

Fatty acid profiles of highly migratory resources from the Southeastern Pacific Ocean, Chile: A potential tool for biochemical and nutritional traceability

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ABSTRACT

The traceability of fish species and their resulting food products is essential to maintain the global supply of these goods, allowing us to distinguish and reconstruct the origin and history of their production chain. One way to trace food is through biochemical determinations, which aid in identifying their origin quickly. In the present study, the fatty acid profiles of 18 highly migratory fishery resource species from the Southeastern Pacific Ocean were analyzed. *Xiphias gladius* presented the greatest abundance and concentration of fatty acids, strongly characterized by the presence of saturated, monounsaturated, and polyunsaturated fatty acids. A similar trend of high diversity in all classes of fatty acids was observed in tuna species (i.e. *Thunnus alalunga*; *T. albacares*; *T. obesus*), *Ruvettus pretiosus* and *Lepidocybium flavobrunneum*. In turn, *Lampris guttatus*, *Makaira indica*, and *Tetrapturus audax* presented an intermediate diversity of fatty acids and the highest amount of saturated and monounsaturated fatty acids of the evaluated species. Finally, *Luvarus imperialis*, *Coryphaena hippurus* and the sharks (*Lamna nasus*; *Alopias vulpinus*; *Prionace glauca*; *Isurus oxyrinchus*; *Sphyrna zygaena*) presented a low diversity of fatty acids, with only saturated fatty acids strongly predominating. Regarding the total concentration of fatty acids, the highest average values were recorded in *X. gladius*, *L. flavobrunneum* and *R. pretiosus*. The present study revealed notorious differences in the fatty acid composition of the muscle of highly migratory fishery resource species from the Southeastern Pacific Ocean off the coast of Chile, with the swordfish showing the best fatty acid profile. These results are the first step necessary to characterize the fatty acid profiles of the different fisheries in Chile.

Subjects Aquaculture, Fisheries and Fish Science, Biochemistry, Ecology, Marine Biology, Zoology

Keywords Fishery, Migratory Species, Traceability, Lipids, Fatty acids

INTRODUCTION

Traceability is an essential concept defined as "the possibility of finding and following the trace, through all the stages of production, transformation and distribution, of a food, a feed, an animal destined for production of food or a substance intended to be incorporated into food or feed or likely to be" (Badia-Melis, Mishra & Ruíz-García, 2015; Salampasis, Tektonidis & Kalogianni, 2012). In this way, we will consider traceability as a tool that allows us to distinguish and reconstruct the species, its origin and history of the production chain of a food product, recognizing all its phases, including capture, harvest, production, processing, storage, and distribution, among others (Badia-Melis, Mishra & Ruiz-García, 2015; Bosona & Gebresenbet, 2013).

Currently, the identification of highly migratory species from the Southeastern Pacific Ocean in Chile (swordfish, *Xiphias gladius*; blue shark, *Prionace glauca*; shortfin mako shark, *Isurus oxyrinchus*; porbeagle shark, *Lamna nasus*; and the mahi-mahi, *Coryphaena hippurus*) is carried out through species identification guides prepared with taxonomic criteria specific to each analyzed species (Parot, 2020), using information on the morphology of adult specimens and conspicuous characteristics, whether these are meristic or morphometric. Problems in species identification arise when a species must be classified by visible body parts alone (e.g. trunk or fins of a shark). For example, in the case of tuna, it is difficult to carry out a taxonomic recognition based on external morphology; in fact, it is only feasible to identify species based on the morphology of the liver and the composition of its fats.

In addition, the problem of identifying highly migratory species occurs more frequently during unloading process, when only the trunk is available (in gutted specimens without heads, tails or fins) (Clark, 2015; Miller, Jessel & Mariani, 2012). In this case, other morphological identification characters must be used, such as the presence of keels, notches, coloration, denticles on the skin, and, in some cases, the distribution of fats in cross-sections of the fillet or muscle tissue (Hernández et al., 2010; Mello, de Carvalho & Brito, 2013; Stefanni et al., 2021).

Seafood can be traced through the use of different tools (Ricardo et al., 2015). The identification and quantification of fatty acids is an effective tool to trace marine products (Ricardo et al., 2017). Fatty acids are key molecules in organisms because they are part of the cell membrane, they participate in different physiological processes and are an important energy source (Dalsgaard et al., 2003; Tocher & Glencross, 2015). These molecules can be affected by the species, their diet or habitat conditions and can even vary among different species, different stages of development or different seasons of the year (Sargent et al., 1999). Despite the variability of fatty acids, these can trace the geographic origin of a product because fatty acids are closely related to organisms lower on the food chain, such as phytoplankton or zooplankton. (Dalsgaard et al., 2003; Fonseca et al., 2022). This further confirms the importance of applying new and innovative methods for the biochemical traceability of marine species and fishery products of highly migratory resources in the Southeastern Pacific Ocean off the coast of Chile.

Particularly, biochemical determinations allow us to identify the species and its origin quickly and efficiently, immediately after the unloading process.

It has been found that in highly productive marine ecosystems, such as the Humboldt Current System, highly migratory species considered as top predators (i.e. sharks, tuna, marlins, swordfish), demonstrate a link between their diet (prey consumption) and the fatty acid profiles of their organs and/or tissues (Barría et al., 2020; Lazo-Andrade et al., 2023; Quispe-Machaca et al., 2021; Segura-Cobena et al., 2021; Hu et al., 2022). In particular, the lipids and/or fats of the prey are directly transferred and stored conservatively in the predators' organs (Beckmann et al., 2013; Xu, Pethybridge & Li, 2022; Meyer et al., 2019). Subsequently, as required, these lipids are mobilized and used for various key physiological functions within their ontogeny (e.g. growth, reproduction, homeostasis) (Leigh, Papastamatiou & German, 2017; Alderete-Macal, Caraveo-Patiño & Hoyos-Padilla, 2020; Meyer et al., 2017; Meyer et al., 2021). Within highly migratory predator species, different eating habits and hunting behaviors of their prey have also been described. For example, in the case of shark species (e.g. *Prionace glauca*, *Isurus oxyrinchus*), tuna (e.g. *Thunnus albacares*, *Thunnus alalunga*), and mahi-mahi fish (e.g. *Coryphaena hippurus*) a voracious and generalist habit has been reported (Méndez, 2021). In turn, in marlin species (e.g. *Makaira indica*, *Tetrapturus audax*) and swordfish (e.g. *Xiphias gladius*) the consumption of cephalopod species has been described as the main prey (Lazo-Andrade et al., 2021; Lazo-Andrade et al., 2023; Zhang et al., 2023). Particularly, the swordfish *X. gladius* has demonstrated a specialist hunting habit for the jumbo squid (Ibáñez, González & Cubillos, 2004); swordfish have been reported to first stab and then cut their prey with the sword of their mouth structure (Berkovitz & Shellis, 2017; Preti et al., 2023).

Most of these bony and cartilaginous fish species present a trophic and/or reproductive migratory pattern (for a conceptual model see: Lazo-Andrade et al., 2021; Lazo-Andrade et al., 2023; Barría et al., 2020) from equatorial water zones to cold temperate zones of the Southeastern Pacific Ocean. These fishes aim to consume high-energy value prey necessary to sustain the metabolic expenditure involved in traveling long distances, as well as storing sufficient energy for their subsequent reproduction (Guzmán-Rivas et al., 2023a; Guzmán-Rivas et al., 2023b; Segura-Cobena et al., 2021; Meekan et al., 2022). These bioenergetic-adaptive attributes are characterized by the consumption of prey with a specific profile and/or fatty acid footprint that are also rich in lipids, and the posterior conservative storage of the energy from these prey in the organs. Fatty acid profiles can thus be used as a biochemical and nutritional traceability tool for these species that support important fisheries in the Humboldt System (Barría et al., 2020; Lazo-Andrade et al., 2023; Santos et al., 2020).

The study model species (Table 1, Fig. 1) are considered: i) top predators that consume prey with high amounts of fat and/or energy; ii) the fatty acid profiles in their tissues reflect the food consumed, which is transferred and stored conservatively in their muscle; iii) the fatty acid profiles may vary, not only depending on the prey consumed through a characteristic hunting habit and/or behavior, but also due to their phylogeny and/or taxonomic group of evolutionary origin. It is thus expected that the model species studied present interspecific variations in the

fatty acid profiles of their muscle. This tool can be useful not only to identify the biochemical traceability of fish species at the tissue level, but also their nutritional condition and fillet quality. Therefore, in the present study, we analyzed the fatty acid composition in highly migratory species obtained from Humboldt marine ecosystem off the coast of Chile.

MATERIALS AND METHODS

Ethical declaration

This study was guided in accordance with the Act on Welfare and Management of Marine Animals, and they comply with the current Chilean animal care and manipulation legislation of the fishery resources (SUBPESCA). Consequently, to prevent the pain of the fishes during their collection and handling, they were put to sleep with a cold shock (Law 20.380, Ministry of Health and Ethics Committee, Chile) (Robb & Kestin, 2002).

Sample collection and analyzed species

Scientific observers from the Fisheries Development Institute-IFOP, within the framework of the Highly Migratory Fisheries Resources Project (Biological-Fisheries Aspects (IFOP, MINECON)), collected tissue samples (muscle) of highly migratory species captured on vessels of the trawler and industrial longline fishing fleets aimed at capturing swordfish; some species were included in the bycatch category (Barría *et al.*, 2020; Guzmán-Rivas *et al.*, 2023) (Table 1). All specimens were identified, measured, weighed, and sexed on board the boats.

A total of 18 highly migratory fishery resource species from the Southeastern Pacific Ocean were analyzed (Fig. 2), of which 03 corresponded to tuna species (i.e. albacore, yellowfin, bigeye), 05 to shark species (i.e. porbeagle, common thresher, blue, shortfin mako, hammerhead), 08 to other species of large fish (i.e. mahi-mahi, swordfish, louvar, escolar, skipjack, oil, butterfly kingfish, sun) and 02 to species of billfish (i.e. black, striped). For more details, including scientific names, common names and number of samples analyzed per species, see (Table 1, Fig. 1).

Muscle samples were taken between the first and second dorsal fins at a depth of approximately 20 mm from the skin to the underlying connective tissue or muscle tissue for cartilaginous fish; for bony fish these samples were extracted from the trunk (Barría *et al.*, 2020). After obtaining the samples, they were immediately placed on dry ice to be transported and stored at -80 °C in a freezer until the subsequent biochemical traceability analysis (measured as their fatty acid compositions) in the Hydrobiological Resources Laboratory of the Universidad Católica de la Santísima Concepción, Chile. Here, the muscle samples from highly migratory fishery resource species were vacuum- and cold-dried at -80°C in a freeze-dryer (Operon, FDU-7012). Then, they were sonicated (MRC, AC-120H) and stored in 15 mL centrifuge tubes for the immediate analysis of their fatty acid compositions.

Fatty acid compositions

First, the lipid content was extracted from 20 mg of the dry weight using the gravimetric method developed by *Folch, Lees & Sloane Stanley (1957)* and supplemented by *Cequier-Sánchez et al. (2008)*. This method used dichloromethane:methanol (2:1) as an organic solvent. Then, the fatty acid compositions were determined following the method used by *Malzahn et al. (2007)* and *Urzúa et al. (2012)*, where fatty acid methyl esters (FAMES) were measured from the total lipids extracted. These lipids were esterified by incubation with methanolic sulfuric acid in a Thermo Shaker (Model: DBSO-001) at 70°C for 1 h. Then, the fatty acids were obtained by washing with n-Hexane. This washing was performed three times using 6 mL, 3 mL, and 3 mL of the respective solvent. At the end of each wash, each mixture was vortexed and the upper phase was added to a new previously primed amber bottle. Finally, the fatty acids were concentrated using a sample concentrator (MD 200) supplemented with nitrogen gas. The FAMES were measured using a gas chromatograph (Agilent, model 7890A) at a set temperature with a DB-225 column (J and W Scientific, 30 m long, 0.25 mm interior diameter, and 0.25 µm thick film). FAMES were quantified using the C23:0 fatty acid as an internal standard according to *Malzahn et al. (2007)*, with Agilent chromatography software (ChemStation, USA). FAMES were then identified by comparison with known standards of fatty acids of marine origin (using certified material, Supelco 37, mixture FAME 47,885 – U).

Statistical analysis

Statistical tests were performed using the Rstudio v.1.1.453 (R v.3.3.3) and PRIMER-E (PRIMER6 v.6.1.16 and PERMANOVA + v.1.0.6) programs. The advanced statistical analyses described by: *Sokal & Rohlf (1995)*; *Zuur, Ieno & Smith (2007)*; *Clarke & Gorley (2015)*; a confidence level of 95% ($p < 0.05$) was also applied. To identify the species through their species/specific fatty acid profiles, a Bray-Curtis similarity and similarity matrix were carried out with their respective multivariate analyses: i) multidimensional scaling (MDS) and ii) principal coordinates (PcoA). In addition, a similarity analysis (ANOSIM) was performed to determine similar species and/or groups with a determination coefficient close to zero ($R = 0$). For very different species and/or groups, a determination coefficient close to one ($R = 1$) was utilized. Subsequently, a similarity percentage analysis (SIMPER) was carried out to determine the percentage of contribution of the different types of fatty acids in the different species analyzed. Finally, a multivariate permutation analysis (PERMANOVA) was used to compare the fatty acid profiles of the diverse species.

RESULTS

Fatty acid compositions and PCoA

The fatty acid compositions presented highly significant differences among the analyzed species (PERMANOVA, Pseudo-F= 18.875; $P < 0.001$). That is, a distinctive and characteristic fatty acid composition was identified for each study species; these biochemical/physiological traits are reflected in the amount (i.e. concentration) and diversity (i.e. different types) of fatty acids observed in the muscle (tissue samples of 20 mg of dry weight, DW) of each species.

In terms of diversity and composition of fatty acids, swordfish (*Xiphias gladius*) consistently presented the **greatest diversity** of fatty acids, strongly characterized by the presence of all classes of fatty acids (saturated, monounsaturated, polyunsaturated-n3, and polyunsaturated-n6). A similar trend of **high diversity** in all classes of fatty acids was observed in tuna species (i.e. albacore: *Thunnus alalunga*; yellowfin: *T. albacares*; bigeye: *T. obesus*), oilfish (*Ruvettus pretiosus*) and escolar fish (*Lepidocybium flavobrunneum*). In turn, sunfish (*Lampris guttatus*) and marlins (black: *Makaira indica*; striped: *Tetrapturus audax*) presented an **intermediate diversity** of fatty acids, though the greater presence of saturated and monounsaturated fatty acids was noteworthy in these species. Finally, the louvar fish (*Luvarus imperialis*), the mahi-mahi (*Coryphaena hippurus*) and the sharks (porbeagle: *Lamna nasus*; common thresher: *Alopias vulpinus*; blue: *Prionace glauca*; shortfin mako: *Isurus oxyrinchus*; hammerhead: *Sphyrna zygaena*) presented a **low diversity** of fatty acids, where only saturated fatty acids strongly predominated. For more details regarding the different types of fatty acids detected in the diverse species see Table 2.

Regarding the total concentration of fatty acids, the highest average values were recorded in swordfish (3.56 ± 0.4 mg), oilfish (2.34 ± 0.44 mg) and escolar fish (3.38 ± 0.57 mg), intermediate values in striped marlin (1.67 ± 0.15 mg), butterfly kingfish (1.10 ± 0.21 mg), yellowfin tuna (0.67 ± 0.13 mg), albacore (0.59 ± 0.12 mg) and bigeye tuna (0.63 ± 0.08 mg), and the lowest values in blue sharks (0.13 ± 0.01 mg), shortfin mako sharks (0.1 ± 0.01 mg), hammerhead sharks (0.05 ± 0.01 mg), and mahi-mahi fish (0.06 ± 0.004 mg). For more details regarding the fatty acid contents determined for each species, see Table 2.

When considering the saturated fatty acids, palmitic acid (C16:0) was observed in the greatest amounts in swordfish (0.59 ± 0.4 mg 20 mg^{-1} DW), followed by albacore (0.3 ± 0.24 mg 20 mg^{-1} DW). The monounsaturated fatty acid found in the highest concentrations was oleic acid (C18:1n9) in species of escolar fish (2.04 ± 0.88 mg 20 mg^{-1} DW), oilfish (1.36 ± 1.04 mg 20 mg^{-1} DW) and swordfish (1.31 ± 0.84 mg 20 mg^{-1} DW). For the polyunsaturated fatty acids, the eicosapentanoic (EPA, C20:5n3) and docohexaenoic acids (DHA, C22:6n3) were abundant in swordfish (0.09 ± 0.07 mg 20 mg^{-1} DW) and escolar fish (0.08 ± 0.04 mg 20 mg^{-1} DW) (Table 2, Fig. 3).

MDS and PCoA

The multidimensional scaling analysis (MDS) revealed differences in the distribution of the fatty acid profiles of the analyzed species (2 dimensions with stresses of 0.1; Fig. 4). Notorious groupings were observed for each species, in which their fatty acid profiles were conspicuously separated and/or distant depending on the species: i) swordfish (*X. gladius*: green triangles), ii) oilfish (*R. pretiosus*: yellow border triangles), and iii) escolar fish (*L. flavobrunneum*: blue inverted triangles). They were also clearly grouped according to taxa: i) swordfish (*X. gladius*), ii) oilfish (*R. pretiosus*), iii) sunfish (*L. guttatus*), iv) tuna (albacore: *T. alalunga*; yellowfin: *T. albacares*; big eye: *T. obesus*; escolar fish: *L. flavobrunneum*; butterfly kingfish: *G. melampus*), v) sharks (porbeagle: *L. nasus*; common thresher: *A. vulpinus*; blue: *P.*

glauca; shortfin mako: *I. oxyrinchus*; hammerhead: *S. zygaena*), and finally, very close to these species of chondrichthyans, the mahi-mahi fish (*C. hippurus*). For further details see: Fig. 3 and Fig. 4.

ANOSIM and SIMPER

The similarity analysis (ANOSIM) confirmed that the fatty acid profiles of the evaluated species were statistically significant, and very different among them, with a global coefficient of determination (Global R) that includes all the paired comparisons of $R=0.761$ (values of R close to 1 indicate very different fatty acid profiles among species; with a significance level of 0.1%; and 999 permutations). For details regarding all the paired comparisons, see Table S1 in the supplementary materials section.

In turn, the similarity percentage analysis (SIMPER) indicated that the greatest contribution to this differentiation was provided by the fatty acids oleic (C18:1n9), palmitic (C16:0), stearic (C18:0), eicosenoic (C20:1), and DHA (C22:6n3). The SIMPER also demonstrated that the species swordfish (*X. gladius*), oilfish (*R. pretiosus*), escolar fish (*L. flavobrunneum*), shortfin mako shark (*I. oxyrinchus*) and mahi-mahi fish (*C. hippurus*) contributed the most to the significant differences found among the fatty acid profiles. For more details see Table S2 in the supplementary materials section.

DISCUSSION

In the present study, we effectively determined the fatty acid compositions of the highly migratory species obtained from the fishing fleets off the coast of Chile. These findings confirm the importance of using this method for the biochemical traceability of species and fishery products of highly migratory resources in Chile (Lazo-Andrade et al., 2021; Quispe-Machaca et al., 2022). This method can be used to distinguish between species and/or origin, based on the fatty acid profiles of their tissues (i.e., muscle and/or fillet), which in this case constitute the main part of the body intended as food for human consumption (Barria et al., 2020; Leal et al., 2015; Ricardo et al., 2015).

The traceability of fishery resources through the analysis of fatty acids, as a potential tool to determine the geographical origin of the species, has important implications for their sustainable exploitation within an ecosystem and precautionary approach (Guzmán-Rivas et al., 2021; Lazo-Andrade et al., 2021). Together with DNA analyses, this biochemical tool (e.g. fatty acids) could allow us to quickly and efficiently determine and/or distinguish the species and its geographical origin (capture zone) immediately after the unloading process at the port and subsequently at the processing plant (Leal et al., 2015; Stowasser, Pond & Collins, 2009). Additionally, identifying the nutritional profile of fishery resources allows us to promote the exploitation of certain species that have a healthier and more sustainable origin throughout the entire production chain (from capture at sea, landing, processing and finally making it to the consumer's plate) (Gong et al., 2018; Molkentin et al., 2015).

In the case of highly migratory fishery resource species, our study highlights the high diversity of all classes of fatty acids (saturated; mono-unsaturated; poly-unsaturated) in swordfish (*Xiphias gladius*), oilfish (*Ruvettus pretiosus*), tuna (albacore: *Thunnus alalunga*; yellowfin: *T. albacares*; big eye: *T. obesus*) and fish (escolar: *Lepidocybium flavobrunneum*; butterfly kingfish: *Gasterochisma melampus*). On the contrary, a low diversity of fatty acids was found in the evaluated species of sharks and/or cartilaginous fish (porbeagle: *Lamna nasus*; common thresher: *Alopias vulpinus*; blue: *Prionace glauca*; shortfin mako shark: *Isurus oxyrinchus*; hammerhead: *Sphyrna zygaena*), in which only saturated fatty acids predominated. These differences in the fatty acid profiles can be explained not only by differences associated with a phylogenetic and/or taxon trait (i.e. comparisons between bony fishes vs. cartilaginous fishes and/or sharks), but also by the geographic origin of the species (i.e. high latitude species vs. low latitude species) (Pethybridge et al., 2010; Prato & Biandolino, 2012). In turn, the low diversity of fatty acids in the shark species analyzed in this study may be related to an ancestral evolutionary trait of common diversification in tropical environments, where saturated fatty acids have predominated (Shadwick, Farrell & Brauner, 2015). These fatty acids in marine organisms are highly important in cellular homeostasis processes and physiological processes that adapt to different temperatures (Shadwick, Farrell & Brauner, 2015).

From an ecophysiological point of view, particularly regarding the structure, function and interaction with the environment, fatty acids play fundamental roles in the biophysical process of homeoviscous adaptation in fishes (Ernst, Ejsing & Antonny, 2016). This complex process allows fishes to maintain an optimal level of fluidity in their cell membrane and body tissue, depending on the water temperature (i.e. in cold temperatures, polyunsaturated fatty acids predominate vs. warm temperatures where saturated fatty acids predominate (Howell & Matthews, 1991)). This may explain the high displacement capacity of these species from warm to cold temperate environments/waters of the Humboldt Current System due to the high homeoviscous capacity present in their tissues and membranes (Shadwick, Farrell & Brauner, 2015; Malekar et al., 2018; Leigh, Papastamatiou & German, 2017; Lazo-Andrade et al., 2023).

In addition, within an ecosystem approach, differences or similarities in the composition of fatty acids can be associated with the degree of physiological and trophic specialization of each organism (e.g. swordfish are considered specialists, while sharks are considered generalists (Lazo-Andrade et al., 2021; Munroe, Simpfendorfer & Heupel, 2014)), as well as their trophic spatial position (Kainz et al., 2017) within the marine food web. For example, in our study, the fatty acid profiles of some species (*I. oxyrinchus*, *C. hippurus*) did not provide sufficient distinctive information to aid in their classification, indicating that they could present a similar trophic level and voracious feeding behavior as species previously described by Letelier et al. (2009); Lopez, Meléndez & Barriá (2009); and Lopez, Barriá & Meléndez (2012). On the contrary, cephalopod species has been described as the main prey item of billfish and swordfish species, which is consequently reflected in the fatty acid profiles of their tissues and/or organs (Quispe-Machaca et al., 2021; Quispe-Machaca et al., 2022; Hu et al., 2023; Guzmán-Rivas et al., 2023). Particularly, the swordfish *X. gladius* has demonstrated a specialist hunting habit on

the jumbo squid (Ibáñez, González & Cubillos, 2004), first stabbing and then cutting their prey with the sword of their mouth structure (Berkovitz & Shellis, 2017; Preti et al., 2023). Here, recent findings on the use of fatty acids as biomarkers of the interaction between two highly migratory resources of the southern Humboldt System revealed the degree of preference that swordfish have for preying on jumbo squid, particularly the consumption of its digestive gland, indicated by the fatty acids signal (Hu et al., 2022; Lazo-Andrade et al., 2023; Guzmán Rivas et al., 2023).

These data could be used as reference information in other fisheries across Chile. They could also be used as a data reference to trace geographic origin. Consequently, future studies with an integral and ecosystemic approach should incorporate: i) other organs of the body, such as the liver and the gonad, which are also considered potential fishery products with high added value; ii) the capture area and sex of the organisms; iii) a complementary tool for molecular identification through the genetic analysis of species.

CONCLUSION

The present study revealed notorious differences in the fatty acid compositions of the muscle of highly migratory fishery resource species of the Southeastern Pacific Ocean, off the coast of Chile. Swordfish had the highest abundance and concentration of fatty acids, followed by escolar fish and oilfish, while the hammerhead shark had the lowest abundance and concentration of fatty acids. These results are the first step needed to characterize the fatty acid profiles of the diverse fisheries in Chile.

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