected in five countries (Chile,

Colombia, Italy, Spain, and Peru) showed non-significant similar relationship only between

Chile and Peru (Chi-square, $p = 0.27$). All other relationships showed signs of significant

deviation (Fig. 4). This finding was mainly driven by the strong contrast in mislabeling rates

observed across the countries analyzed. Colombia exhibited an extremely high misleading rate,

while Spain, Peru, and Chile had moderate to high levels, and Italy had a very low mislabeling

rate. Detailed mislabeling results for each country are shown in panel B of Supplementary

Table S1.

3.7.2   Mislabeling per distribution channel

The analysis revealed that mislabeling rates varied significantly among the different

distribution channels. The highest overall mislabeling rate was found in the inspection category

at 64% (195/303, 95% CI [58.8-69.5]). This was followed by restaurants at 36% (76/210, 95%

CI [30-42.9]), wholesale markets at 27.3% (38/139, 95% CI [20.6-35.3]), markets at 22.8%

(52/228, 95% CI [17.8-28.7]), supermarkets at 12.2% (53/434, 95% CI [9.4-15.6]), warehouse

at 10.5% (21/200, 95% CI [6.9-15.6]), fish landings at 5.9% (12/203, 95% CI [3.3-10.1]), and

large scale retailers at 3.57% (1/28, CI [0.63-17.7]) (Fig. 5). The "market" category

encompassed samples collected from the following subsectors: ethnic shops, delicacy shops,

fishmongers, open air markets, retail markets, handicraft markets, fish markets, retailers, and

local commerce.

The mislabeling rate observed at the inspection category was significantly higher than in all

other categories (Chi-square, $p < 0.05$). This discrepancy can be attributed to the elevated

mislabeling rate within this category compared to others. It is important to note that most

samples from this category were obtained through seizures at official control points, which

tend to contain a higher percentage of fraudulent items. Out of the 303 samples analyzed in

this category, 194 (64%) were processed shark fins that were falsely declared as fish bladders

at an airport in Colombia (Cardeñosa et al., 2023).

The mislabeling rate at restaurants was significantly higher (Chi-square, $p < 0.05$) compared

to other categories, except for wholesale and markets, where the rates were statistically similar

($p > 0.05$). Excluding the inspection category, restaurants exhibited the highest mislabeling

rate, while the lowest rate was found at fish landings. This outcome was anticipated, as the

initial stages of the supply chain have fewer opportunities for mislabeling. This result aligns

with several studies that have shown that mislabeling tends to increase further along the supply

chain (Pardo et al., 2016; Marín et al., 2018).

3.7.3 Mislabeling per seafood type

The estimated overall mislabeling rates for the different types of seafood analyzed were highest

for gastropods at 50% (3/6, 95% CI [18.8-81.2]), followed by finfish at 33.2% (293/882, 95%

CI [30.2-36.4]), sharks at 20.2% (68/337, 95% CI [16.2-24.8], bivalves at 16.1% (78/485, 95%

CI [13.2-19.8]), batoids at 15.4% (4/26, 95% CI [6.2-33.5]), and cephalopods at 5.1% (2/39,

95% CI [1.4-16.9]) (Fig. 5). A global Chi-square test indicated a strong significant difference

($p < 0.05$) in the mislabeling rates among the assessed groups (batoids, bivalves, cepahlopods,

finfish, and sharks). Subsequent multiple comparison analyses identified significant

differences among three groups: finfish vs. cephalopods (Fisher's exact test, $p < 0.05$), finfish

vs. bivalves (Chi-square, $p < 0.05$), and finfish vs. sharks (Chi-square, $p < 0.05$) (Fig. 5). The

finfish group exhibited the highest significant mislabeling rate. This is likely due to its high

species diversity, the variety of commercial forms, and economic incentives, all of which make

this category more susceptible to mislabeling or substitution. In contrast, the smaller sample

sizes in other categories, such as batoids and cephalopods, reduce the statistical power to detect

meaningful differences. Additionally, the unequal group sizes may influence the robustness of

comparisons across seafood categories.

The most frequently encountered substitute species were three threatened shark species. A total

of 161 samples, initially labeled as fish bladders (typically sourced from certain finfish species)

were actually shark fins from two species: *Carcharhinus falciformis* (n=114, IUCN status: VU)

and *Sphyrna lewini* (n=47, IUCN status: CR). The third species, *Prionace glauca* (n=38, IUCN

status: NT), was found being used not only as a substitute for other sharks (i.e. hammerheads,

shortfin makos, and smooth-hounds) but also for various finfish products (i.e. dolphinfish, rock

seabass, and fish bladder). These findings highlight serious conservation concerns, particularly

given the involvement of highly threatened species, demanding urgent policy actions and

enforcement measurements.

The current review identified a total of 27 Peruvian seafood items labeled as "*tollo de leche*".

Out of these samples, two were finfish, while the remaining 25 belonged to five different shark

species. Notably, three of these shark species (*A. pelagicus*, *I. oxyrinchus*, and *S. zygaena*) are

classified as threatened by the IUCN. In Peru, the term "*tollo de leche*" was originally

designated for a single species: the Critically Endangered humpback smooth-hound shark, *M.*

whitneyi (Elliot et al., 1996; Chirichigno & Cornejo, 2001). However, a recent study revealed

that this term is now being used to refer to small-sized specimens of various shark species

(Núñez & Gozzer-Wuest, 2019). The use of conflicting market names, which constitutes a form

of mislabeling (Ahles et al., 2025), can result in overfishing of vulnerable species, hinder the

enforcement of regulations, and limit consumers' ability to make informed choices (Almerón-

Souza et al., 2018). To address these issues, efforts should focus on improving labeling

accuracy and eliminating conflicting names by creating a standardized list of unique market

names (Marín et al., 2018).

Among the invertebrate seafood samples analyzed, the most commonly mislabeled species was

the Chilean blue mussel *M. chilensis*. This bivalve was substituted with three different species:

Aulacomya atra, which was detected in 12 samples collected from a supermarket in Chile

(Colihueque et al., 2020), and *M. galloprovincialis* or *M. edulis*, which were found in 15

products from European commerce (Gense et al., 2021). Another bivalve, the Peruvian scallop

(*A. purpuratus*), was the most commonly used substitute species. This scallop species was used

to replace two types of European scallops: the variegated scallop (*Mimachlamys varia*) in Spain,

with 45 substituted samples, and two samples of king scallops labeled as *Pecten maximus* and

Pecten sp. in Germany. The year-round availability of farmed Peruvian scallop positions this

species as a potential substitute for wild, seasonally available local European scallops

(Parrondo et al., 2021).

958   4. Conclusions and future perspectives

959   This research presents the first comprehensive global survey of DNA-based methods used to

960   identify seafood species from the ESPO, with particular focus on species diversity,

961   conservation status, and issues related to mislabeling. The findings from this review contribute

962   significantly to our understanding of past, present, and future trends in molecular methods that

963   support traceability, regulation, and effective management of ESPO species. Among the

identification methods, Sanger sequencing technology stands out as the most frequently utilized due to its high efficiency and accuracy. However, faster and more cost-effective techniques, such as species-specific primers and multiplex PCR, were also identified in the reviewed studies, mostly targeting vulnerable species like sharks and seahorses. Despite the great potential of HTS-based methods for authenticating seafood species, few studies have explored their utility in ESPO products. Notably, no research has yet explored the application of emergent molecular species identification technologies, such as CRISPR-based platforms, for seafood authentication in the ESPO. This relatively new technology has the potential to revolutionize seafood authentication, as indicated by recent studies reporting higher specificity and sensitivity levels, as well as shorter processing times compared to traditional DNA identification methods (Ying et al., 2022; Moorthy et al., 2025).

This study also conducted the first meta-analysis on the mislabeling of ESPO seafood products sold globally, revealing an overall mislabeling rate of 24.8%. As expected, the highest rates of mislabeling were detected in the final stages of the supply chain. A significant finding from this review is that threatened shark species were not only the most frequently mislabeled but also the most commonly encountered substitute species. This raises important concerns about conservation, fishery management, trade, and regulation of vulnerable resources. In light of this, laudable shark conservation initiatives, like the "Shark Free Ceviche" seal (Díaz-Ferguson et al., 2024), which has already been implemented in Colombia, should be replicated or adopted in more ESPO nations like Ecuador and Peru, which are major players in global shark fishing, trade, and consumption.

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Figure legends

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Fig. 1. Sankey diagram illustrating the relationships between target seafood species and DNA

markers. The width of each connector is proportional to the number of articles reporting the

use of each DNA marker. The molecular methods associated with the DNA markers are shown,

along with their corresponding article reference numbers (in brackets), which can be found in

Table 1.

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Fig. 2. Pie charts in Panel A show the taxonomic diversity of the seafood species identified

using DNA-based methods. Species detected were grouped into five major taxonomic

categories: fish (blue), mollusks (pale blue), crustaceans (dark grey), cetaceans (green), and

holothurians (orange). Wedge sizes represent the proportion of identified species assigned to

each category, based on the number of species identified across all reviewed studies. Panel B

shows a pie chart illustrating the proportion of total species, which are categorized by their

conservation statuses, according to data from the IUCN. The satellite pie chart shows the

proportions and taxonomic diversity of threatened species (Vulnerable: VU, Endangered: EN,

and Critically Endangered: CR). These include sharks (blue), batoids (deep sky blue), finfish

(pale blue), gastropods (dark grey), and chimaeras (light grey).

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Fig. 3. Results of the global meta-analysis for seafood from the Eastern South Pacific Ocean

(ESPO). The heat map illustrates the countries from which seafood samples were collected and

analyzed. Color intensity indicates the mislabeling rate calculated for each country, as

displayed in the mislabeling rate color scale. The back-to-back bar graph in Panel A presents

the overall global rates of mislabeled and correctly labeled samples, along with rates specific

to each seafood category. The back-to-back bar graph in Panel B depicts the proportions of

mislabeled and correctly labeled samples observed in individual countries, categorized by

seafood type. Confidence intervals (95% CI) for the mislabeling rates in each country are

provided in brackets. "N" indicates sample size, and "M" denotes the mislabeling rate.

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1622 **Fig. 4.** Mislabeling rates by A) continent and B) country. Bars represent the mislabeling rate,

1623 error bars indicate the 95% confidence intervals. The relationship between the mislabeling rates

1624 in Europe and South America showed no significant deviation. Bars labeled with different

1625 lowercase letters are significantly different at $p < 0.05$. Statistical significance was determined

1626 using either the Chi-square test or Fisher's exact test, depending on the sample size.

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1628 **Fig. 5.** Mislabeling rates by A) supply chain stage and B) seafood type. Bars represent the

1629 mislabeling rate, error bars indicate the 95% confidence intervals. Bars labeled with different

1630 lowercase letters are significantly different at $p < 0.05$. Statistical significance was determined

1631 using either the Chi-square test or Fisher's exact test, depending on the sample size.

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1637 **Supplementary File legends**

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Supplementary Table S1: Metadata of samples included in the global mislabeling analysis of

Eastern South Pacific seafood. Panel B shows detailed mislabeling rates results per each

analyzed category

Supplementary File S1: R scripts used to determine confidence intervals

Supplementary File S2: R scripts used to analyze the statistical significance of mislabeling

rates grouped by Continent

Supplementary File S3: R scripts used to analyze the statistical significance of mislabeling

rates grouped by Country

Supplementary File S4: R scripts used to analyze the statistical significance of mislabeling

rates grouped by Supply Chain Distribution Channel

Supplementary File S5: R scripts used to analyze the statistical significance of mislabeling

rates grouped by Seafood Type

Supplementary File S6: descriptive analysis of the primers used in the reviewed articles

Table 1. List of articles reviewed in this study.

Nº	Authors	Publication year	Journal (Language)	Target species	Method	DNA markers	ESPO seafood species type (supply channel and country of origin)	Conducted in	Passed screening Levels	Samples (n) in meta-analysis	Reference
1	Toro	1998	Journal of Shellfish Research (English)	Mussels	PCR-RFLP	ITS, PAPM	Wild (Chile)	CANADA	1	—	Toro (1998)
2	Rego et al.	2002	Journal of Agricultural and Food Chemistry (English)	Mussels	PCR-RAPD	Random	Wild (Chile)	SPAIN	1	—	Rego et al. (2002)
3	Rehbein	2002	Journal of Aquatic Food Product Technology (English)	Fish	PCR-RFLP SSCP	CYTB	Commercial (IFOMA Germany, imported from Chile and Peru)	GERMANY	1 and 2	—	Rehbein (2002)
4	Jérôme et al.	2003a	Journal of Agricultural and Food Chemistry (English)	Sardines	PCR-RFLP	CYTB	Commercial (supermarket in France, canned in Peru)	FRANCE	1, 2, and 3	1	Jérôme et al. (2003a)
5	Jérôme et al.	2003b	Journal of Agricultural and Food Chemistry (English)	Sardines	FINS	CYTB	Commercial (supermarket in France, origin Chile and Peru)	FRANCE	1, 2, and 3	6	Jérôme et al. (2003b)
6	Perez and García-Vazquez	2004	Journal of Food Protection (English)	Hake	PCR-RFLP	5S rDNA, CYTB	Wild (Chile)	SPAIN	1	—	Perez and García-Vazquez (2004)
7	Toro et al.	2005	Journal of Shellfish Research (English)	Mussels	PCR-RFLP	ITS, PAPM	Wild (Chile)	CHILE	1	—	Toro et al. (2005)
8	Olivares-Paz et al.	2006	Investigaciones Marinas (Spanish)	Keyhole limpets	PCR-RFLP	CYTB	Wild (Chile)	SPAIN/CHILE	1	—	Olivares-Paz et al. (2006)
9	Marín et al.	2007	Journal of Shellfish Research (English)	Abalone	PCR-RAPD	RANDOM	Research facility (Chile)	CHILE	1	—	Marín et al. (2007)
10	Aguilera-Muñoz et al.	2008	Gayana (English)	Mollusks	PCR and band size polymorphism	ITS1, ITS2	Commercial (Chile, Mexico)	CHILE	1 and 2	—	Aguilera-Muñoz et al. (2008)

11	Hernández et al.	2008	Journal of Fish Biology (English)	Shark fins	Multiplex PCR-SSP	ITS2	Commercial (drying facility, commercial storage warehouse in Chile)	CHILE	1, 2, and 3	200	Hernández et al. (2008)
12	Espiñeira et al.	2009a	Journal of Agricultural and Food Chemistry (English)	Bivalves	FINS	18S rDNA	Wild (Chile, Peru)	SPAIN	1	—	Espiñeira et al. (2009a)
13	Espiñeira et al.	2009b	European Food Research and Technology (English)	Salmon, trout, bream	FINS, PCR-RFLP	CYTB	Wild (Peru) and commercial (supermarket, Chile)	SPAIN	1 and 2	—	Espiñeira et al. (2009b)
14	Hernández et al.	2010	Hidrobiológica (English)	Shark fins	PCR-SSP	ITS2	Commercial (storage warehouse, Chile)	CHILE	1 and 2	—	Hernández et al. (2010)
15	Tzika et al.	2010	Conservation Genetics (English)	Cetaceans	DNA sequencing	CYTB	Commercial (markets, Peru)	SWITZERLAND/ PERU	1 and 2	—	Tzika et al. (2010)
16	Aranceta-Garza et al.	2011	Food Control (English)	Abalone	PCR-SSCP	18S rDNA	Commercial and wild (Retail market in Mexico, imported from Chile and Peru)	MEXICO	1, 2, and 3	2	Aranceta-Garza et al. (2011)
17	Fernández-Tajes et al.	2011	European Food Research and Technology (English)	Mussels	PCR-RFLP	PAPM, COI	Commercial and wild (Spanish supermarket, imported from Chile)	SPAIN	1, 2, and 3	80	Fernández-Tajes et al. (2011)
18	Ha et al.	2011	Journal of Agricultural and Food Chemistry (English)	Abalone	FINS	16S rRNA, (COI was used as auxiliary marker)	Commercial (wholesale and retail outlets in Hong Kong, imported from Chile)	HONG KONG/UK	1, 2, and 3	2	Ha et al. (2011)
19	Herrero et al.	2011	Food Chemistry (English)	Salmon	qPCR-SSP	ITS1	Commercial (supermarket in Chile)	SPAIN	1 and 2	—	Herrero et al. (2011)

20	Ardura et al.	2012	Fisheries Research (English)	Fish	DNA sequencing	16S rRNA	Commercial (Spanish producers, species origin: Peru)	SPAIN	1, 2, and 3	2	Ardura et al. (2012)
21	Caballero et al.	2012	Molecular Ecology Resources (English)	Sharks	Multiplex PCR-SSP, DNA sequencing	COI, ITS2	Commercial (landings in Colombia)	COLOMBIA	1 and 2	—	Caballero et al. (2012)
22	Haye et al.	2012	Food Control (English)	Crabs	DNA sequencing	COI	Commercial (seafood market and food store in Chile)	CHILE	1 and 2	—	Haye et al. (2012)
23	Näumann et al.	2012	Informationen aus der Fischereiforschung (German)	Scallops	DNA sequencing	16S rRNA	Commercial (Imported or local commerce in Germany, imported from Peru)	GERMANY	1, 2, and 3	1	Näumann et al. (2012)
24	Horreo et al.	2013	Journal of the Science of Food and Agriculture (English)	Several animal species	DNA sequencing	16S rRNA	Commercial (imported from Peru)	SPAIN	1, 2, and 3	1	Horreo et al. (2013)
25	Marín et al.	2013	Food Control (English)	Scallops	Multiplex PCR-SSP	16S rRNA	Commercial (landings and market in Peru)	JAPAN	1, 2, and 3	3	Marín et al. (2013)
26	Chairi and Rebordinos	2014	Journal of Agricultural and Food Chemistry (English)	Anchovies	Multiplex PCR-SSP	5S rDNA	Wild (Chile)	SPAIN	1	—	Chairi and Rebordinos (2014)
27	Santaclara et al.	2014	Food Chemistry (English)	Ling fish	FINS	COI	Wild (Chile)	SPAIN	1	—	Santaclara et al. (2014)
28	Marín et al.	2015	Fisheries Science (English)	Scallops	DNA sequencing	16S rRNA	Commercial (landings in Peru)	JAPAN	1, 2, and 3	8	Marín et al. (2015)
29	Velez-Zuazo et al.	2015	Fisheries Research (English)	Sharks	DNA sequencing	COI	Commercial (landings in Peru)	PERU	1 and 2	—	Velez-Zuazo et al. (2015)
30	Galal-Khallaf et al.	2016	Food Chemistry (English)	Shrimps/ Cephalopods	DNA sequencing	COI, 16S rRNA	Commercial (supermarkets in Spain and Egypt,	SPAIN/EGYPT	1, 2, and 3	18	Galal-Khallaf et al. (2016)

								imported from Ecuador and Chile)			
31	Pliego Cárdenas et al.	2016	American Malacological Bulletin (English)	Octopus	DNA sequencing	COI, COIII, 16S rRNA	Commercial (artisanal fishery in Ecuador)	MEXICO/ ECUADOR	1, 2, and 3	7	Pliego Cárdenas et al. (2016)
32	Sanchez et al.	2016	Fisheries Science (English)	Cephalopods	DNA sequencing	16S rRNA	Wild (Peru)	JAPAN	1	—	Sanchez et al. (2016)
33	Velasco et al.	2016	Heliyon (English)	Anchovies	FINS	CYTB	Commercial (markets, supermarkets, and specialized stores in Spain, origin Chile and Peru)	SPAIN	1, 2, and 3	11	Velasco et al. (2016)
34	Abbadi et al.	2017	Journal of the Science of Food and Agriculture (English)	Bivalves	HTS Pyroseq	COI, 16S rRNA	Commercial (customs premises, market in Italy, imported from Chile)	ITALY	1, 2, and 3	44	Abbadi et al. (2017)
35	Jilberto et al.	2017	Food Chemistry (English)	Mussels	HRM, RFLP	PAPM	Wild (Chile)	SPAIN	1	—	Jilberto et al. (2017)
36	Marín et al.	2017	Aquaculture Research (English)	Scallops	Multiplex PCR-SSP	16S rRNA	Commercial (landings in Peru and supermarket in UK, imported from Peru)	JAPAN	1, 2, and 3	65	Marín et al. (2017)
37	Canales-Aguirre et al.	2018	Revista de Biología Marina y Oceanografía (English)	Fish	DNA sequencing	COI	Commercial (artisanal fishery in Chile)	CHILE	1 and 2	—	Canales-Aguirre et al. (2018)
38	Marín et al.	2018	Plos One (English)	Crustacean, fish, gastropods, mollusks	DNA sequencing	COI, 12S rRNA, 16S rRNA, Control Region	Commercial (landings, wholesales, markets, supermarkets, restaurants in Peru)	PERU	1, 2, and 3	120	Marín et al. (2018)

39	Mora et al.	2018	Salud y Tecnología Veterinaria (Spanish)	Fish	qPCR-SSP	ATP6, Control Region	Commercial (supermarkets in Peru)	PERU	1 and 2	—	Mora et al. (2018)
40	Shehata et al.	2018	Food Control (English)	Fish	DNA sequencing	COI	Commercial (Canadian Food and Inspection Agency surveillance) across Canada, imported from Chile and Peru)	CANADA	1, 2, and 3	9	Shehata et al. (2018)
41	Giusti et al.	2019	Food Control (English)	Anchovies	DNA sequencing	CYTB	Commercial (large-scale retail distribution in Italy, imported from Chile)	CHILE	1, 2, and 3	9	Giusti et al. (2019)
42	Hu et al.	2019	Science and Technology of Food Industry (Chinese)	Sea cucumber	DNA sequencing	COI, 16S rRNA	Commercial (supermarket in China, species origin: Peru)	CHINA	1, 2, and 3	1	Hu et al. (2019)
43	Larraín et al.	2019	Scientific Reports (English)	Mussels	RFLP	COI, 16S rRNA, PAPM, ITS, MAC-1, 18S rDNA	Wild (Chile)	CHILE	1	—	Larraín et al. (2019)
44	Shehata et al.	2019	Food Research International (English)	Fish	DNA sequencing	COI	Commercial (Canadian Food and Inspection Agency surveillance across Canada, imported from Chile, Colombia, Ecuador and Peru)	CANADA	1, 2, and 3	12	Shehata et al. (2019)

45	Yu et al.	2019	Journal of Food Hygiene and Safety (Korean)	Cephalopods	DNA sequencing	COI, 16S rRNA	Commercial (market in South Korea, imported from Chile and Peru)	KOREA	1, 2, and 3	5	Yu et al. (2019)
46	Biffi et al.	2020	Scientific Reports (English)	Cephalopods, fish, cetaceans	DNA sequencing	COI	Commercial (landings, wholesale, retail, supermarket, restaurants in Peru)	PERU	1, 2, and 3	413	Biffi et al. (2020)
47	Cabanillas-Torpoco et al.	2020	Zootaxa (English)	Sawfish	DNA sequencing	COI	Commercial (landings in Peru)	PERU	1 and 2	—	Cabanillas-Torpoco et al. (2020)
48	Colihueque et al.	2020	Recent Patents on Food, Nutrition & Agriculture (English)	Mussels	PCR-RFLP	18S rDNA	Commercial (supermarkets in Chile)	CHILE	1, 2, and 3	95	Colihueque et al. (2020)
49	Prida et al.	2020	Foods (English)	Salmon, trout	PCR-RFLP	CYTB	Commercial (restaurants in Chile)	CHILE	1, 2, and 3	84	Prida et al. (2020)
50	Cañedo-Apolaya et al.	2021	Diversity (English)	Angel shark	DNA sequencing	COI	Commercial (landings and wholesale in Peru)	PERU	1 and 2	—	Cañedo-Apolaya et al. (2021)
51	Costa et al.	2021	Molecular Phylogenetics and Evolution (English)	Squids	DNA sequencing	COI, 16S rRNA, Rhodopsin	Commercial (markets in Ecuador and Peru)	BRAZIL	1 and 2	—	Costa et al. (2021)
52	Gense et al.	2021	Foods (English)	Bivalves	NHT NGS-Metabar-coding	16S rRNA	Commercial (delicacy shop in Austria, imported from Peru)	AUSTRIA	1, 2, and 3	16	Gense et al. (2021)
53	Kappel et al.	2021	Analytical and Bioanalytical Chemistry (English)	*Penaeus* shrimps	Microarray, DNA sequencing	COI, 16S rRNA	Commercial (retailer in Germany, declared origin: Ecuador)	GERMANY	1, 2, and 3	1	Kappel et al. (2021)

54	Klapper and Schröder	2021	Food Control (English)	Scallops	Multiplex qPCR, DNA sequencing	16S rRNA	Commercial (artisanal fishery in Chile)	GERMANY	1, 2, and 3	2	Klapper and Schröder (2021)
55	Marín et al.	2021	Journal for Nature Conservation (English)	Fish	qPCR-SSP, DNA sequencing	COI, 16S rRNA	Commercial (landings, wholesale, and markets in Peru)	PERU	1, 2, and 3	61	Marín et al. (2021)
56	Parrondo et al.	2021	Food Control (English)	Scallops	DNA sequencing	16S rRNA	Commercial (fish shops, supermarkets, and restaurants in Spain imported from Chile or Peru)	SPAIN	1, 2, and 3	77	Parrondo et al. (2021)
57	Quintrel et al.	2021	Foods (English)	Mussels	PCR-RFLP, qPCR-HRM	PAPM	Wild and commercial (Chile)	CHILE	1 and 2	—	Quintrel et al. (2021)
58	Velez-Zuazo et al.	2021	Food Control (English)	Fish	DNA sequencing	COI	Commercial (fish markets, restaurants, and supermarkets in Peru)	PERU	1 and 2	—	Velez-Zuazo et al. (2021)
59	Xing et al.	2021	Food Control (English)	Sea cucumber	DNA sequencing	COI, 16S rRNA	Commercial (supermarket in China, origin: Peru)	CHINA	1, 2, and 3	1	Xing et al. (2021)
60	Asorey et al.	2022	Food Chemistry: Molecular Sciences (English)	Mussels	HRM, FINS	PAPM, H1C	Commercial (growing center in Chile)	CHILE	1, 2, and 3	61	Asorey et al. (2022)
61	Dufflocq et al.	2022	Food Control (English)	Swordfish	DNA sequencing	COI	Commercial (fish market, open-air market, and Supermarkets in Chile)	CHILE	1, 2, and 3	47	Dufflocq et al. (2022)
62	Giusti et al.	2022	Food Control (English)	Mussels	PCR-RFLP	PAPM	Commercial (national large retailers, ethnic shop (Italy,	ITALY	1, 2, and 3	23	Giusti et al. (2022)

							imported from Chile)				
63	Manzanillas-Castro and Acosta-López	2022	Biodiversity (English)	Sharks	Multiplex PCR-SSP	ITS2	Commercial (fish market in Ecuador)	ECUADOR	1 and 2	—	Manzanillas-Castro and Acosta-López (2022)
64	Marín et al.	2022	Marine and Fisheries Sciences (English)	Fish	DNA sequencing	COI, Control Region	Commercial (landings in Peru)	PERU	1, 2, and 3	96	Marín et al. (2022)
65	Villate-Moreno et al.	2022	PeerJ (English)	Sharks	DNA sequencing	NAD2	Commercial (landings in Colombia)	COLOMBIA	1 and 2	—	Villate-Moreno et al. (2022)
66	Wenne et al.	2022	Aquaculture (English)	Mussels	MassARRAY SNP Genotyping	M7	Commercial (market in Poland, imported from Chile)	POLAND	1 and 2	—	Wenne et al. (2022)
67	Alfaro-Cordova et al.	2023	Conservation Genetics Resources (English)	Devil rays	DNA sequencing	COI	Commercial (landings in Peru)	PERU	1 and 2	—	Alfaro-Cordova et al. (2023)
68	Cardeñosa et al.	2023	Animal Conservation (English)	Sharks fins	qPCR-SSP, DNA sequencing	ITS2, COI	Commercial (shark fin seizure at El Dorado International Airport-Colombia)	COLOMBIA	1, 2, and 3	194	Cardeñosa et al. (2023)
69	Vera et al.	2023	Revista Peruana de Biología (Spanish)	Jewelfish	DNA sequencing	COI	Commercial (landings in Peru)	PERU	1 and 2	—	Vera et al. (2023)
70	Ehemann et al.	2024a	Fish Biology (English)	*Urotrygon* rays	DNA sequencing	COI, NAD2	Commercial (landings in Ecuador and Peru)	MEXICO	1 and 2	—	Ehemann et al. (2024a)
71	Ehemann et al.	2024b	Taxonomy (English)	*Gymnura* rays	DNA sequencing	COI	Commercial (landings in Peru)	MEXICO/PERU	1 and 2	—	Ehemann et al. (2024b)
72	Gil et al.	2024	Journal of the Science of Food and Agriculture (English)	Shrimp/prawns	DNA sequencing	COI	Commercial (supermarket and fishmongers in Spain, imported from Ecuador)	SPAIN	1, 2, and 3	12	Gil et al. (2024)

73	Ortiz-Moriano et al.	2024	Food Control (English)	Shrimp/ prawns	DNA sequencing	COI, 16S rRNA	Commercial (supermarkets in Spain, imported from Ecuador)	SPAIN	1, 2, and 3	1	Ortiz-Moriano et al. (2024)
74	Tiktak et al.	2024	Plos One (English)	Finfish, sharks, rays	DNA sequencing, LOC-LAMP	COI, ITS2, Control Region	Commercial (fishing ports and markets in Ecuador)	UK/ECUADOR	1 and 2	—	Tiktak et al. (2024)
75	Marín et al.	2025	Plos One (English)	Shellfish/ fish	DNA sequencing, qPCR-SSP, PCR-SSP, multiplex PCR	COI, 16S rRNA, 12S rRNA	Commercial and wild (landings, wholesale, markets, supermarkets in Peru)	PERU	1, 2, and 3	15	Marín et al. (2025)

Table 2. Species diversity found in the articles reviewed by the present study.

Group	Order	Family	Scientific name	Common name	Identification method	Genetic marker	Product presentation	Retailer (city-country)	IUCN status	(GenBank)/[BOLD] accessions	References
Chondrichthyes											
Sharks	Carcharhiniformes	Carcharhinidae	*Carcharhinus brachyurus*	Copper shark	DNA sequencing	Control Region	—	Commercial fishery (Peru)	VU	—	Benavides et al. (2011)
						COI	Fin or muscle from landed specimen	Landing (La Libertad-Peru)		(KJ146027)	Velez-Zuazo et al. (2015)
			Carcharhinus cerdale	Pacific smalltail shark	DNA sequencing	NAD2	Fresh whole body	Landing (Colombia)	CR	(OM165094 to OM165097)	Villate-Moreno et al. (2022)
			Carcharhinus falciformis	Silky shark	DNA sequencing	COI	Whole fillet or chopped fillet	Retail (Lima-Peru)	VU	—	Biffi et al. (2020)
					Multiplex PCR-SSP	ITS2	Fresh meat	Fish Market (Santo Domingo-Ecuador)		—	Manzanillas-Castro and Acosta-López (2022)
					DNA sequencing	NAD2	Fresh whole body	Landing (Colombia)		(OM165098 to OM165107)	Villate-Moreno et al. (2022)
					DNA sequencing, qPCR-SSP	COI	Dried fin	Shark fin seizure (El Dorado International Airport-Colombia)		—	Cardeñosa et al. (2023)
			Carcharhinus leucas	Bullshark	DNA sequencing	NAD2	Fresh whole body	Landing (Colombia)	VU	(OM165108)	Villate-Moreno et al. (2022)
					DNA sequencing, qPCR-SSP	COI	Dried fin	Shark fin seizure (El Dorado International Airport-Colombia)		—	Cardeñosa et al. (2023)
			Carcharhinus limbatus	Blacktip shark	DNA sequencing	NAD2	Fresh whole body	Landing (Colombia)	VU	(OM165109 to OM165111)	Villate-Moreno et al. (2022)
			Carcharhinus longimanus	Oceanic whitetip shark	DNA sequencing	COI	Muscle	Fishing port (Playa Mía, Manta, Manabí Province-Ecuador)	CR	—	Tiktak et al. (2024)
			Carcharhinus obscurus	Dusky shark	Multiplex PCR-SSP, DNA sequencing	COI, ITS2	Dried pectoral fin	Drying facility, Commercial storage warehouse (Caldera, Coquimbo, Paico-Chile)	EN	—	Hernández et al. (2008)

			DNA sequencing	COI	Fin or muscle from landed specimen	Landing (La Libertad-Peru)		(KJ146021)	Velez-Zuazo et al. (2015)
	Galeocerdo cuvier	Tiger shark	DNA sequencing	COI	Skin or muscle samples	Landing (Buenaventura-Colombia); seized from illegal fisheries (Malpelo Sanctuary-Colombia)	NT	(JN315435)	Caballero et al. (2012)
			DNA sequencing, qPCR-SSP	COI	Dried fin	Shark fin seizure (El Dorado International Airport-Colombia)		—	Cardeñosa et al. (2023)
			DNA sequencing	COI	Muscle	Fish market Santa Rosa (Salinas, Santa Elena Province-Ecuador)		—	Tiktak et al. (2024)
	Prionace glauca	Blue shark	Multiplex PCR-SSP	ITS2	Dried pectoral fin	Drying facility, Commercial storage warehouse (Caldera, Coquimbo, Paico-Chile)	NT	—	Hernández et al. (2008)
			Multiplex PCR-SSP	ITS2	Fresh whole individual, dried fin	Commercial storage warehouse (Paico-Chile)		—	Hernández et al. (2010)
			DNA sequencing	COI	Fin or muscle from landed specimen	Landing (La Libertad and Moquegua-Peru)		(KJ146042, KJ146043, KJ146044)	Velez-Zuazo et al. (2015)
			DNA sequencing	COI	Frozen and refrigerated fillets, dried, fish fritters	Market (Lambayeque-Peru); Restaurant, Supermarket (La Libertad-Peru)		(MH194440, MH194441, MH194480, MH194481, MH194484)	Marín et al. (2018)
			DNA sequencing	COI	Whole fillet or chopped fillet	Retail (Tumbes-Peru); Retail, Supermarket, Wholesale (Lima-Peru)		—	Biffi et al. (2020)
			DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)		—	Velez-Zuazo et al. (2021)
			Multiplex PCR-SSP	ITS2	Fresh meat	Fish Market (Santo Domingo-Ecuador)		—	Manzanillas-Castro and Acosta-López (2022)

	Species	Common name	Method	Marker	Sample type	Source	Status	Accession	Reference
	Rhizoprionodon longurio	Pacific sharpnose shark	DNA sequencing	NAD2	Fresh whole body	Landing (Colombia)	VU	(OM165170 to OM165178)	Villate-Moreno et al. (2022)
Sphyrnidae	*Sphyrna corona*	Scalloped bonnethead	DNA sequencing	NAD2	Fresh whole body	Landing (Colombia)	CR	(OM165179)	Villate-Moreno et al. (2022)
	Sphyrna lewini	Scalloped hammerhead	Multiplex PCR-SSP	ITS2	Dried pectoral fin	Drying facility, Commercial storage warehouse (Caldera, Coquimbo, Paico-Chile)	CR	—	Hernández et al. (2008)
			Multiplex PCR-SSP, DNA sequencing	COI, ITS2	Skin or muscle samples	Landing (Buenaventura-Colombia); seized from illegal fisheries (Malpelo Sanctuary-Colombia)		(JN315436 to JN315443)	Caballero et al. (2012)
			Multiplex PCR-SSP	ITS2	Fresh meat	Fish Market (Santo Domingo-Ecuador)		—	Manzanillas-Castro and Acosta-López (2022)
			DNA sequencing	NAD2	Fresh whole body	Landing (Colombia)		(OM165180 to OM165194)	Villate-Moreno et al. (2022)
			DNA sequencing, qPCR-SSP	COI	Dried fin	Shark fin seizure (El Dorado International Airport-Colombia)		—	Cardeñosa et al. (2023)
			DNA sequencing	COI	Muscle	Fishing port (Playa Mía, Manta, Manabí Province-Ecuador)		—	Tiktak et al. (2024)
	Sphyrna media	Scoophead	DNA sequencing	NAD2	Fresh whole body	Landing (Colombia)	CR	(OM165195)	Villate-Moreno et al. (2022)
	Sphyrna tiburo	Bonnethead	DNA sequencing	NAD2	Fresh whole body	Landing (Colombia)	EN	(OM165196 to OM165197)	Villate-Moreno et al. (2022)
	Sphyrna zygaena	Smooth hammerhead	Multiplex PCR-SSP	ITS2	Dried pectoral fin	Cooperative traders	VU	—	Hernández et al. (2008)
			DNA sequencing	COI	Skin or muscle samples	Landing (Buenaventura-Colombia); seized from illegal fisheries (Malpelo Sanctuary-Colombia)		(JN315444, JN315445)	Caballero et al. (2012)

			DNA sequencing	COI	Fin or muscle from landed specimens	Landing (La Libertad and Lambayeque-Peru)		(KJ146045)	Velez-Zuazo et al. (2015)
			DNA sequencing	COI	Fresh headless, fish fritters	Landing (Tumbes-Peru), Wholesale, Market, Restarurant (La Libertad-Peru)		(MH194422, MH194431, MH194471 to MH194475, MK070513)	Marín et al. (2018)
			DNA sequencing	COI	Whole fillet or chopped fillet	Retail, Wholesale (Lima-Peru); Retail (Tumbes-Peru)		—	Biffi et al. (2020)
			DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)		(MN880591 to MN880593)	Marín et al. (2022)
			DNA sequencing	NAD2	Fresh whole body	Landing (Colombia)		(OM165198 to OM165199)	Villate-Moreno et al. (2022)
	Triakidae	*Galeorhinus galeus*	Tope shark	DNA sequencing	ITS2	Dried pectoral fin	Drying facility, Commercial storage warehouse (Caldera, Coquimbo, Paico-Chile)	CR	—	Hernández et al. (2008)
				DNA sequencing	COI	Fin or muscle from landed specimen	Landing (La Libertad and Moquegua-Peru)		(KJ146028, KJ146029)	Velez-Zuazo et al. (2015)
		Mustelus albipinnis	Whitemargin smooth-hound	DNA sequencing	NAD2	Fresh whole body	Landing (Colombia)	LC	(OM165112 to OM165117)	Villate-Moreno et al. (2022)
		Mustelus henlei	Brown smooth-hound	DNA sequencing	NAD2	Fresh whole body	Landing (Colombia)	LC	(OM165118 to OM165135)	Villate-Moreno et al. (2022)
		Mustelus lunulatus	Sicklefin smooth-hound	DNA sequencing	COI	Refrigerated fillet	Supermarket (Lima-Peru)	LC	(MH194496)	Marín et al. (2018)
				DNA sequencing	COI	Whole fillet or chopped fillet	Supermarket (Lima-Peru); Retail (Tumbes-Peru)		—	Biffi et al. (2020)
				DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)		(MN880526, MN880605)	Marín et al. (2022)
				DNA sequencing	NAD2	Fresh whole body	Landing (Colombia)		(OM165136 to OM165166)	Villate-Moreno et al. (2022)
				DNA sequencing	COI	Muscle	Fish market Santa Rosa (Salinas, Santa Elena Province-Ecuador)		—	Tiktak et al. (2024)
		Mustelus mento	Speckled smooth-hound	DNA sequencing	COI	Whole fillet or chopped fillet	Supermarket (Lima-Peru)	CR	—	Biffi et al. (2020)

		Mustelus whitneyi	Humpback smooth-hound	DNA sequencing	COI	Fresh, refrigerated fillet	Wholesale, Supermarket (La Libertad-Peru); Multimarket (Callao-Peru)	CR	MH194477, MH194478, MH194506)	Marín et al. (2018)
				DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, Supermarket (Lima-Peru)		—	Velez-Zuazo et al. (2021)
				DNA sequencing	COI	Fresh whole body	Landing (Piura and Tumbes-Peru)		(MN880507 to MN880509, MN880531, MN880532, MN880606)	Marín et al. (2022)
Lamniformes	Alopiidae	*Alopias pelagicus*	Pelagic thresher	Multiplex PCR-SSP, DNA sequencing	COI	Skin or muscle samples	Landing (Buenaventura-Colombia); seized from illegal fisheries (Malpelo Sanctuary-Colombia)	EN	(JN315423 to JN315434)	Caballero et al. (2012)
				DNA sequencing	COI	Fin or muscle from landed specimen	Landing (La Libertad-Peru)		(KJ406022 to KJ406026)	Velez-Zuazo et al. (2015)
				DNA sequencing	COI	Fresh fillet, headless	Retail (Lima and Tumbes-Peru)		(MH194433, MH194456, MH194476)	Marín et al. (2018)
				DNA sequencing	COI	Whole fillet or chopped fillet	Retail (Lima and Tumbes-Peru)		—	Biffi et al. (2020)
				DNA sequencing	COI	Dried fillet	Market (Ancash-Peru)		(MN839531)	Marín et al. (2021)
				Multiplex PCR-SSP	ITS2	Fresh meat	Fish Market (Santo Domingo-Ecuador)		—	Manzanillas-Castro and Acosta-López (2022)
				DNA sequencing, qPCR-SSP	COI	Dried fin	Shark fin seizure at El Dorado International Airport (Bogotá-Colombia)		—	Cardeñosa et al. (2023)
				DNA sequencing, LOC-LAMP	COI Control Region	Muscle	Fish market Santa Rosa (Salinas, Santa Elena Province-Ecuador)		—	Tiktak et al. (2024)
		Alopias superciliosus	Bigeye thresher	Multiplex PCR-SSP	ITS2	Dried pectoral fin	Drying facility, Commercial storage warehouse (Caldera,	VU	—	Hernández et al. (2008)

Family	Species	Common name	Method	Marker	Sample	Location	Status	Accession	Reference
						Coquimbo, Paico-Chile)			
			DNA sequencing	COI	Whole fillet or chopped fillet	Retail (Lima-Peru)		—	Biffi et al. (2020)
			DNA sequencing, LOC-LAMP	COI ITS2	Muscle	Fish market Santa Rosa (Salinas, Santa Elena Province-Ecuador)		—	Tiktak et al. (2024)
	Alopias vulpinus	Thresher	Multiplex PCR-SSP	ITS2	Dried pectoral fin	Drying facility, Commercial storage warehouse (Caldera, Coquimbo, Paico-Chile)	VU	—	Hernández et al. (2008)
			DNA sequencing	COI	Whole fillet or chopped fillet	Retail (Lima-Peru)		—	Biffi et al. (2020)
Lamnidae	*Isurus oxyrinchus*	Shortfin mako	Multiplex PCR-SSP	ITS2	Dried pectoral fin	Drying facility, Commercial storage warehouse (Caldera, Coquimbo, Paico-Chile)	EN	—	Hernández et al. (2008)
			Multiplex PCR-SSP	ITS2	Fresh whole individual, dried fin	Commercial storage warehouse (Paico-Chile)		—	Hernández et al., 2010
			DNA sequencing	COI	Fin or muscle from landed specimen	Landing (La Libertad and Moquegua-Peru)		(KJ146030 to KJ146038)	Velez-Zuazo et al. (2015)
			DNA sequencing	COI	Fresh fillet	Multimarket (Lima-Peru)		(MH194507)	Marín et al. (2018)
			DNA sequencing	COI	Whole fillet or chopped fillet	Restaurant, Retail, Supermarket, Wholesale (Lima-Peru)		—	Biffi et al. (2020)
			DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)		—	Velez-Zuazo et al. (2021)
			DNA sequencing	COI	Meat slice	Fish market (Santiago-Chile)		—	Dufflocq et al. (2022)
			Multiplex PCR-SSP	ITS2	Fresh meat	Fish Market (Santo Domingo-Ecuador)		—	Manzanillas-Castro and Acosta-López (2022)
			DNA sequencing, Control Region	COI ITS2	Muscle	Artisanal fishing port (Esmeraldas Province-Ecuador)		—	Tiktak et al. (2024)

	Order	Family	Species	Common name	Method	Marker	Sample type	Location	Status	Accession	Reference
			Isurus paucus	Longfin mako	Multiplex PCR-SSP	ITS2	Dried pectoral fin	Drying facility, Commercial storage warehouse (Caldera, Coquimbo, Paico-Chile)	EN	—	Hernández et al. (2008)
			Lamna nasus	Porbeagle	Multiplex PCR-SSP	ITS2	Dried pectoral fin	Drying facility, Commercial storage warehouse (Caldera, Coquimbo, Paico-Chile)	VU	—	Hernández et al. (2008)
					Multiplex PCR-SSP	ITS2	Fresh whole individual, dried fin	Commercial storage warehouse (Paico-Chile)		—	Hernández et al. (2010)
					DNA sequencing	COI	Fin or muscle from landed specimen	Landing (Piura, La Libertad, Ancash, Lima, or Moquegua-Peru)		(KJ146039, KJ146040, KJ146041)	Velez-Zuazo et al. (2021)
					DNA sequencing	COI	Meat slice	Fish market, Open-air Market (Santiago-Chile)		—	Dufflocq et al. (2022)
	Orectolobiformes	Rhincodontidae	*Rhincodon typus*	Whale shark	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	EN	(MH194458)	Marín et al. (2018)
	Squatiniformes	Squatinidae	*Squatina armata*	Angel shark	DNA sequencing	COI	Fresh whole body	Wholesale (Lambayeque-Peru), Bayovar Port (Piura-Peru)	CR	[PMVTB046-20, PMVTB047-20, PMVTB067-20, PMVTB068-20]	Cañedo-Apolaya et al. (2021)
			Squatina californica	Pacific angelshark	DNA sequencing	COI	Whole fillet or chopped fillet	Retail (Tumbes-Peru)	NT	—	Biffi et al. (2020)
					DNA sequencing	COI	Whole body	Punta Pico coast (Tumbes-Peru)		[FMCT1223-19]	Cañedo-Apolaya et al. (2021)
Batoids	Myliobatiformes	Dasyatidae	*Hypanus dipterurus*	Diamond stingray	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	VU	(MH194454)	Marín et al. (2018)
			Hypanus longus	Longtail stingray	DNA sequencing	COI	Muscle	Fish market Santa Rosa (Salinas, Santa Elena Province-Ecuador)	VU	—	Tiktak et al. (2024)
			Pteroplatytrygon violacea	Pelagic stingray	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	LC	(MH194470)	Marín et al. (2018)
		Gymnuridae	*Gymnura afuerae*	Butterfly ray	DNA sequencing	COI	Fresh whole body, fresh fillet	Landing (Tumbes-Peru)	NT	(MH194463, MH194465)	Marín et al. (2018)
					DNA sequencing	COI	Fresh whole body	Isla de Lobos (Peru)		(PP756688 to PP756691)	Ehemann et al. (2024b)
		Myliobatidae	*Aetobatus laticeps*	Pacific eagle ray	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	VU	(MH194470)	Marín et al. (2018)
			Mobular birostris	Giant manta	DNA sequencing	COI	Whole body or pectoral fins	Landing (Tumbes-Peru)	EN	[Project Code: DBPDC]	Alfaro-Cordova et al. (2023)

			Species	Common name	Method	Marker	Sample type	Location	Status	Accession	Reference
			Mobula mobular	Devil fish	DNA sequencing	COI	Fresh whole body and fillet, dried, tortilla	Landing, Market (Tumbes-Peru); Market (Lambayeque-Peru); Restaurant (La Libertad-Peru)	EN	(MH194439, MH194451 to MH194453, MH194455, MH194457, MH194461, MH194464, MH194469, MH194482, MK070514, MK070516)	Marín et al. (2018)
					DNA sequencing	COI	Whole body or pectoral fins	Landing (La Libertad and Tumbes-Peru)		[Project Code: DBPDC]	Alfaro-Cordova et al. (2023)
			Mobula munkiana	Munk's devil ray	DNA sequencing	COI	Whole body or pectoral fins	Landing (La Libertad and Tumbes-Peru)	VU	[Project Code: DBPDC]	Alfaro-Cordova et al. (2023)
			Mobula tarapacana	Chilean devil ray	DNA sequencing	COI	Whole body or pectoral fins	Landing (La Libertad-Peru)	EN	[Project Code: DBPDC]	Alfaro-Cordova et al. (2023)
			Mobula thurstoni	Smoothtail mobula	DNA sequencing	COI	Whole body or pectoral fins	Landing (La Libertad and Tumbes-Peru)	EN	[Project Code: DBPDC]	Alfaro-Cordova et al. (2023)
			Myliobatis chilensis	Chilean eagle ray	DNA sequencing	COI	Refrigerated and fresh fillets, dried	Market (Lambayeque-Peru); Market, Supermarket (La Libertad-Peru)	VU	(MH194450, MH194479, MH194483, MH194485)	Marín et al. (2018)
					DNA sequencing	COI	Whole fillet or chopped fillet	Retail (Lima-Peru)		—	Biffi et al. (2020)
			Myliobatis longirostris	Snouted eagle ray	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	VU	(MH194462)	Marín et al. (2018)
		Urotrygonidae	*Urotrygon chilensis*	Blotched stingray	DNA sequencing	COI, NAD2	Fresh whole body	Landing (Manta, Punta Blanca, Santa Rosa-Ecuador), (Tumbes -Peru)	NT	(PP179040 to PP179043)	Ehemann et al. (2024a)
	Rajiformes	Arhynchobatidae	*Sympterygia brevicaudata*	Shorttail fanskate	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	NT	(MH194468)	Marín et al. (2018)
	Rhinopristiformes	Pristidae	*Pristis pristis*	Common sawfish	DNA sequencing	COI	Fresh whole body	Landing (Máncora-Peru)	CR	[PMFSH636-20]	Cabanillas-Torpoco et al. (2020)
		Rhinobatidae	*Pseudobatos planiceps*	Pacific guitarfish	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	VU	(MH194460)	Marín et al. (2018)
	Torpediniformes	Narcinidae	*Narcine entemedor*	Giant electric ray	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	VU	(MH194459, MH194488, MK070517)	Marín et al. (2018)
Holocephali	Chimaeriformes	Callorhinchidae	*Callorhinchus callorynchus*	Plownose chimaera	DNA sequencing	COI	Whole fillet or chopped fillet	Supermarket (Lima-Peru)	VU	—	Biffi et al. (2020)

Osteichthyes											
Finfish	Acanthuriformes	Lobotidae	*Lobotes pacifica*	Pacific tripletail	DNA sequencing	COI	Whole fillet or chopped fillet	Restaurant, Supermarket (Lima-Peru)	LC	—	Biffi et al. (2020)
					DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)		—	Velez-Zuazo et al. (2021)
					DNA sequencing	COI	Fresh whole body	Market (Piura-Peru)		(MN839527)	Marín et al. (2021)
		Luvaridae	*Luvarus imperialis*	Luvar	DNA sequencing	COI	Whole fillet or chopped fillet	Wholesale (Lima-Peru)	LC	—	Biffi et al. (2020)
	Acropomatiformes	Malakichthyidae	*Hemilutjanus macrophthalmos*	Grape-eye seabass	DNA sequencing	COI	Fresh whole body	Wholesale (Piura-Peru)	DD	(MN839520)	Marín et al. (2021)
					DNA sequencing	COI	Fresh whole body	Landing (Piura and Tumbes-Peru)		(MN880513, MN880589)	Marín et al. (2022)
					DNA sequencing, Multiplex PCR-SSP	COI	Fresh whole body, cooked	Landing and Wholesale (Piura-Peru), Restaurant (Tumbes-Peru)		(PP092953)	Marín et al. (2025)
	Atheriniformes	Atherinopsidae	*Odontesthes regia*	Chilean silverside	DNA sequencing	COI	Fried and fresh fillets	Restaurant (Lima-Peru)	LC	(MH194518, MH194550)	Marín et al. (2018)
					DNA sequencing	COI	Whole or fillet	(Canada, imported from Peru)		—	Shehata et al. (2018)
					DNA sequencing	COI	Whole fillet or chopped fillet	Retail (Lima-Peru)		—	Biffi et al. (2020)
					DNA sequencing	COI	Fresh whole body	Market (Ancash-Peru)		(MN839513)	Marín et al. (2021)
	Blenniiformes	Labrisomidae	*Labrisomus philippii*	Chalapo clinid	DNA sequencing	COI	Cooked whole body	Restaurant (Lima-Peru)	LC	(MH194519)	Marín et al. (2018)
	Carangaria *incertae sedis*	Centropomidae	*Centropomus unionensis*	Yellowfin snook	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	LC	(MN880528)	Marín et al. (2022)
		Sphyraenidae	*Sphyraena ensis*	Mexican barracuda	DNA sequencing	COI	Fresh whole body	Multimarket (Lima-Peru)	LC	(MH194547)	Marín et al. (2018)
	Carangiformes	Carangidae	*Selene peruviana*	Peruvian moonfish	DNA sequencing	COI	Whole fillet or chopped fillet	Wholesale (Lima-Peru)	LC	—	Biffi et al. (2020)
			Seriola lalandi	Yellowtail amberjack	DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)	LC	—	Velez-Zuazo et al. (2021)
			Seriola peruana	Fortune jack	DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)	LC	—	Velez-Zuazo et al. (2021)
			Seriola rivoliana	Longfin yellowtail	DNA sequencing	COI	Marinated ceviche	Restaurant (Lima-Peru)	LC	(MH194546)	Marín et al. (2018)

				DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)		(MN880603)	Marín et al. (2022)
		Trachinotus paitensis	Paloma pompano	DNA sequencing	COI	Whole fillet or chopped fillet	Supermarket (Lima-Peru)	LC	—	Biffi et al. (2020)
				DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)		(MN880583 to MN880587)	Marín et al. (2022)
				DNA sequencing	COI	Fresh whole body	Market (Ancash-Peru)		(PP092957)	Marín et al. (2025)
		Trachurus murphyi	Chilean jack mackerel	RFLP-SSCP	Cytb	Fishmeal	International Fishmeal and Oil Manufacturers' Association, IFOMA (Germany, imported from Chile)	DD	—	Rehbein (2002)
				DNA sequencing	COI	Whole fillet or chopped fillet	Wholesale (Lima-Peru)		—	Biffi et al. (2020)
	Coryphaenidae	*Coryphaena hippurus*	Common dolphinfish	DNA sequencing	COI	Steamed fillet, marinated ceviche, fresh whole body, stir-fried, deep fried fillet, fish roe, fish burger	Landing (Tumbes-Peru); Restaurant (La Libertad-Peru); Supermarket (Ancash-Peru); Multimarket, Restaurant, Supermarket (Lima-Peru)	LC	(MH194438, MH194444, MH194449, MH194511, MH194512, MH194520, MH194521, MH194535, MH194542, MK070511)	Marín et al. (2018)
				DNA sequencing	COI	Whole, frozen	Retailer, Importer (Canada, imported from Peru)		—	Shehata et al. (2019)
				DNA sequencing	COI	Whole fillet or chopped fillet	Restaurant, Supermarket, Wholesale (Lima-Peru)		—	Biffi et al. (2020)
				DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)		—	Velez-Zuazo et al. (2021)
	Istiophoridae	*Istiompax indica*	Black marlin	DNA sequencing	COI	Whole fillet or chopped fillet	Retail (Lima and Tumbes-Peru)	LC	—	Biffi et al. (2020)
		Istiophorus platypterus	Indo-Pacific sailfish	DNA sequencing	COI	Whole fillet or chopped fillet	Retail (Tumbes-Peru)	VU	—	Biffi et al. (2020)
		Kajikia audax	Striped marlin	DNA sequencing	COI, Control Region	Fresh whole body	Landing (Tumbes-Peru)	LC	(MH194486, MK070523)	Marín et al. (2018)
				DNA sequencing	COI	Whole fillet or chopped fillet	Landing (Tumbes-Peru)			Biffi et al. (2020)
		Makaira nigricans	Blue marlin	DNA sequencing	COI	Whole fillet or chopped fillet	Retail (Lima-Peru)	VU	—	Biffi et al. (2020)

	Rachycentridae	*Rachycentron canadum**	Cobia	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	LC	(MN839528)	Marín et al. (2021)
	Xiphiidae	*Xiphias gladius*	Swordfish	DNA sequencing	COI	Fish fritters, fresh headless	Landing (Tumbes-Peru); Market, Restaurant (La Libertad-Peru)	NT	(MH194430, MH194432, MH194466, MK070512)	Marín et al. (2018)
				DNA sequencing	COI	Whole, refrigerated	Importer (Canada, imported from Ecuador)		—	Shehata et al. (2019)
				DNA sequencing	COI	—	Restaurant, Retail, Supermarket, Wholesale (Lima-Peru)		—	Biffi et al. (2020)
				DNA sequencing	COI	Meat slice	Fish market, Open-air Market, Supermarket (Santiago-Chile)		—	Dufflocq et al. (2022)
Centrarchiformes	Aplodactylidae	*Aplodactylus punctatus*	Zamba marblefish	DNA sequencing	COI	Whole fillet or chopped fillet	Wholesale (Lima-Peru)	NE	—	Biffi et al. (2020)
	Kyphosidae	*Girella freminvillii*	Black sea chub	DNA sequencing	COI	Whole fillet or chopped fillet	Wholesale (Lima-Peru)	LC	—	Biffi et al. (2020)
Clupeiformes	Alosidae	*Sardinops sagax*	South American pilchard	RFLP-SSCP	Cytb	Fishmeal	International Fishmeal and Oil Manufacturers' Association, IFOMA (Germany, imported from Chile)	LC		Rehbein (2002)
				PCR-RFLP	Cytb	Canned	Supermarket (France, canned in Peru)		—	Jérôme et al. (2003a)
				FINS	Cytb	Canned	Supermarket (France, origin Chile and Peru)		(AY394046, AY394047)	Jérôme et al. (2003b)
	Clupeidae	*Strangomera bentincki*	Araucanian herring	RFLP-SSCP	Cytb	Fishmeal	International Fishmeal and Oil Manufacturers' Association, IFOMA (Germany, imported from Chile)	LC	—	Rehbein (2002)
				FINS	Cytb	Canned	Supermarket (France, origin Chile and Peru)		(AY394050)	Jérôme et al. (2003b)
	Dorosomatidae	*Opisthonema medirastre*	Middling thread herring	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	LC	(MN839514)	Marín et al. (2021)
	Engraulidae	*Engraulis ringens*	Anchoveta	RFLP-SSCP	Cytb	Fishmeal	International Fishmeal and Oil Manufacturers' Association, IFOMA (Germany, imported from Chile and Peru)	LC	—	Rehbein (2002)
				DNA sequencing	16S rRNA	Fish feed: Canned (whole fish), salty (without bones)	Spanish producers and pet shop (species origin: Peru)		—	Ardura et al. (2012)
				DNA sequencing	16S rRNA	Fish feed: Canned in oil	Imported (species origin: Peru)		(HQ623641)	Horreo et al. (2013)

				FINS	Cytb	Fresh, canned	Markets, Supermarkets, and specialized stores (Spain, origin Chile and Peru)		—	Velasco et al. (2016)
				PCR-SSP	5S rDNA	Fresh	(Valparaíso-Chile)		(JX070024-JX070033)	Chairi and Rebordinos (2014)
				DNA sequencing	COI	Canned, frozen burger	Supermarket (Ancash and La Libertad-Peru)		(MH194490, MH194491, MK070518, MK070519, MH194537)	Marín et al. (2018)
				DNA sequencing	Cytb	In oil	Large-scale retail distribution (Tuscany-Italy, imported from Chile)		—	Giusti et al. (2019)
		Ethmidium maculatum	Pacific menhaden	DNA sequencing	COI	Fresh whole body	Market (Lima-Peru)	DD	(MH194494, MH194495)	Marín et al. (2018)
				DNA sequencing	COI	Whole fillet or chopped fillet	Wholesale (Lima-Peru)			Biffi et al. (2020)
Eupercaria *incertae sedis*	Haemulidae	*Anisotremus interruptus*	Burrito grunt	DNA sequencing	COI	Fresh whole body	Market (La Libertad-Peru)	LC	(MH194448, MK070515)	Marín et al. (2018)
				DNA sequencing	COI	Fresh whole body	Wholesale (Piura-Peru)		(MN839517)	Marín et al. (2021)
				DNA sequencing	COI	Fresh whole body	Landing (Piura-Peru)		(MN880558)	Marín et al. (2022)
				DNA Sequencing, PCR-SSP	COI	Fresh whole body, cooked	Restaurant and Wholesale (Piura-Peru)		(PP092956, PV562156)	Marín et al. (2025)
		Anisotremus scapularis	Peruvian grunt	DNA sequencing	COI	Fried, fresh, steamed whole body	Market, Restaurant (Ancash-Peru); Restaurant (La Libertad and Piura-Peru)	LC	(MH194443, MH194500, MH194522, MH194526)	Marín et al. (2018)
				DNA sequencing	COI	Whole fillet or chopped fillet	Supermarket (Lima-Peru)		—	Biffi et al. (2020)
				DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)		—	Velez-Zuazo et al. (2021)
				DNA sequencing	COI	Fresh whole body	Market (Ancash-Peru)		(MN839516)	Marín et al. (2021)
				DNA sequencing	COI	Fresh whole body	Landing (Piura-Peru)		(MN880542)	Marín et al. (2022)
		Haemulon scudderii	Grey grunt	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	LC	(MN839518)	Marín et al. (2021)
				DNA sequencing	COI	Fresh whole body	Wholesale (Piura-Peru)		(PQ459803 to PQ459804)	Marín et al. (2025)

Family	Species	Common name	Method	Gene	Sample	Origin	Status	Accession	Reference
	Isacia conceptionis	Cabinza grunt	DNA sequencing	COI	Whole fillet or chopped fillet	Wholesale (Lima-Peru)	LC	—	Biffi et al. (2020)
			DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)		—	Velez-Zuazo et al. (2021)
Labridae	*Decodon melasma*	Blackspot wrasse	DNA sequencing	COI	Fresh whole body	Landing (Piura-Peru)	LC	(MN880543)	Marín et al. (2022)
Lutjanidae	*Lutjanus argentiventris*	Yellow snapper	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	LC	(MN880525, MN880602)	Marín et al. (2022)
Malacanthidae	*Caulolatilus affinis*	Bighead tilefish	DNA sequencing	COI	Whole fillet or chopped fillet	Supermarket (Lima-Peru)	LC	—	Biffi et al. (2020)
	Caulolatilus princeps	Ocean whitefish	DNA sequencing	COI	Fresh whole body	Landing (Piura-Peru)	LC	(MN880554)	Marín et al. (2022)
Sciaenidae	*Cilus gilberti*	Corvina drum	DNA sequencing	COI	Whole fillet or chopped fillet	Restaurant, Supermarket (Lima-Peru)	DD	—	Biffi et al. (2020)
	Cynoscion albus	Whitefin weakfish	DNA sequencing	COI	Whole fillet or chopped fillet	Supermarket (Lima-Peru)	DD	—	Biffi et al. (2020)
			DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)			Velez-Zuazo et al. (2021)
	Cynoscion analis	Peruvian weakfish	qPCR-SSP	ATPase6	Fresh whole body	Wholesale and supermarket (Ancash, Lambayeque, Lima-Peru)	LC	—	Mora et al. (2018)
			DNA sequencing	COI	Fresh whole body	Landing (Piura-Peru)		(MN880521)	Marín et al. (2022)
	Cynoscion phoxocephalus	Cachema weakfish	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	LC	(MN880604)	Marín et al. (2022)
	Cynoscion praedatorius	Boccone weakfish	DNA sequencing	COI	Fried	Restaurant (La Libertad-Peru)	DD	(MH194447)	Marín et al. (2018)
			DNA sequencing	COI	Whole fillet or chopped fillet	Retail, Supermarket, Wholesale (Lima-Peru)		—	Biffi et al. (2020)
			DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)		—	Velez-Zuazo et al. (2021)
	Cynoscion stolzmanni	Stolzmann's weakfish	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	LC	(MN880529)	Marín et al. (2022)
	Cheilotrema fasciatum	Arnillo drum	DNA sequencing	COI	Fresh whole body	Market (Ancash-Peru)	LC	(MH194527)	Marín et al. (2018)
			DNA sequencing	COI	Fresh whole body	Market (Ancash-Peru)		(MN839519)	Marín et al. (2021)
	Larimus acclivis	Steeplined drum	DNA sequencing	COI	Fresh whole body	Landing (Piura-Peru)	LC	(MN880556)	Marín et al. (2022)

		Paralonchurus peruanus	Peruvian banded croaker	DNA sequencing	COI	Steamed whole body	Restaurant (La Libertad-Peru)	LC	(MH194442)	Marín et al. (2018)
				DNA sequencing	COI	Fresh whole body	Market (Ancash-Peru)		(PP092959)	Marín et al. (2025)
		Pareques lanfeari	Royal highhat	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	LC	(MN880527)	Marín et al. (2022)
		Umbrina xanti	Polla drum	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	LC	(MN880599)	Marín et al. (2022)
	Sparidae	*Calamus brachysomus*	Pacific porgy	DNA sequencing	COI	Fresh whole body	Landing (Piura-Peru)	LC	(MN880544)	Marín et al. (2022)
				DNA sequencing	COI	Fresh whole body	Wholesale (Piura-Peru)		(PP092958)	Marín et al. (2025)
Gadiformes	Merlucciidae	*Macruronus magellanicus*	Patagonian grenadier	RFLP-SSCP	Cytb	Fishmeal	International Fishmeal and Oil Manufacturers' Association, IFOMA (Germany, imported from Chile)	NE	—	Rehbein (2002)
		Merluccius gayi	South Pacific hake	PCR-RFLP	Cytb, 5S rDNA	Fresh whole body	(Chile)	DD	—	Perez and Garcia-Vazquez (2004)
				qPCR-SSP	Control Region	Whole body	Wholesale and supermarket (Ancash, Lambayeque, Lima-Peru)		—	Mora et al. (2018)
				DNA sequencing	COI	Marinated ceviche	Restaurant (La Libertad-Peru)		(MH194428)	Marín et al. (2018)
				DNA sequencing	COI	Whole, refrigerated	Retailer (Canada, imported from Peru)		—	Shehata et al. (2019)
				DNA sequencing	COI	Whole fillet or chopped fillet	Retail, Wholesale (Lima-Peru)		—	Biffi et al. (2020)
				DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)		—	Velez-Zuazo et al. (2021)
				DNA sequencing	COI	Fresh whole body	Market (Ancash-Peru)		(PP092962)	Marín et al. (2025)
		Merluccius peruanus	Peruvian hake	qPCR-SSP	Control Region	Whole fillet or chopped fillet	Wholesale and supermarket (Ancash, Lambayeque, Lima-Peru)	NE	—	Mora et al. (2018)
Lampriformes	Lampridae	*Lampris guttatus*	Opah	DNA sequencing	COI	Fresh fillet	Multimarket (Lima-Peru)	LC	(MH194505)	Marín et al. (2018)
				DNA sequencing	COI	Whole fillet or chopped fillet	Retail, Wholesale (Lima-Peru)		—	Biffi et al. (2020)
Mugiliformes	Mugilidae	*Mugil cephalus*	Flathead grey mullet	DNA sequencing	COI	Whole fillet or chopped fillet	Restaurant, Retail, Wholesale (Lima-Peru)	LC	—	Biffi et al. (2020)

				DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)		—	Velez-Zuazo et al. (2021)
				DNA sequencing	COI	Fresh whole body	Market (Ancash-Peru)		(PP092963)	Marín et al. (2025)
Ophidiiformes	Ophidiidae	*Brotula clarkae*	Pacific bearded brotula	DNA sequencing	COI	Whole fillet or chopped fillet	Restaurant, Supermarket (Lima-Peru)	DD	—	Biffi et al. (2020)
				DNA sequencing	COI	Fresh whole body	Landing (Piura and Tumbes-Peru)		(MN880510, MN880535, MN880573, MN880574, MN880577, MN880578, MN880579, MN880607)	Marín et al. (2022)
		Brotula ordwayi	Ordway's brotula	DNA sequencing	COI	Fresh whole body	Landing (Piura and Tumbes-Peru)	LC	(MN880511, MN880568)	Marín et al. (2022)
		Genypterus chilensis	Red cusk-eel	FINS	COI	Fresh	(Chile)	NE	—	Santaclara et al. (2014)
		Genypterus maculatus	Black cusk-eel	FINS	COI	Fresh	(Chile)	NE	—	Santaclara et al. (2014)
		Lepophidium negropinna	Specklefin cusk eel	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	LC	(MN880512, MN880569, MN880570 to MN880572)	Marín et al. (2022)
Perciformes	Anthiadidae	*Acanthistius pictus*	Brick seabass	DNA sequencing	COI	Whole fillet or chopped fillet	Supermarket, Wholesale (Lima-Peru)	LC	—	Biffi et al. (2020)
				DNA sequencing	COI	Fresh whole body	Wholesale (Lambayeque-Peru)		(MN839525)	Marín et al. (2021)
				DNA sequencing	COI	Fresh whole body	Landing (Piura-Peru)		(MN880541)	Marín et al. (2022)
		Anthias noeli	Rosy jewelfish	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	NE	[FMCT1282N21, FMCT1283N21, FMCT1284N21, FMCT1285N21, FMCT1237N19]	Vera et al. (2023)
		Hemanthias peruanus	Splittail bass	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	LC	(MN880600)	Marín et al. (2022)
		Hemanthias signifer	Damsel bass	DNA sequencing	COI	Whole fillet or chopped fillet	Supermarket (Lima-Peru)	LC	—	Biffi et al. (2020)
		Pronotogrammus multifasciatus	Threadfin bass	DNA sequencing	COI	Whole fillet or chopped fillet	Retail (Tumbes-Peru)	LC	—	Biffi et al. (2020)

Family	Species	Common name	Method	Marker	Sample	Source	Status	Accession	Reference
Epinephelidae	*Alphestes immaculatus*	Pacific mutton hamlet	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	LC	(MN880524)	Marín et al. (2022)
			DNA Sequencing, PCR-SSP	COI, 16S rRNA	Fresh whole body	Wholesale (Lambayeque-Peru)		(PQ459846 to PQ459848, PP092955)	Marín et al. (2025)
	Cephalopholis colonus	Pacific creole-fish	DNA sequencing	COI	Whole fillet or chopped fillet	Supermarket (Lima-Peru), Landing (Tumbes-Peru)	LC	—	Biffi et al. (2020)
			DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)		(MN880594 to MN880596)	Marín et al. (2022)
	Epinephelus analogus	Spotted grouper	DNA sequencing	COI	Fresh whole body	Wholesale (Piura-Peru)	LC	(PP092961)	Marín et al. (2025)
	Epinephelus quinquefasciatus	Pacific goliath grouper	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	DD	(MN880588)	Marín et al. (2022)
	Hyporthodus acanthistius	Rooster hind	DNA sequencing	COI	Whole fillet or chopped fillet	Supermarket, Wholesale (Lima-Peru)	VU	—	Biffi et al. (2020)
			DNA sequencing	COI	Fresh whole body	Market (Tumbes-Peru)		(MN839521)	Marín et al. (2021)
			DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)		(MN880575)	Marín et al. (2022)
	*Hyporthodus cifuentesi***	Olive grouper	DNA sequencing	COI	Fresh whole body	Wholesale (Piura-Peru)	LC	(MN839523)	Marín et al. (2021)
	Hyporthodus niphobles	Star-studded grouper	DNA sequencing	COI	Whole fillet or chopped fillet	Supermarket, Wholesale (Lima-Peru)	LC	—	Biffi et al. (2020)
			DNA sequencing	COI	Fresh whole body	Landing (Piura and Tumbes-Peru)		(MN880506, MN880520, MN880536, MN880537, MN880566, MN880567, MN880576, MN880590, MN880608)	Marín et al. (2022)
			DNA sequencing	COI	Fresh whole body	Market (Tumbes-Peru)		(PP092960)	Marín et al. (2025)
	Mycteroperca xenarcha	Broomtail grouper	DNA sequencing	COI	Cooked fish meat	Restaurant (Lima-Peru)	DD	(MH194543)	Marín et al. (2018)
			DNA sequencing	COI	Fresh whole body	Wholesale (Piura-Peru)		(MN839523)	Marín et al. (2021)
			DNA sequencing	COI	Fresh whole body	Landing (Piura and Tumbes-Peru)		(MN880516, MN880557, MN880561 to MN880565)	Marín et al. (2022)
Nototheniidae	*Dissostichus eleginoides*	Patagonian toothfish	DNA sequencing	COI	Whole or fillet	(Canada, imported from Chile)	NE	—	Shehata et al. (2018)
			DNA sequencing	COI	Whole, refrigerated	Retailer (Canada, imported from Chile)	NE	—	Shehata et al. (2019)

		Dissostichus mawsoni	Antartic toothfish	DNA sequencing	COI	Whole, frozen	Retailer (Canada, imported from Chile)		—	Shehata et al. (2019)
	Sebastidae	*Sebastes oculatus*	Patagonian redfish	DNA sequencing	COI	Whole fillet or chopped fillet	Wholesale (Lima-Peru)	LC	—	Biffi et al. (2020)
	Serranidae	*Diplectrum conceptione*	Sand-perch	DNA sequencing	COI	Whole fillet or chopped fillet	Retail, Wholesale (Lima-Peru)	LC	—	Biffi et al. (2020)
		Diplectrum pacificum	Inshore sand perch	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	LC	(MN880597)	Marín et al. (2022)
		Paralabrax callaensis	Southern rock bass	DNA sequencing	COI	Fresh whole body	Landing (Piura and Tumbes-Peru)	DD	(MN880538, MN880539, MN880559)	Marín et al. (2018)
				DNA sequencing	COI	Fresh whole body	Market (Ancash-Peru)		(MN839525)	Marín et al. (2021)
				DNA Sequencing, Multiplex PCR-SSP	COI, 16S rRNA	Fresh, cooked	Landing and Market (Tumbes-Peru), Market (Ancash-Peru), Restaurant (Piura)		(PP092943 to PP092947, PP087227 and PPP087228)	Marín et al. (2025)
		Paralabrax humeralis	Peruvian rock seabass	DNA sequencing	COI	Marinated ceviche, fish fritters	Restaurant (Ancash and Piura-Peru)	DD	(MH194499, MH194524, MH194541)	Marín et al. (2018)
				DNA sequencing	COI	Whole fillet or chopped fillet	Supermarket, Wholesale (Lima-Peru)		—	Biffi et al. (2020)
				DNA sequencing	COI	Fresh whole body	Market (Ancash-Peru)		(MN839526)	Marín et al. (2021)
				DNA sequencing	COI	Fresh whole body	Landing (Piura-Peru)		(MN880503 to MN880505, MN880514, MN880517, MN880533, MN880534, MN880540)	Marín et al. (2022)
				DNA Sequencing, Multiplex PCR-SSP	COI, 16S rRNA	Fresh, cooked	Market (Tumbes, Piura, La Libertad, Ancash-Peru), Restaurant (Ancash-Peru)		(PQ459836 to PQ459845, PP092948 to PP092952, PPP087229 and PV491563)	Marín et al. (2025)
	Triglidae	*Prionotus stephanophrys*	Lumptail searobin	DNA sequencing	COI	Fish fritters, fresh pieces	Market, Restaurant (Ancash-Peru)	LC	(MH194492, MH194531)	Marín et al. (2018)
				DNA sequencing	COI	Whole fillet or chopped fillet	Retail, Wholesale (Lima-Peru)		—	Biffi et al. (2020)
				DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)		—	Velez-Zuazo et al. (2021)
				DNA sequencing	COI	Fresh whole body	Market (Tumbes-Peru)		(MN839515)	Marín et al. (2021)

Order	Family	Species	Common name	Method	Marker	Sample type	Source (Location)	Status	Accession	Reference
				DNA sequencing	COI	Fresh whole body	Market (Tumbes-Peru)		(PQ459813 to PQ459814)	Marín et al. (2025)
Pleuronectiformes	Cynoglossidae	*Symphurus chabanaudi*	Chabanaud's tonguefish	DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)	LC	(PP092966)	Marín et al. (2025)
	Paralichthyidae	*Ancylopsetta dendritica*	Three-spot flounder	DNA sequencing	COI	Fresh whole body	Wholesale (Piura-Peru)	LC	(PP092964)	Marín et al. (2025)
		Cyclopsetta querna	Toothed flounder	DNA sequencing	COI	Whole fillet or chopped fillet	Restaurant, Supermarket, Wholesale (Lima-Peru)	LC	—	Biffi et al. (2020)
				DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)		—	Velez-Zuazo et al. (2021)
				DNA sequencing	COI, 12S rRNA	Fresh whole body, cooked	Landing (Tumbes-Peru), Restaurant (Tumbes-Peru)		(PP092965, PV505011, PV562161)	Marín et al. (2025)
		Etropus ectenes	Sole flounder	DNA sequencing	COI	Marinated ceviche	Restaurant (La Libertad-Peru)	LC	(MH194424, MH194425)	Marín et al. (2018)
				DNA Sequencing, PCR-SSP	COI	Fresh whole body	Landing (Tumbes-Peru)		(PP092942)	Marín et al. (2025)
		Hippoglossina tetrophthalma	Fourspot flounder	DNA sequencing	COI	Fresh whole body	Wholesale (Lambayeque-Peru)	LC	(MN839530)	Marín et al. (2021)
				DNA sequencing	COI	Fresh whole body	Landing (Tumbes-Peru)		(MN880530)	Marín et al. (2022)
		Paralichthys adspersus	Fine flounder	DNA sequencing	COI	Whole fillet or chopped fillet	Restaurant, Supermarket (Lima-Peru)	LC	—	Biffi et al. (2020)
				DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)		—	Velez-Zuazo et al. (2021)
				DNA Sequencing, PCR-SSP	COI	Fresh whole body	Market and Aquaculture facility (Ancash-Peru)		(PP092941, PQ459815 to PQ459825)	Marín et al. (2025)
		Paralichthys woolmani	Speckled flounder	DNA sequencing	COI	Whole fillet or chopped fillet	Restaurant, Supermarket (Lima-Peru)	DD	—	Biffi et al. (2020)
				DNA sequencing	COI	Fresh whole body	Landing (Piura and Tumbes-Peru)		(MN880555, MN880580 to MN880582)	Marín et al. (2022)
				DNA sequencing	12S rRNA	Cooked	Retail (Tumbes-Peru)		(PV505012)	Marín et al. (2025)
Salmoniformes	Salmonidae	*Oncorhynchus kisutch**	Coho salmon	PCR-RFLP	Cytb	Uncooked muscled	Sushi roll restaurant (Osorno, Puerto Montt-Chile)	NE	—	Prida et al. (2020)

Order	Family	Species	Common name	Method	Gene	Product	Source	Status	Accession	Reference
		Oncorhynchus mykiss*	Rainbow trout	DNA sequencing	COI	Whole, frozen	Importer, Retailer (Canada, imported from Chile and Peru)	NE	—	Shehata et al. (2019)
				PCR-RFLP	Cytb	Uncooked muscled	Sushi roll restaurant (Iquique, Osorno, Puerto Montt, Quellón, Viña del Mar, Temuco, Valparaíso-Chile)		—	Prida et al. (2020)
		Oncorhynchus tshawytscha*	Chinook salmon	PCR-RFLP	Cytb	Uncooked muscled	Sushi roll restaurant (Osorno, Temuco-Chile)	NE	—	Prida et al. (2020)
		Salmo salar*	Atlantic salmon	qPCR-SSP	ITS1		Supermarket (Chile)	NT	—	Herrero et al. (2011)
				DNA sequencing	COI	Fillet vacuum packaged	Multimarket (Lima-Peru)		(MH194516)	Marín et al. (2018)
				DNA sequencing	COI	Whole or fillet	(Canada, imported from Chile)		—	Shehata et al. (2018)
					COI	Whole frozen, refrigerated	Importer, Registered plant, (Canada, imported from Chile)		—	Shehata et al. (2019)
				PCR-RFLP	Cytb	Uncooked muscle	Sushi roll restaurant (Antofagasta, Concepción, Iquique, Osorno, Puerto Montt, Quellón,Temuco, Validivia, Valparaíso, Viña del Mar-Chile)		—	Prida et al. (2020)
		Salmo trutta*	Sea trout	PCR-RFLP, FINS	Cytb	—	(Peru)	LC	—	Espiñeira et al. (2009b)
Scombriformes	Bramidae	*Brama australis*	Southern rays bream	PCR-RFLP, FINS	Cytb	Fresh, processed	Supermarket (Chile)	NE	—	Espiñeira et al. (2009b)
		Xenobrama microlepis	Golden pomfret	DNA sequencing	COI	Fresh	Artisanal fishery (Calbuco-Chile)	NE	(KX497160, KX497161)	Canales-Aguirre et al. (2018)
	Centrolophidae	*Schedophilus haedrichi*	Mocosa ruff	DNA sequencing	COI	Fresh whole body, steamed fillet	Market, Restaurant (La Libertad-Peru)	LC	(MH194423, MH194446)	Marín et al. (2018)
				DNA sequencing	COI	Whole fillet or chopped fillet	Supermarket, Wholesale (Lima-Peru)		—	Biffi et al. (2020)
				DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)		—	Velez-Zuazo et al. (2021)

				DNA sequencing	COI	Fresh whole body	Market (La Libertad-Peru)		(MN839529)	Marín et al. (2021)
				DNA sequencing	COI	Fresh whole body	Landing (Piura-Peru)		(MN880515)	Marín et al. (2022)
				DNA sequencing, Multiplex PCR-SSP	COI	Fresh, cooked	Market and Restaurant (La Libertad-Peru), Landing (Tumbes-Peru), Wholesale (Piura and Lambayeque-Peru)		(PP092954, PV562157, PQ459805 to PQ459809)	Marín et al. (2025)
		Seriolella violacea	Palm ruff	DNA sequencing	COI	Whole fillet or chopped fillet	Supermarket, Wholesale (Lima-Peru)	LC	—	Biffi et al. (2020)
				DNA sequencing	COI	Fresh whole body	Landing (Piura-Peru)		(MN880601)	Marín et al. (2022)
	Gempylidae	*Lepidocybium flavobrunneum*	Escolar	DNA sequencing	COI	Whole fillet or chopped fillet	Restaurant (Lima-Peru)	LC	—	Biffi et al. (2020)
		Thyrsites atun	Snoek	DNA sequencing	COI	Whole or fillet	(Canada, imported from Chile)	NE		Shehata et al. (2018)
	Scombridae	*Acanthocybium solandri*	Wahoo	DNA sequencing	COI	Whole fillet or chopped fillet	Retail (Lima-Peru)	LC	—	Biffi et al. (2020)
		Katsuwonus pelamis	Skipjack tuna	DNA sequencing	COI	Whole fillet or chopped fillet	Landing (Tumbes-Peru)	LC	—	Biffi et al. (2020)
				DNA sequencing	COI	Muscle	Fishing port (Playa Mía, Manta, Manabí Province-Ecuador)		—	Tiktak et al., (2024)
		Sarda chiliensis	Eastern Pacific bonito	DNA sequencing	COI	Fried fillet	Restaurant (La Libertad-Peru)	LC	(MH194515)	Marín et al. (2018)
				DNA sequencing	COI	Whole fillet or chopped fillet	Retail, Restaurant, Supermarket, Wholesale (Lima-Peru)		—	Biffi et al. (2020)
				DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)		—	Velez-Zuazo et al. (2021)
		Scomber japonicus	Chub mackerel	RFLP-SSCP	Cytb	Fishmeal	International Fishmeal and Oil Manufacturers' Association, IFOMA (Germany, imported from Peru)	LC	—	Rehbein (2002)
				DNA sequencing	COI	Whole fillet or chopped fillet	Wholesale (Lima-Peru)		—	Biffi et al. (2020)
		Scomberomorus sierra	Pacific sierra	DNA sequencing	COI	Whole fillet or chopped fillet	Wholesale (Lima-Peru)	LC	—	Biffi et al. (2020)
				DNA sequencing	COI	Fresh whole body	Landing (Piura-Peru)		(MN880519)	Marín et al. (2022)

			Thunnus albacares	Yellowfin tuna	DNA sequencing	COI	Whole fillet or chopped fillet	Restaurant, Retail, Supermarket, Wholesale (Lima-Peru); Landing, Retail (Tumbes-Peru)	LC	—	Biffi et al. (2020)
					DNA sequencing	COI	Fresh, refrigerated, or frozen	Fish market, Restaurant, or Supermarket (Lima-Peru)		—	Velez-Zuazo et al. (2021)
					DNA sequencing	COI, Control Region	Fresh whole body	Landing (Tumbes-Peru)		(MN880518, MN880522, MN880616, MN880618)	Marín et al. (2022)
	Syngnathiformes	Syngnathidae	*Hippocampus ingens*	Pacific seahorse	PCR-SSP	16S rRNA	Fresh whole body (seized by Peruvian authorities)	Seizure from Landing (Ancash-Peru)	VU	—	Marín et al. (2021)
					qPCR-SSP, direct qPCR-SSP, DNA Sequencing	16S rRNA	Dried	Donations (Ancash, Lima, and Piura-Peru)		(MN839505 to MN839510)	Marín et al. (2021)
	Tetraodontiformes	Tetraodontidae	*Sphoeroides annulatus*	Bullseye puffer	DNA sequencing	COI	Whole fillet or chopped fillet	Wholesale (Lima-Peru)	LC	—	Biffi et al. (2020)
Mollusca											
Bivalvia	Adapedonta	Pharidae	*Ensis macha*	Razor clam	FINS	18S rDNA	Frozen or preserved	(Chile, Peru)	NE	—	Espiñeira et al. (2009a)
	Arcida	Arcidae	*Anadara tuberculosa*	Pustulose ark	DNA sequencing	COI	Marinated ceviche	Restaurant (La Libertad-Peru)	NE	(MH194436)	Marín et al. (2018)
	Cardiida	Donacidae	*Donax obesulus*	Wedge clam	DNA sequencing	COI	Fresh whole body	Market (Ancash-Peru)	NE	(MH194540)	Marín et al. (2018)
		Semelidae	*Semele corrugata*	Clam	DNA sequencing	COI	Fresh whole body	Market (Ancash-Peru)	NE	(MH194538)	Marín et al. (2018)
		Solecurtidae	*Tagelus dombeii*	Hard razor clam	FINS	18S rDNA	Frozen or preserved	(Chile, Peru)	NE	—	Espiñeira et al. (2009a)
					DNA sequencing	COI	Boiled, fresh cut in pieces, marinated ceviche	Market, Restaurant (Ancash-Peru); Multimarket (Lima-Peru)		(MH194523, MH194539, MH194548)	Marín et al. (2018)
			Tagelus peruanus	Razor clam	FINS	18S rDNA	Frozen or preserved	(Peru)	NE	(EU660762)	Espiñeira et al. (2009a)
	Mytilida	Mytilidae	*Aulacomya atra*		PCR-RFLP	ITS	Fresh	Corral Bay (Chile)	NE	—	Toro (1998)

		Chilean ribbed mussel	PCR-RFLP	18S rDNA	Fresh whole body	Supermarket (Osorno-Chile)		—	Colihueque et al. (2020)
			PCR-RFLP	PAPM	Raw	(Chile)		—	Quintrel et al. (2021)
	Choromytilus chorus	Choro mussel	PCR-RFLP	ITS	Fresh	Corral Bay (Chile)	NE	(EU636218)	Toro (1998)
			PCR and band size polimorphism	ITS1, ITS2	Fresh	(Concepción-Chile)		—	Aguilera-Muñoz et al. (2008)
			PCR-RFLP	PAPM	Raw	(Chile)		—	Quintrel et al. (2021)
	Mytilus chilensis	Chilean mussel	PCR-RFLP	ITS	Fresh	Corral Bay (Chile)	NE	—	Toro (1998)
			RAPD	RANDOM	Fresh	Puerto Aguirre (Chile)		—	Rego et al. (2002)
			PCR-RFLP	ITS, PAPM	Fresh	8 natural populations (from Arauco to Punta Arenas-Chile)		—	Toro et al. (2005)
			PCR-RFLP	COI, PAPM	Frozen	Supermarket (Chile)		—	Fernández-Tajes et al. (2011)
			HTS-Pyroseq	COI, 16S rRNA	Fresh, frozen	Customs premises (Italy, imported from Chile)		(KR078006)	Abbadi et al. (2016)
			HRM	PAPM	Fresh	Wild (Chile)		—	Jilberto et al. (2017)
			PCR-RFLP	COI, 16S rRNA, PAPM, ITS, MAC-1, 18S rDNA	Fresh	Wild populations (Chile)		—	Larraín et al. (2019)
			PCR-RFLP	18S rDNA	Frozen whole body	Supermarket (Osorno-Chile)		—	Colihueque et al. (2020)
			HRM	PAPM	Canned, frozen pre-cooked	(Chile and Germany imported from Chile)		—	Quintrel et al. (2021)
			HRM, FINS	PAPM, H1C	Fresh	Growing center (Reloncaví Sound and Dichato-Chile)		(MT949777 to MT949820, MT949830 to MT949837)	Asorey et al. (2022)
			PCR-RFLP	PAPM	Pre-cooked, frozen	National large retailers, Ethnic shop (Italy, imported from Chile)		—	Giusti et al. (2022)
			PCR and SNPs genotyping	PAPM	Whole body	Market (Poland, imported from Chile)		—	Wenne et al. (2022)
	Mytilus edulis	Blue mussel	HRM	PAPM	Fresh	Wild (Chile)	NE	—	Jilberto et al. (2017)

Order	Family	Species	Common name	Method	Marker	Sample state	Origin		Accession	Reference
		Mytilus galloprovincialis*	Mediterranean mussel	PCR-RFLP	ITS, PAPM	Fresh	8 natural populations (from Arauco to Punta Arenas-Chile)	NE	—	Toro et al. (2005)
				HRM	PAPM	Fresh	(Chile)		—	Jilberto et al. (2017)
		Perumytilus purpuratus	Purple mussel	PCR-RFLP	ITS	Fresh	Corral Bay (Chile)	NE	—	Toro (1998)
				PCR-RFLP	PAPM	Fresh	(Chile)		—	Quintrel et al. (2021)
Ostreida	Ostreidae	*Ostrea chilensis*	Chilean flat oyster	FINS	18S rDNA	Frozen or preserved	(Chile)	NE	—	Espiñeira et al. (2009a)
Pectinida	Pectinidae	*Argopecten purpuratus*	Peruvian scallop	FINS	18S rDNA	Frozen or preserved	(Peru)	NE	(EU660808, EU660809)	Espiñeira et al. (2009a)
				DNA sequencing	16S rRNA	Frozen	Imported or local commerce (Hamburg, Germany, imported from Peru)		—	Näumann et al. (2012)
				Multiplex PCR-SSP	16S rRNA	Fresh, processed	Landed by commercial diver (Pisco and Piura-Peru), market (Peru)		—	Marín et al. (2013)
				DNA sequencing	16S rRNA	Fresh	Landed by commercial diver (Ancash, Lima, Pisco, and Piura-Peru)		(KJ000134 to KJ000141)	Marín et al. (2015)
				Multiplex PCR-SSP	16S rRNA	Fresh, processed	Landed by commercial diver (Pisco and Piura-Peru); Supermarket (London-UK)		—	Marín et al. (2017)
				Multiplex PCR-SSP	16S rRNA	Fresh, ceviche, seafood rice	Restaurant (Lima-Peru)		(MH194434, MH194544)	Marín et al. (2018)
				NGS Metabarcoding	16S rRNA	Frozen	Delicacy shop (Austria, imported from Peru)		—	Gense et al. (2021)
				DNA sequencing	16S rRNA	Frozen, cooked	Supermarket, Restaurant (Germany, origen not declared, probably Chile or Peru)		—	Klapper and Schröder (2021)
				DNA sequencing	16S rRNA	Frozen, cooked	Supermarket, Fish shops (Cantabrian Coast-Spain), Restaurants (Asturias, Galicia, Segovia-Spain), (imported from Chile or Peru)		(MT126344 to MT126356)	Parrondo et al. (2021)

Class	Order	Family	Species	Common name	Method	Gene	Product	Origin	Status	Accession	Reference
					DNA Sequencing, PCR-SSP, qPCR-SSP, direct qPCR-SSP	16S rRNA	Fresh, cooked, frozen	Market and Supermarket (Ancash-Peru), Landing (Piura and Pisco-Peru), Restaurant (Ancash and Piura-Peru)		(PP087160 to PP087193, PV491562)	Marín et al. (2025)
	Venerida	Mesodesmatidae	*Mesodesma donacium*	Macha clam	FINS	18S rDNA	Frozen or preserved	(Chile)	NE	(EU660756, EU0757)	Espiñeira et al. (2009a)
		Veneridae	*Ameghinomya antiqua*	Cancellated clam	FINS	18S rDNA	Frozen or preserved	(Chile)	NE	(EU660742, EU660743)	Espiñeira et al. (2009a)
			Leukoma thaca	Taca clam	FINS	18S rDNA	Frozen or preserved	(Chile)	NE	(EU660752, EU660753)	Espiñeira et al. (2009a)
Cephalopoda	Myopsida	Loliginidae	*Doryteuthis gahi*	Patagonian squid	DNA sequencing	COI	Steamed rings	Restaurant (Piura-Peru)	LC	(MH194501)	Marín et al. (2018)
					DNA Sequencing, PCR-SSP	COI, 16S rRNA	Fresh, cooked	Restaurant (Ancash and Piura-Peru), Market (Ancash and Tumbes-Peru)		(PQ459851 to PQ459852, PV562158)	Marín et al. (2025)
			Lolliguncula argus	Argus brief squid	DNA sequencing	COI, 16S rRNA, Rhodopsin	Whole individual	Market (Machalilla-Ecuador)	DD	(MN787690, MN787710, MN787730)	Costa et al. (2021)
			Lolliguncula diomedeae	Dart squid	DNA sequencing	COI, 16S rRNA, Rhodopsin	Whole individual	Market (Isla Santa Clara, Marta-Ecuador, Talara-Peru)	DD	(MN787672 to MN787677, MN787692 to MN787697, MN787712 to MN787717)	Costa et al. (2021)
					DNA sequencing	16S rRNA	Fresh tentacles	Landing (Tumbes-Peru)		(PQ459849 to PQ459850)	Marín et al. (2025)
			Lolliguncula panamensis	Panama brief squid	DNA sequencing	COI, 16S rRNA, Rhodopsin	Whole individual	Market (Posorja, Río Verde-Ecuador, Talara-Peru)	DD	(MN787678 to MN787682, MN787698 to MN787702, MN787718 to MN787722)	Costa et al. (2021)
	Octopoda	Octopodidae	*Octopus mimus*	Changos octopus	DNA sequencing	COI	Boliled, grilled, seafood rice	Restaurant (Ancash and Lima-Peru)	LC	(MH194493, MH194502, MH194545)	Marín et al. (2018)
					DNA sequencing	COI, COIII, 16S rRNA	Arm tissue	Las Palmeras zone at the Salinas seaside (Santa Elena-Ecuador)		—	Pliego Cárdenas et al. (2016)
	Oegopsida	Ommastrephidae	*Dosidicus gigas*	Jumbo flying squid	DNA sequencing	COI, 16S rRNA	Frozen	Supermarkets (Cairo, Menoufia, and Qalyubia-Egypt, imported from Chile)	DD	(KJ879299 to KJ879303)	Galal-Khallaf et al. (2016)

					Method	Gene	Product	Location	Status	Accession	Reference
					DNA sequencing	16S rRNA	—	(Peru)		(LC063230 to LC063237)	Sánchez et al. (2016)
					DNA sequencing	COI, 16S rRNA	Chopped, Sliced, Seasoned	Market (South Korea, imported from Chile and Peru)		—	Yu et al. (2018)
					DNA sequencing	COI	Marinated ceviche, frozen seafood mix	Restaurant (La Libertad-Peru); Supermarket (Ancash-Peru)		(MH194426, MH194427, MH194533)	Marín et al. (2018)
					DNA sequencing	COI	—	Retail, Supermarket, Wholesale (Lima-Peru)		—	Biffi et al. (2020)
					DNA sequencing	COI	Cooked tentacles	Restaurant (Lambayeque-Peru)		(PV562159 and PV562160)	Marín et al. (2025)
Gastropoda	Lepetellida	Fissurellidae	*Fissurella bridgesii*	Lapa cheqche	PCR-RFLP	Cytb	Fresh	(Chile)	NE	—	Olivares-Paz et al. (2006)
			Fissurella crassa	Thick keyhole limpet	PCR-RFLP	Cytb	Fresh	(Chile)	NE	—	Olivares-Paz et al. (2006)
					PCR and band size polimorphism	ITS1, ITS2	Fresh	(Concepción-Chile)		(EU636216)	Aguilera-Muñoz et al. (2008)
					DNA sequencing	COI, 16S rRNA, ITS	Fresh	(Concepción-Chile)		(EU636211, EU636216)	Aguilera-Muñoz et al. (2008)
			Fissurella cumingi	Lapa rosada	PCR-RFLP	Cytb	Fresh	Wild population (Chile)	NE	—	Olivares-Paz et al. (2006)
			Fissurella latimarginata	Lapa negra	PCR-RFLP	Cytb	Fresh	Wild population (Chile)	NE	—	Olivares-Paz et al. (2006)
			Fissurella limbata	Lapa ploma	PCR-RFLP	Cytb	Fresh	Wild population (Chile)	NE	—	Olivares-Paz et al. (2006)
			Fissurella maxima	Lapa criolla	PCR-RFLP	Cytb	Fresh	Wild population (Chile)	NE	—	Olivares-Paz et al. (2006)
			Fissurella nigra	Key-hole limpet	PCR-RFLP	Cytb	Fresh	Wild population (Chile)	NE	—	Olivares-Paz et al. (2006)
			Fissurella oriens	Small banded keyhole limpet	PCR-RFLP	Cytb	Fresh	Wild population (Chile)	NE	—	Olivares-Paz et al. (2006)
			Fisurella picta	Large banded keyhole limpet	PCR-RFLP	Cytb	Fresh	Wild population (Chile)	NE	—	Olivares-Paz et al. (2006)
			Fissurella pulchra	Lapa rosada	PCR-RFLP	Cytb	Fresh	Wild population (Chile)	NE	—	Olivares-Paz et al. (2006)
			Fisurella radiosa	Lapa	PCR-RFLP	Cytb	Fresh	Wild population (Chile)	NE	—	Olivares-Paz et al. (2006)
		Haliotidae	*Haliotis discus hannai**	Pacific abalone	RAPD	RANDOM	Fresh	Reseach facility (Chile)	EN	—	Marín et al. (2007)
					PCR and band size polimorphism	ITS1, ITS2	Fresh, canned	(Coquimbo-Chile; Baja California-Mexico)		(EU636215)	Aguilera-Muñoz et al. (2008)

Order	Family	Species	Common name	Method	Target	Product	Origin	Status	Accession	Reference
				DNA sequencing	COI, 16S rRNA, ITS	Fresh	(Coquimbo-Chile)		(EU636202, EU636208, EU636215)	Aguilera-Muñoz et al. (2008)
		Haliotis rufescens*	Red abalone	RAPD	RANDOM	Fresh	Reseach facility (Chile)	CR	—	Marín et al. (2007)
				PCR and band size polimorphism	ITS1, ITS2	Fresh, canned	(Coquimbo-Chile), (Baja California-Mexico, imported from Chile)		(EU636214)	Aguilera-Muñoz et al. (2008)
				DNA sequencing	COI, 16S rRNA, ITS	Fresh	(Coquimbo-Chile)		(EU636201, EU636207, EU636214)	Aguilera-Muñoz et al. (2008)
Neogastropoda	Muricidae	*Chorus giganteus*	Top shell whelk	PCR and band size polimorphism	ITS1, ITS2	Fresh, processed	(Concepción-Chile)	NE	—	Aguilera-Muñoz et al. (2008)
		Concholepas concholepas	Chilean abalone	PCR and band size polimorphism	ITS1, ITS2	Fresh, canned	(Concepción-Chile), (Baja California-Mexico, imported from Chile)	NE	—	Aguilera-Muñoz et al. (2008)
				DNA sequencing	COI, 16S rRNA, ITS	Fresh	(Concepción-Chile)		—	Aguilera-Muñoz et al. (2008)
				PCR-SSCP	18S	Fresh, Canned	Retail market (Mexico)		(HM775291)	Aranceta-Garza et al (2011)
				FINS	COI, 16S rRNA	Dried	Wholesale and retail outlets (Hong Kong, imported from Chile)		—	Ha et al. (2011)
		Thaisella chocolata	Chocolate rock shell	PCR and band size polimorphism	ITS1, ITS2	Fresh, processed	(Antofagasta-Chile)	NE	—	Aguilera-Muñoz et al. (2008)
				DNA sequencing	COI, 16S rRNA, ITS	Fresh	(Antofagasta-Chile)		(EU636204, 636210)	Aguilera-Muñoz et al. (2008)
				DNA sequencing	COI	Marinated ceviche, fresh cut in pieces	Market, Restaurant (Ancash-Peru)		(MH194525, MH194530)	Marín et al. (2018)
Trochida	Tegulidae	*Tegula atra*	Smooth black trochid	PCR and band size polimorphism	ITS1, ITS2	Fresh, processed	(Concepción-Chile)	NE	(EU636217)	Aguilera-Muñoz et al. (2008)

					Method	Marker	Product	Source		Accession	Reference
					DNA sequencing	COI, 16S rRNA, ITS	Fresh	(Concepción-Chile)		(EU636206, EU636212, EU636217)	Aguilera-Muñoz et al. (2008)
Crustacea											
Crabs	Decapoda	Cancridae	*Cancer plebejus*	Chilean crab	DNA sequencing	COI	Raw crab chelipeds	Seafood market (Coquimbo-Chile, 29° 57′ S)	NE	—	Haye et al. (2012)
			Cancer porteri	Boco	DNA sequencing	COI	Raw crab chelipeds, Canned chelipeds	Food store, Seafood market (Coquimbo-Chile, 29° 57′ S)	NE	—	Haye et al. (2012)
			Metacarcinus edwardsii	Mola rock crab	DNA sequencing	COI	Frozen chelipeds, Frozen minced meat, Frozen chelipeds	Food store, Seafood market (Coquimbo-Chile, 29° 57′ S)	NE	—	Haye et al. (2012)
			Romaleon setosum	Rock-crab	DNA sequencing	COI	Raw crab chelipeds, Canned chelipeds, and frozen crab meat, Frozen minced meat	Food store, Seafood market (Coquimbo-Chile, 29° 57′ S)	NE	—	Haye et al. (2012)
					DNA sequencing	COI	Crab meat	Supermarket (Ancash-Peru)		(MH194536)	Marín et al. (2018)
		Platyxanthidae	*Homalaspis plana*	Blackberry crab	DNA sequencing	COI	Crab claws, Canned chelipeds, Frozen minced meat	Food store, Seafood market (Coquimbo-Chile, 29° 57′ S)	NE	—	Haye et al. (2012)
			Platyxanthus orbignyi	Purple crab	DNA sequencing	COI	Marinated ceviche, fresh	Restaurant (La Libertad-Peru)	NE	(MH194445)	Marín et al. (2018)
Shrimps		Penaeidae	*Penaeus (Litopenaeus) vannamei*	Whiteleg shrimp	DNA sequencing	COI, 16S rRNA	Frozen	Supermarkets (Oviedo, Principality of Asturias-Spain, imported from Ecuador)	NE	(KJ879313-KJ879314)	Galal-Khallaf et al. (2016)
					DNA sequencing	COI	Marinated ceviche, fresh	Restaurant (La Libertad-Peru); Supermarket (Ancash-Peru)		(MH194437, MH194528)	Marín et al. (2018)
					DNA sequencing, PCR-MICROARRAY	COI, 16S rRNA	—	Retailer (Germany, declared origin: Ecuador)		—	Kappel et al. (2021)
					DNA sequencing	COI	Fresh, frozen, boiled	Supermarket, Fishmongers (Madrid-		—	Gil et al. (2024)

								Spain, imported from Ecuador)			
					DNA sequencing	COI	Peeled	Supermarket (Asturias-Spain, imported from Ecuador)		—	Ortiz-Moriano et al. (2024)
Echinodermata											
Sea cucumber	Dendrochirotida	Cucumariidae	*Athyonidium chilensis*	Burrowing shaggy sea cucumber	DNA sequencing	COI, 16S rRNA	Dried	Supermarket (China, origin: Peru)	NE	—	Hu et al. (2019)
					Mini barcoding	COI	Dried	Supermarket (China, origin: Peru)		—	Xing et al. (2022)
Cetaceans											
Dolphins	Cetartiodactyla	Delphinidae	*Delphinus delphis*	Common dolphin	DNA sequencing	tRNA-Glu to Cytb	Meat pieces or whole body	Fish market (Ancash and La Libertad-Peru)	LC	(HM572302) (HM572297 to HM572301)	Tzika et al. (2010)
					DNA sequencing	COI	Whole fillet or chopped fillet	Retail (Lima-Peru)		—	Biffi et al. (2020)
			Lagenorhynchus obscurus	Dusky dolphin	DNA sequencing	tRNA-Glu to Cytb	Meat pieces or whole body	Fish market (Ancash and La Libertad-Peru)	LC	(HM572303 to HM572305)	Tzika et al. (2010)
			Tursiops truncatus	Bottlenose dolphin	DNA sequencing	tRNA-Glu to Cytb	Meat pieces or whole body	Fish market (Ancash and La Libertad-Peru)	LC	(HM572307 to HM572320)	Tzika et al. (2010)
Porpoises		Phocoenidae	*Phocoena spinipinnis*	Burmeister's porpoise	DNA sequencing	tRNA-Glu to Cytb	Meat pieces or whole body	Fish market (Ancash and La Libertad-Peru)	NT	(HM572306)	Tzika et al. (2010)

*Introduced species for commercial purposes.
**This species is not found in Peruvian waters; it likely represents an imported item from Ecuador, where it occurs naturally.

Fig. 1

Fig. 2

A) BIODIVERSITY

GASTROPODS   BIVALVIA   CEPHALOPODS

15%
6 species

0.7%
1 species

11.2%
17 species

42.5%
17 species

14.3%
1 species

19.7%
30 species

42.5%
17 species

FINFISH
SHARKS
BATOIDS
CHIMAERAS

CRUSTACEANS
3.4%
7 species

85.7%
6 species

CRABS

SHRIMPS

68.4%
104 species

MOLLUSKS 19.6%
40 species

CETACEANS 2%
4 species

FISH 74.5%
152 species

HOLOTHURIANS 0.5%
1 species

TOTAL = 204 SPECIES

B) IUCN STATUS

LC
39.2%

NT
4.4%

VU
10.8%

THREATENED

SHARKS (VU: 9, EN: 6, CR: 9)
BATOIDS (VU: 8, EN: 4, CR: 1)
FINFISH (VU: 4)
GASTROPODS (EN: 1, CR: 1)
CHIMAERAS (VU: 1)

13 spp.
29.5%

EN
5.4%

24 spp.
54.6%

4 spp.
9.1%

DD
8.3%

CR
5.4%

NE
26.5%

1 sp.
2.3%

2 spp.
4.5%

Fig. 3

GLOBAL MISLABELING ANALYSIS OF SEAFOOD SPECIES FROM THE EASTERN SOUTH PACIFIC OCEAN

MISLABELING

100%   75%   50%   25%   0%

Correctly labeled   **Mislabeled**

A

Global mislabeling of ESPO species

16 countries (39 articles)
N=1,806
Mislabeled=24.8%
95% CI [22.9 to 26.9%]

	Correctly labeled	Mislabeled
TOTAL 75.2%		24.8%
Finfish 66.8%		33.2%
Sharks 79.8%		20.2%
Bivalves 83.7%		16.3%
Batoids 84.6%		15.4%
Crustaceans 100%		
Cephalopods 94.9%		5.1%
Gastropods 50%		50%
Holothurians 100%		
Chimaeras 100%		
Cetaceans 100%		

1400 1300 1200 1100 1000 900 800 700 600 500 400 300 200 100 0 100 200 300 400 500 600 700

Number of samples

B

SOUTH AMERICA (ESPO)

PERU (N=774 M=16.2%) [13.7-18.9]
- Finfish 85.9% — 14.1%
- Sharks 65.7% — 34.3%
- Batoids 84.6% — 15.4%
- Bivalves 96.3% — 3.7%
- Cephalopods 100%
- Crustaceans 100%
- Gastropods 100%
- Chimaeras 100%
- Cetaceans 100%

CHILE (N=487, M=11.5%) [8.9-14.7]
- Sharks 89.5% — 10.5%
- Finfish 82.4% — 17.6%
- Bivalves 92.3% — 7.7%

COLOMBIA (N=194, M=100%) [97.7-100]
- 100% Sharks

ECUADOR (N=9, M=0%) [0-29.9]
- Cephalopods 100%
- Finfish 100%

NORTH AMERICA

MEXICO (N=2, M=50%) [9.5-90.5]
- Gastropods 50% — 50%

CANADA (N=21 M=4.76%) [0.08-22.7]
- Finfish 95.2% — 4.8%

EUROPE

SPAIN (N=193, M=25.4%) [19.8-31.9]
- Bivalves 70.7% — 29.3%
- Finfish 58.6% — 21.4%
- Crustaceans 100%

ITALY (N=76, M=1.3%) [0-7.8]
- Bivalves 100%
- Finfish 88.9% — 11.1%

GERMANY (N=4, M=50%) [15-85]
- Bivalves 33.3% — 66.7%
- Crustaceans 100%

FRANCE (N=7, M=0%) [0-35.4]
- Finfish 100%

ENGLAND (N=5, M=0%) [0-35.4]
- Bivalves 100%

AUSTRIA (N=16, M=93.8%) [71.7-98.9]
- Bivalves 6.2% — 93.8%

AFRICA

EGYPT (N=9, M=0%) [0-30]
- Cephalopods 100%

ASIA

SOUTH KOREA (N=5, M=40%) [11.8-76.9]
- Cephalopods 60% — 40%

HONG KONG (N=2, M=100%) [34.2-100]
- 100% Gastropods

CHINA (N=2, M=0%) [0-65.8]
- Holothurians 100%

450 400 350 300 250 200 150 100 50 0 50 100 150 200

Number of samples

Fig. 4

Fig. 5