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Revealing the illegal harvesting of Manila clams (*Ruditapes philippinarum*) using fatty acid profiles of the adductor muscle

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Author's contribution:

Conceived and designed the experiments: R.M., F.R. and R.C. Performed the experiments: R.M., F.R and A.S. Analyzed the data: R.M., F.R., R.B., M.R.M.D. and R.C. Contributed reagents/materials/analysis tools: S.D., S.A.O.S., M.R.M.D. and R.C. All authors wrote and reviewed the manuscript.

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| 1 | Revealing the illegal harvesting of Manila clams (Ruditapes philippinarum) using |
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| 24 | Abstract |
| 25 | The Manila clam (Ruditapes philippinarum) is one of the most traded bivalves in the world. |
| 26 | Knowing its harvesting location is therefore paramount to guarantee the safety of consumers. |
| 27 | The present study employs fatty acid (FA) profiles of the adductor muscle (AM) to reveal the |
| 28 | most likely harvesting location of four batches of Manila clams suspected of having been |
| 29 | illegally sourced from the Tagus estuary. In this ecosystem, where the collection of Manila |

30 clams is currently prohibited for food safety reasons, illegal, unreported and unregulated 31 (IUU) capture is known to occur. In order to trace the geographic origin of these four batches 32 of Manila clams, a reference model based on the FA profiles of the AM was developed with 33 specimens originating from the two most representative ecosystems supplying the trade-chain of this species in mainland Portugal (the Tagus estuary and Ria de Aveiro), as well as Ría de 34 35 Vigo, a production area outside Portugal and that is also an important supplier. The ability of this model to allocate clams to its origin ecosystem was evaluated using independent datasets, 36 with an allocation success of 100% (all samples were correctly assigned to its origin 37 ecosystem, thus validating the model). Based on the reference model established, the 38 39 harvesting location of the four batches suspected of originating from ongoing IUU in the 40 Tagus estuary was investigated. Specimens from 3 of the 4 batches screened were classified, as most likely originating from the Tagus estuary (with a likelihood ranging from 90% up to 41 42 100%). These results highlight the potential of this approach to fight the IUU capture of Manila clams, as this practice endangers important habitats and threatens public health. 43

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45 Keywords: traceability, mislabeling, bivalves, food safety, lipid markers

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1. Introduction

Marine bivalves, such as oysters, mussels, cockles and clams are among the most consumed seafood products worldwide. The Manila clam (*Ruditapes philippinarum*) is one of the most representative of such bivalves, with a production in 2017 of over 35.000 tons in Europe alone (FAO, 2019). Native from South-east Asia (Indo-Pacific), *R. philippinarum* is an invasive species in European coasts (Humphreys et al., 2015), where it was introduced in the early 1970's. In Iberian Peninsula, this species has been reported since late 1980's (Campos

& Cachola, 2005; Chiesa et al., 2017), presenting currently well-stablished populations which
turned it an important economic resource in this area (FAO, 2019).

56 Despite their high nutritional value, bivalves can at times threaten human health. Due to their 57 suspension feeding nature, bivalves can accumulate pathogenic bacteria, being this especially dangerous for human health if consumed raw or lightly cooked (Cook, 1991; Wright, Fan, & 58 59 Baker, 2018), as well as metals and metalloids present in the water (Karouna-Renier, Snyder, Allison, Wagner, & Ranga Rao, 2007; Velez, Figueira, Soares, & Freitas, 2015). These issues 60 61 are related with water and sediment quality of the harvesting location (Li, Yu, Song, & Mu, 2006; Stabili, Terlizzi, & Cavallo, 2013). In order to safeguard public health, the European 62 63 Union (EU) already produced several pieces of legislation (Regulation (EC) No 853/2004, 64 No 854/2004, No 2073/2005 and No 1021/2008) classifying bivalves harvesting areas according to the levels of Escherichia coli they display per g of bivalves flesh and 65 intravalvular liquid (EC, 2004a, 2004b, 2005, 2008). Moreover, to ensure the traceability of 66 each batch of seafood traded in the European Union, it also stablished several labelling 67 regulations (Regulation (European Commission (EC)) No 104/2000 and No 1224/2009; 68 Regulation (EU) No 404/2011 and No 1379/2013) (EC, 2000, 2009; EU, 2011, 2013). The 69 70 more recent and demanding of these labeling regulations (Regulation (EU) No 1379/2013) 71 (EU, 2013) stipulates, among other specifications, that marketed seafood products need to 72 display the catch area, production method and fishing gear used. In this way, the development 73 of traceability tools for origin certification is paramount to avoid seafood mislabeling, being 74 key to ensure safety for human consumption (Leal, Pimentel, Ricardo, Rosa, & Calado, 2015; Moretti, Turchini, Bellagamba, & Caprino, 2003). 75

Environmental factors, such as temperature, salinity and sediment type, influence the spatial
distribution of bivalves (Gosling, 2003) modulating their fatty acids (FA) profile (Calado &
Leal, 2015). For instance, high salinity fluctuations and low temperatures influence the

79 structure and fluidity of cell membranes. This results in a lower saturated FA (SFA) content, 80 that stabilize bilayer cellular membranes, with these biomolecules being replaced by polyunsaturated FA (PUFA), which allow higher membrane fluidity (Fokina, Ruokolainen, 81 82 Bakhmet, & Nemova, 2015; Nemova, Fokina, Nefedova, Ruokolainen, & Bakhmet, 2013). Other driving factor of the FA composition in bivalve tissues is trophic history, with the 83 predominance of certain FA revealing their dietary regimes (Calado & Leal, 2015; Prato, 84 Danieli, Maffia, & Biandolino, 2010). The FAs 16:0, 16:1n-7 and 20:5n-3 (eicosapentaenoic 85 acid, EPA) in bivalves tissues reveal the consumption of diatoms, while PUFA 18:3n-3 and 86 18:2n-6 of green microalgae, 22:6n-3 (docosahexaenoic acid, DHA) and 18:4n-3 of 87 88 dinoflagellates, and odd chain FA (15:0 and 17:0) and 18:1n-7 of detritus/bacteria (among 89 others, Calado & Leal, 2015; Dalsgaard, John, Kattner, Müller-Navarra, & Hagen, 2003; Ezgeta-Balić, Najdek, Peharda, & Blažina, 2012; Fujibayashi, Nishimura, & Tanaka, 2016; 90 91 Nerot et al., 2015). These indicative features allow to apply the profiling of FA signatures of tissues from different marine species for multiple scopes, such as identifying their feeding 92 habitats (e.g. Coelho et al., 2011; Xu, Xu, Zhang, Peng, & Yang, 2016), diet composition 93 (e.g. Bosley, Copeman, Dumbauld, & Bosley, 2017; White et al., 2017), seasonal variations 94 in dietary habits (e.g. Soler-Membrives, Rossi, & Munilla, 2011) or trace their geographic 95 96 origin (Ricardo, Maciel, Domingues, & Calado, 2017; Ricardo et al., 2015; Zhang, Liu, Li, & 97 Zhao, 2017).

98 The FA profile of the adductor muscle (AM) proved to be suitable in geographic origin 99 traceability studies targeting diverse bivalve species, such as cockles (*Cerastoderme edule*; 100 Ricardo et al., 20157, 2015), scallops (*Pecten maximus*; Grahl-Nielsen, Jacobsen, 101 Christophersen, & Magnesen, 2010) and clams (*Astarte sulcata*; Olsen, Grahl-Nielsen, & 102 Schander, 2009). The AM is of particular interest in traceability studies, mainly due to its

high content in polar lipids, which prevents short-term turnover in the FA profile related to
dietary shifts (Grahl-Nielsen et al., 2010; Leal et al., 2015; Olsen et al., 2009).

105 To avoid the fraudulent mislabeling of seafood geographic origin, it is important to develop 106 and refine traceability tools. Therefore, the present study aimed to develop a model based on 107 the FA profile of the AM that could indicate the most likely harvesting location of four 108 batches of *R. philippinarum* suspected of having been illegally harvested from the Tagus 109 estuary (where the harvesting of Manila clams is forbidden due to food safety issues). A two-110 step approach was employed to develop this model: i) Manila clam samples harvested from 111 three ecosystems (the Tagus estuary and Ria de Aveiro, two Portuguese ecosystems that 112 supply ~95% of the whole Manila clam traded in Portugal, and Ría de Vigo, a Spanish 113 ecosystem that is also an important supplier of this species to the Portuguese market) were used to validate a predictive model to trace their geographic origin; and following the 114 validation of the predictive model ii) the FA profile of the AM of clams suspected of 115 originating from the Tagus estuary were screened to verify if these clams had indeed been 116 117 harvested in this area where their capture is illegal.

118

- 119 **2. Material and methods**
- 120 **2.1 Study areas and clam collection**

Thirty specimens of *R. philippinarum* were collected in May 2018 in the Tagus estuary (Te, Portugal), Ria de Aveiro (RAv, Portugal) and Ría de Vigo (RV, Spain) (3 ecosystems X 30 replicates = 90 samples; Figure 1). These ecosystems play an important role in the Portuguese trade of *R. philippinarum*, with these clams being intensively harvested in these locations. However, it must be highlighted, that regardless of the Tagus estuary being the main source of Manila clams supplying the Portuguese trade, and most likely the Spanish trade as well, the harvesting of Manila clams is currently illegal in this ecosystem due to food safety issues.

128 Recurrent apprehensions of several tons of this bivalve originating from the illegal, 129 unreported and unregulated (IUU) capture of this bivalve are commonly reported on Portuguese and Spanish media, with authorities from both countries continuously pursuing 130 inspection actions to fight this practice. The specimens collected from these three ecosystems 131 were used to assemble a predictive reference model to assign the most likely place of origin 132 133 to sampled Manila clams (see below). Stakeholders provided 4 batches of Manila clams whom they strongly suspected had been illegally harvested from the Tagus estuary, with the 134 1st batch of 12 clams being obtained from a retailer (Rt), the 2nd batch of 7 clams from a 135 wholesaler (Ws) and the 3rd and 4th batches of 30 clams each originating from two separated 136 137 tanks from a depuration center (DC1 and DC2).

All samples were collected fresh, stored in aseptic bags and kept refrigerated until arrival to the laboratory. All specimens were taxonomically confirmed as *R. philippinarum* and the AM was dissected, freeze-dried and stored at -80 °C until the FA analysis was performed.

141

142 **2.2. Fatty acids analysis**

Methyl esters of fatty acids (FAME) were obtained through transmethylation, using a 143 144 modified method from Aued-Pimentel, Lago, Chaves, & Kumagai (2004). In brief, 5-10 mg 145 of the adductor muscle was suspended in 1 mL n-hexane, 0.2 mL of methanolic solution 146 KOH (2 M) and 2 mL saturated NaCl solution, followed by intense vortexing. Posteriorly, the samples were centrifuged at 2000 rpm for 5 minutes, with the organic phase then being 147 148 collected. The FAME obtained were injected and analyzed by gas chromatography-mass 149 spectrometry (GC-MS - QP2010 Ultra, Shimadzu, Kyoto, Japan), equipped with an autosampler, a DB-FFAP column with 30 m length, 0.32 mm internal diameter and 0.25 µm film 150 thickness (J&W Scientific, Folsom, CA). The column was initially programed to 80 °C, 151 increasing 25 °C min⁻¹ until 160 °C, 2 °C min⁻¹ from 160 to 220 °C and 30 °C min⁻¹ from 220 152

to 250 °C, using helium as the carrier gas, at a flow of 1.8 mL min⁻¹. All FAME were 153 154 identified using the equipment built-in software by comparing retention times, the mass spectrum of each relative to mixed FAME standards (C4-C24, Supelco 37 Component Fame 155 156 Mix) and standard spectra from the library "AOCS Lipid Library" (http://lipidlibrary.aocs.org/). 157

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2.3. Data and statistical analysis

160 The relative FA composition was obtained for each sample, being calculated as the mean and 161 standard deviation for each FA per sampling group. All FA were classified either as saturated 162 FA (SFA), monounsaturated FA (MUFA), polyunsaturated FA (PUFA) or highly unsaturated 163 FA (HUFA). Usually, FA with \geq 2 double bonds are only classified as PUFA, however, for a 164 better characterization of the FA profile, these biomolecules were separated in the present 165 study as PUFA (FAs displaying 2 or 3 double bonds) and HUFA (FAs with \geq 4 double 166 bonds).

167 The relative FA composition of each sample was submitted to a log (x + 1) transformation 168 and a dissimilitary matrix between samples was obtained using the Bray-Curtis coefficient. 169 The existence of significant differences (p < 0.05) between the FA profiles of the AM of 170 clams from different ecosystems was investigated trough a one-way analysis of similarity 171 (ANOSIM). Additionally, a similarity percentage analysis (SIMPER) was performed to find 172 which FAs contributed the most to the separation recorded between pairs of ecosystems.

A reference model was built using a canonical analysis of principal coordinates (CAP) with the groups corresponding to the ecosystems of origin of the Manila clams surveyed, namely Te, RAv and RV. First, to evaluate the accuracy of the reference model, an independent training and test datasets was produced. The matrix with all samples was randomly split with a ratio of 0.67 to 0.33, resulting in training and test matrices with 60 samples (20 replicates

178 per ecosystem) and 30 samples (10 replicates per ecosystem), respectively. Following this 179 procedure, a CAP was performed under the training dataset. The generated model was then evaluated introducing samples of the test dataset, one group at a time, verifying in which 180 181 ecosystem the samples were allocated. Finally, the reference model with all sites per ecosystem (30 replicates per ecosystem = 90 samples) was built. This model was used to 182 183 verify the most likely harvesting location of the samples suspected of originating from the Tagus estuary provided by the stakeholders, namely Rt, Ws, DC1 and DC2, through their 184 allocation to one of the following locations: Te, RAv or RV. 185

186 To justify the allocation of the samples suspected of originating from the Tagus estuary to the 187 ecosystems, under each FA, nonparametric Nemenyi tests were performed to investigate the 188 existence of significant differences (p < 0.05) between pairs of sampling groups.

Multivariate analysis (CAP, ANOSIM and SIMPER) were performed using PRIMER v7 with
the add-on PERMANOVA+ (Anderson, Gorley, & Clarke, 2008; Clarke & Gorley, 2015),
while the Nemenyi tests were performed using R environment v3.2.5 (R Core Team, 2016).

192

193 **3. Results**

The mean relative abundance of each FA per sampling group is presented in Table 1. A total of 26 FAs were identified, being HUFA the most dominant class (50-53%), with eicosapentaenoic (20:5n-3; EPA) and docosahexaenoic (22:6n-3; DHA) acids being the most relevant ones, followed by SFA (22-26%), with the predominance of palmitic (16:0; PA) and stearic (18:0) acids. The least represented classes were MUFA (13-18%), mostly present due to oleic (18:1n-9) and eicosenoic (20:1n-9/11) acids, and PUFA (7-12%), with docosadienoic (22:2n-6) acid being the most predominant.

The results of global and pairwise ANOSIM tests performed under the ecosystems surveyed (Te, RAv and RV) revealed significant differences (p < 0.001), with the higher value of R

203 obtained for the RAv vs. RV comparison (R = 1), followed by Te vs. RV (R = 0.999) and Te 204 vs. RAv (0.877). Results from the SIMPER analysis are presented in Table 2 and revealed that DHA and EPA were, for the three comparisons, the FAs that contributed the most for the 205 206 differences recorded between ecosystems. The lowest mean DHA content was registered for RV (18.80%) and the highest for RAv (30.17%), while the lowest mean EPA content was 207 208 presented by RAv (9.22%) and the highest by RV (17.63%, see Table 1).

209 The CAP results are summarized in Tables 3 and 4 and graphically presented in Figures 2 and 210 3. The evaluation of the CAP model built with the training dataset revealed a high performance (100% of correct allocations, see Table 3). For the reference model built with all 211 212 the ecosystem samples collected, the percentage of the one-leave-out cross-validation was 213 also 100% of correct allocation (see Table 4), being this illustrated by the perfect separation of the group samples shown in the respective CAP diagram (Figure 2). Concerning the most 214 215 likely harvesting location of the four batches of Manila clams suspected of originating from 216 the Tagus estuary, these showed high allocation percentages ($\geq 90\%$) for samples of Rt, Ws and DC2 to TE (see Table 4 and Figure 3 A, B and D, respectively). The sole exception was 217 218 batch DC1, with samples being mostly allocated to RAv (83.3% of allocation) (see Figure 3C and Table 4). 219

220 The results of the Nemenyi tests are summarized in Table 5, where comparisons between the 221 FAs of the AM of Manila clams from the sampled ecosystems and between clams from the batches suspected of originating from the Tagus estuary are presented. Regarding the 222 223 comparisons between ecosystems, Te vs. RAv, Te vs. RV and RAv vs. RV, significant 224 differences were recorded for most of the FAs surveyed (see Table 5). The batches of Manila clams being investigated with most samples classified as Te in the CAP analysis (namely Rt, 225 226 Ws and DC2), displayed only 4 FAs (or less) with significant differences between these 227 groups and Te. It is worth highlighting that these significant differences were always higher

when the comparison was performed with the two other ecosystems surveyed (RAv and RV)
(see Table 5). Concerning DC1, a higher number of FAs presented significant differences in
the comparison Te vs. DC1 than in the comparison RAv vs. DC1. This result is in line with
the allocation of most samples from DC1 to RAv as their most likely harvesting location.
Overall, the results of the Nemenyi tests support the results of the CAP.

233

4. Discussion

The fraudulent mislabeling of geographic origin is a well-known problem in the seafood trade (Leal et al., 2015). The significant differences recorded in the FA profiles of the AM of Manila clams originating from the three ecosystems surveyed in the present study, confirmed the potential of this biochemical tool to trace the geographic origin of bivalves, as already highlighted by previous studies (Grahl-Nielsen et al., 2010; Olsen et al., 2009; Ricardo et al., 2017, 2015).

241 The FA profile of the AM of *R. philippinarum* presented general features similar to other 242 bivalves, such as cockles (Cerastoderme edule; Ricardo et al., 2017, 2015), scallops (Pecten 243 maximus; Grahl-Nielsen et al., 2010) or other clams (Astarte sulcata; Olsen et al., 2009), with 244 the most dominant FAs being 16:0 (PA), 18:0, 20:5n-3 (EPA) and 22:6n-3 (DHA), as well as by the FA classes with PUFA plus HUFA presenting the highest relative abundance, followed 245 by SFA and MUFA. The high contents of *n*-3 HUFA, namely EPA and DHA in the AM of *R*. 246 247 *philippinarum* in all sampling groups screened, is likely related to its phytoplankton diet, as 248 previously suggested for other bivalve species (Ackman, Epstein, & Kelleher, 1974; Nemova 249 et al., 2013). The highest contents on DHA, as in the case of Manila clams originating from 250 RV, suggests the prevalence of a dinoflagellate based diet, whereas specimens from other 251 ecosystems displayed in their AM higher levels of EPA, likely related to a predominant consumption of diatoms (e.g., Dalsgaard et al., 2003; Fujibayashi et al., 2016; Napolitano, 252

253 1999). The areas surveyed in the present work display a latitudinal gradient, being expected 254 that the northernmost ecosystems would likely host specimens with higher levels of 255 unsaturated FA, as these contribute to maintain membrane fluidity in colder waters (Fokina et 256 al., 2015; Nemova et al., 2013). Nevertheless, this pattern was not found in the present study, likely because the latitudinal cline was not sufficient to promote such contrasting water 257 258 temperatures and, as such, to be reflected in the level of unsaturated FA on the AM of R. philippinarium. The FA profile of the AM is influenced by long term dietary tendencies and 259 environmental conditions (Dalsgaard et al., 2003; Napolitano, Pollero, Gayoso, Macdonald, 260 261 & Thompson, 1997; Nerot et al., 2015), thus, the results here obtained reflect the prevalent 262 abiotic and trophic conditions on the ecosystems surveyed.

263 The reference model assembled displayed accuracy values of 100%, as previously obtained by Ricardo, et al. (2017) using the FA profile of the AM of cockles originating from different 264 ecosystems along the Portuguese coast. The high percentage of samples allocation (\geq 90%) to 265 the Tagus estuary from three of the four batches of Manila clams suspected from being 266 267 illegally collected in that ecosystem is in agreement with the suspicions of Portuguese law enforcement agencies that a significant part of *R. philippinarum* traded in mainland Portugal 268 originate from IUU captures. The findings from this study are certainly of concern as: i) the 269 270 Tagus estuary holds a production/capture area classification of C that impairs the trade of live 271 Manila clams, even if depurated (IPMA, 2019); ii) the damaging nature of the harvesting 272 gears employed in this estuary to pursue this IUU fishery, which endangers multiple habitats 273 of the largest wetland zone in Portugal, and one of the biggest in Europe (Ramajal et al., 274 2016); and iii) the study by Chiesa et al. (2018) that refers the high loads of metals and arsenic (As) recorded in the edible tissues of R. philippinarum from the Tagus estuary. 275 276 Overall, the IUU capture of Manila clams in this ecosystem is certainly of concern if live specimens are traded for human consumption, as they pose a serious threat to public health. 277

278 The present study built upon the findings reported by Ricardo, et al. (2017, 2015) that used 279 the FA profile of the AM to trace the geographic origin of the bivalve C. edule. It advanced the state of the art by applying this approach to another commercially relevant bivalve species 280 281 (R. philippinarum) targeted by IUU. The independent training and test datasets employed in 282 the present study to evaluate the reference model, allowed a more reliable and accurate 283 analysis, when compared with one-leave-out cross-validation (Franklin, 2010). The 284 framework presented in this study will help to strengthen food safety measures aiming to 285 fight the fraudulent mislabeling of the geographic origin of seafood, namely for bivalves. Future studies should enhance the robustness of the reference model by including more origin 286 287 ecosystems (even if these only repent a small fraction of the supply chain supporting the trade 288 of Manila clams) and investigate how seasonal and/or interannual variations on the FA profile of the AM may challenge the accuracy of predictive models. 289

290

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Declaration of interest

- 306 The authors declare that they have no conflict of interest.
- 307

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473

474 **Figure captions:**

475 Figure 1. Sampling locations of Manila clams *Ruditapes philippinarum* in mainland Portugal
476 and Spain: Ría de Vigo (8° 43' 9.59"W, 42° 15' 38.44"N), Ria de Aveiro (8° 41' 18.93"W,
477 40° 46' 6.95"N) and Tagus estuary (9° 0' 58.66"W, 38° 45' 16.55"N).

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479 Figure 2. Reference model produced by a canonical analysis of principal coordinates (CAP)
480 based on the fatty acid composition of the adductor muscle of Manila clams *Ruditapes*481 *philippinarum* originating from the Tagus estuary (Te), Ria de Aveiro (RAv) and Ría de Vigo
482 (RV).

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Figure 3. Pinpoint of the harvesting location of the samples suspected of originating from the Tagus estuary produced by a canonical analysis of principal coordinates (CAP) based on the fatty acid composition of the adductor muscle of Manila clams *Ruditapes philippinarum*. The reference model was validated using samples from the Tagus estuary (Te), Ria de Aveiro (RAv) and Ría de Vigo (RV), on which were introduced, one group at a time, samples from the batches originating from Retailer (Rt, A), Wholesaler (Ws, B), Depuration Center tank1 (DC1, C) and Depuration Center tank 2 (DC2, D).

Table 1. Fatty acid profile (presented as % of relative abundance of the total pool of fatty acids) of the adductor muscle of Manila clams *Ruditapes philippinarum* (values are means of replicates \pm SD) collected from the Tagus estuary (Te), Ria de Aveiro (RAv) and Ría de Vigo (RV) and from the four batches of clams with unknown geographic origin, namely Retail (Rt), Wholesaler (Ws) and two different tanks from a depuration center (DC1 and DC2). SFA - Saturated fatty acids; MUFA - Monounsaturated

| | | Sampling groups | | | | | | | | | | | |
|---------------------|-----------------|-----------------|------------------|-----------------|------------------|-----------------|------------------|--|--|--|--|--|--|
| Fatty acids (%) | Te (n=30) | RAv (n=30) | RV (n=30) | Rt (n=12) | Ws (n=7) | DC1 (n=30) | DC2 (n=30) | | | | | | |
| 14:0 | 0.36 ± 0.08 | 0.52±0.13 | 0.80 ± 0.18 | 0.53±0.09 | 0.33±0.06 | 0.41±0.14 | 0.33±0.08 | | | | | | |
| 15:0 | 0.50 ± 0.08 | 0.57 ± 0.10 | 0.43 ± 0.06 | 0.49 ± 0.06 | 0.47±0.03 | 0.40 ± 0.07 | 0.44 ± 0.06 | | | | | | |
| 16:0 | 12.75±0.93 | 13.71±1.66 | 14.04±0.66 | 13.47±0.82 | 12.04±0.56 | 11.34±1.84 | 11.91±0.94 | | | | | | |
| 17:0 | 1.29 ± 0.17 | 1.33±0.14 | 1.01 ± 0.10 | 1.26 ± 0.13 | 1.36±0.16 | 1.45 ± 0.15 | 1.42 ± 0.09 | | | | | | |
| 18:0 | 7.91±0.70 | 9.81±1.22 | 8.07 ± 0.67 | 8.00 ± 0.94 | 8.19±0.71 | 8.86±0.77 | 8.60 ± 0.78 | | | | | | |
| ∑SFA | 22.81±1.96 | 25.94±3.24 | 24.36±1.67 | 23.75±2.04 | 22.39±1.53 | 22.45±2.98 | 22.71±1.94 | | | | | | |
| 16:1 <i>n</i> -9 | 0.18 ± 0.04 | 0.14 ± 0.03 | 0.13±0.03 | 0.15 ± 0.02 | 0.20±0.03 | 0.15 ± 0.04 | 0.17 ± 0.03 | | | | | | |
| 16:1 <i>n</i> -7 | 2.33±0.39 | 1.92±0.36 | 3.88 ± 0.79 | 2.55 ± 0.40 | 2.21±0.61 | 1.78±0.73 | 2.26 ± 0.32 | | | | | | |
| 18:1 <i>n-</i> 9 | 4.79±0.67 | 4.79±0.81 | 3.80±0.49 | 4.33±0.62 | 4.80±0.66 | 4.88 ± 1.29 | 4.66±0.56 | | | | | | |
| 18:1 <i>n</i> -7 | 1.92±0.24 | 1.63±0.17 | 2.67 ± 0.29 | 2.17±0.21 | 1.84 ± 0.14 | 1.29±0.39 | 1.72±0.20 | | | | | | |
| 20:1 <i>n</i> -9/11 | 4.78±0.41 | 4.84±0.56 | 4.08 ± 0.42 | 5.07±0.66 | 4.40±0.37 | 2.93±0.38 | 4.57±0.36 | | | | | | |
| 20:1 <i>n</i> -7 | 2.74±0.25 | 2.41±0.24 | 3.25 ± 0.25 | 3.17±0.23 | 2.75±0.21 | 2.43±0.29 | 2.84±0.26 | | | | | | |
| ∑MUFA | 16.74±1.99 | 15.72±2.17 | 17.81±2.25 | 17.43±2.14 | 16.20 ± 2.01 | 13.47±3.11 | 16.23±1.72 | | | | | | |
| 18:2 <i>n</i> -6 | 0.30 ± 0.05 | 0.23±0.05 | 0.19±0.05 | 0.24±0.05 | 0.29 ± 0.08 | 0.26±0.29 | 0.25 ± 0.05 | | | | | | |
| 18:3 <i>n</i> -3 | 0.84 ± 0.14 | 0.38 ± 0.06 | 0.52±0.10 | 0.63±0.11 | 0.82±0.13 | 0.38±0.20 | 0.75 ± 0.08 | | | | | | |
| 20:2 <i>n</i> -6 | 1.80 ± 0.28 | 1.61±0.32 | 1.69±0.15 | 1.85 ± 0.22 | 1.75±0.17 | 1.08 ± 0.20 | 1.82±0.22 | | | | | | |
| 20:3 <i>n</i> -6 | 0.22±0.06 | 0.11±0.04 | 0.22±0.05 | 0.19 ± 0.04 | 0.24 ± 0.04 | 0.17 ± 0.05 | 0.15±0.03 | | | | | | |
| 22:2 <i>n</i> -9 | 1.18±0.15 | 1.31±0.19 | 0.87±0.13 | 0.92 ± 0.14 | 1.10±0.11 | 2.14±0.44 | 1.09 ± 0.17 | | | | | | |
| 22:2 <i>n</i> -6 | 3.23±0.41 | 2.71±0.41 | 2.91±0.41 | 2.84 ± 0.64 | 3.09±0.40 | $6.90{\pm}1.20$ | 3.33±0.41 | | | | | | |
| 22:3 <i>n</i> -6 | 1.22±0.12 | 0.76±0.09 | 1.47 ± 0.16 | 1.17 ± 0.17 | 1.21±0.15 | 1.00 ± 0.35 | 1.16±0.11 | | | | | | |
| ∑PUFA | 8.79±1.21 | 7.10±1.15 | 7.87±1.05 | 7.83±1.37 | 8.50±1.08 | 11.93±2.72 | 8.55±1.06 | | | | | | |
| 18:4 <i>n</i> -3 | 1.48±0.25 | 1.06±0.16 | 0.91 ± 0.17 | 1.24 ± 0.11 | 1.45±0.18 | 1.13±0.33 | 1.22±0.18 | | | | | | |
| 20:4 <i>n</i> -6 | 3.70±0.34 | 3.50±0.39 | 3.03±0.32 | 3.66 ± 0.40 | 3.69±0.17 | 4.31±0.46 | 3.75±0.26 | | | | | | |
| 20:4 <i>n</i> -3 | 0.72±0.17 | 0.47 ± 0.10 | 0.92±0.15 | 0.74 ± 0.12 | 0.72±0.10 | 0.30 ± 0.07 | 0.69 ± 0.08 | | | | | | |
| 20:5 <i>n</i> -3 | 11.55±0.77 | 9.22±0.67 | 17.63 ± 1.20 | 13.00±1.58 | 11.16±0.93 | $7.30{\pm}1.28$ | 10.80 ± 0.77 | | | | | | |
| 22:4 <i>n</i> -6 | 1.58±0.23 | 1.37±0.19 | 1.92 ± 0.22 | 1.59 ± 0.24 | 1.64±0.32 | 1.75 ± 0.44 | 1.90±0.23 | | | | | | |
| 22:5 <i>n</i> -6 | 2.21±0.62 | 1.44 ± 0.20 | 0.95 ± 0.16 | 1.57 ± 0.12 | 1.96±0.25 | 2.01±0.29 | 1.85 ± 0.17 | | | | | | |
| 22:5 <i>n</i> -3 | 4.45±0.46 | 4.00 ± 0.50 | 5.79 ± 0.56 | 4.85±0.51 | 4.25±0.47 | 5.81±1.02 | 4.57±0.70 | | | | | | |
| 22:6 <i>n</i> -3 | 25.98±1.99 | 30.17±1.77 | $18.80{\pm}1.04$ | 24.34±1.46 | 28.05±1.38 | 29.54±3.98 | 27.73±1.58 | | | | | | |
| ∑HUFA | 51.66±4.83 | 51.24±3.99 | 49.96±3.83 | 50.99±4.54 | 52.92±3.79 | 52.15±7.86 | 52.51±3.97 | | | | | | |

fatty acids; PUFA - Polyunsaturated fatty acids; HUFA - Highly unsaturated fatty acids.

| | Te vs | s. RAv | | Te va | | RAv vs. RV | | | |
|---------------------|-------------|-------------|---------------------|-------------|-------------|------------------|-------------|-------------|--|
| Fatty Acids | Ind. (%) | Cum. (%) | Fatty Acids | Ind. (%) | Cum. (%) | Fatty Acids | Ind. (%) | Cum. (%) | |
| 22:6n-3 | 20.28 | 20.28 | 22:6n-3 | 23.60 | 23.60 | 22:6 <i>n</i> -3 | 28.44 | 28.44 | |
| 20:5 <i>n</i> -3 | 12.34 | 32.61 | 20:5 <i>n</i> -3 | 21.35 | 44.95 | 20:5 <i>n</i> -3 | 23.05 | 51.49 | |
| 18:0 | 10.57 | 43.19 | 16:1 <i>n</i> -7 | 6.13 | 51.09 | 16:1 <i>n</i> -7 | 5.95 | 57.44 | |
| 16:0 | 9.04 | 52.22 | 16:0 | 5.25 | 56.33 | 22:5 <i>n</i> -3 | 5.33 | 62.77 | |
| 18:1 <i>n</i> -9 | 4.56 | 56.78 | 22:5 <i>n</i> -3 | 5.20 | 61.53 | 18:0 | 5.25 | 68.02 | |
| 22:5 <i>n</i> -6 | 4.53 | 61.31 | 22:5 <i>n</i> -6 | 5.00 | 66.53 | 16:0 | 3.98 | 72.00 | |
| 22:5 <i>n</i> -3 | 3.72 | 65.04 | 18:1 <i>n</i> -9 | 4.13 | 70.66 | 18:1 <i>n</i> -9 | 3.35 | 75.36 | |
| 22:2 <i>n</i> -6 | 3.66 | 68.70 | 18:1 <i>n</i> -7 | 2.99 | 73.65 | 18:1 <i>n</i> -7 | 3.17 | 78.53 | |
| 16:1 <i>n</i> -7 | 3.12 | 71.81 | 20:1 <i>n</i> -9/11 | 2.94 | 76.59 | 20:1 <i>n</i> -7 | 2.57 | 81.10 | |
| 20:1 <i>n</i> -9/11 | 3.02 | 74.83 | 18:0 | 2.84 | 79.43 | | | | |
| 22:3 <i>n</i> -6 | 2.67 | 77.50 | 20:4 <i>n</i> -6 | 2.74 | 82.17 | | | | |
| 18:3 <i>n</i> -3 | 2.64 | 80.14 | | | | | | | |

Table 2. Similarity percentage analysis (SIMPER) identifying which fatty acids of the adductor muscle of Manila clams *Ruditapes philippinarum* contributed to the differences recorded between ecosystems. Te: Tagus estuary; RAv: Ria de Aveiro; RV: Ría de Vigo.

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Table 3. Allocation success (by sampling group) of the canonical analysis of principal coordinates (CAP) based on fatty acid profiles of the adductor muscle of Manila clams *Ruditapes philippinarum*. Te: Tagus estuary; RAv: Ria de Aveiro; RV: Ría de Vigo. Evaluation performed with an independent test dataset.

| | Original | Alloca | tion Gro | up | Total per Group | % Correct Allocation | |
|------------|----------|--------|----------|----|--------------------|-------------------------|--|
| | Group - | Te | RAv | RV | | | |
| Reference | Te | 10 | 0 | 0 | 10 | 100 | |
| model | RAv | 0 | 10 | 0 | 10 | 100 | |
| Evaluation | RV | 0 | 0 | 10 | 10 | 100 | |

- i

Table 4. Allocation success (by sampling group) of the canonical analysis of principal coordinates (CAP) based on the fatty acid profiles of the adductor muscle of Manila clams *Ruditapes philippinarum*. Te: Tagus estuary; RAv: Ria de Aveiro; RV: Ría de Vigo; Rt: Retail; Ws: Wholesaler; DC1: Depuration center tank 1; DC2: Depuration center tank 2.

| | Original Group | Allo | cation G | roup | Total per Group | % Correct Allocation (One-leave-out | % Allocation to TE | |
|-------------|-------------------|------|----------|---------|--------------------|---|--------------------------|--|
| | Ĩ | Te | RAv | RV | - | cross-validation) | | |
| Reference | Te | 30 | 0 | 0 | 30 | 100 | - | |
| Model | RAv RV | 0 | 30 | 0 30 | 30 30 | 100 | - | |
| | Rt | 11 | 0 | 1 | 12 | - | 91.7 | |
| Pinpoint of | Ws | 7 | 0 | 0 | 7 | - | 100 | |
| location | DC1 | 5 | 25 | 0 | 30 | G | 16.7 | |
| | DC2 | 27 | 3 | 0 | 30 | | 90 | |
| | | | | | | | | |

| | Te vs RAv | Te vs RV | RAv vs RV | Te vs Rt | RAv vs Rt | RV vs Rt | Te vs Ws | RAv vs Ws | RV vs Ws | Te vs DC1 | RAv vs DC1 | RV vs DC1 | Te vs DC2 | RAv vs DC2 | RV vs DC2 |
|---------------------|-----------|----------|-----------|----------|-----------|----------|----------|-----------|----------|-----------|------------|-----------|-----------|------------|-----------|
| 14:0 | 0.0011 | < 0.0001 | 0.0361 | 0.0169 | > 0.9999 | 0.3161 | 0.9941 | 0.0249 | < 0.0001 | 0.9122 | 0.0558 | < 0.0001 | 0.9235 | < 0.0001 | < 0.0001 |
| 15:0 | 0.3396 | 0.0259 | < 0.0001 | > 0.9999 | 0.6450 | 0.2193 | 0.9996 | 0.5919 | 0.7275 | < 0.0001 | < 0.0001 | 0.7653 | 0.1673 | 0.0001 | 0.9933 |
| 16:0 | 0.2062 | 0.0020 | 0.7841 | 0.5540 | > 0.9999 | 0.9147 | 0.8666 | 0.0884 | 0.0048 | 0.0931 | < 0.0002 | < 0.0001 | 0.3056 | 0.0001 | < 0.0001 |
| 16:1 <i>n</i> -9 | 0.0048 | < 0.0001 | 0.7561 | 0.5602 | 0.9497 | 0.3121 | 0.9395 | 0.0154 | 0.0004 | 0.0521 | 0.9876 | 0.24698 | > 0.9999 | 0.0100 | < 0.0001 |
| 16:1 <i>n</i> -7 | 0.0525 | < 0.0001 | < 0.0001 | 0.9364 | 0.0172 | 0.1876 | 0.9827 | 0.9530 | 0.0046 | 0.0001 | 0.7544 | < 0.0001 | 0.9999 | 0.1265 | < 0.0001 |
| 17:0 | 0.9964 | < 0.0001 | < 0.0001 | 0.9981 | 0.9523 | 0.0310 | 0.9890 | 0.9998 | 0.0036 | 0.0129 | 0.0967 | < 0.0001 | 0.0624 | 0.2914 | < 0.0001 |
| 18:0 | < 0.0001 | 0.9973 | < 0.0001 | 0.9970 | 0.0004 | > 0.9999 | 0.9950 | 0.0163 | > 0.9999 | 0.0013 | 0.1801 | 0.0118 | 0.0346 | 0.0145 | 0.1634 |
| 18:1 <i>n</i> -9 | > 0.9999 | < 0.0001 | < 0.0001 | 0.5994 | 0.7233 | 0.2578 | > 0.9999 | > 0.9999 | 0.0136 | 0.9855 | 0.9979 | 0.0001 | 0.9998 | > 0.9999 | < 0.0001 |
| 18:1 <i>n</i> -7 | 0.0167 | 0.0004 | < 0.0001 | 0.6899 | 0.0009 | 0.6449 | 0.9995 | 0.6692 | 0.0342 | < 0.0001 | 0.4208 | < 0.0001 | 0.2145 | 0.9585 | < 0.0001 |
| 18:2 <i>n</i> -6 | 0.0067 | < 0.0001 | 0.1214 | 0.2028 | 0.9999 | 0.2143 | 0.9999 | 0.4838 | 0.0072 | < 0.0001 | 0.0896 | > 0.9999 | 0.1103 | 0.9632 | 0.0052 |
| 18:3 <i>n</i> -3 | < 0.0001 | < 0.0001 | 0.1481 | 0.1348 | 0.0146 | 0.7863 | > 0.9999 | < 0.0001 | 0.0122 | < 0.0001 | > 0.9999 | 0.1281 | 0.9431 | < 0.0001 | 0.0004 |
| 18:4 <i>n</i> -3 | < 0.0001 | < 0.0001 | 0.3207 | 0.5155 | 0.2360 | 0.0013 | > 0.9999 | 0.0120 | < 0.0001 | < 0.0001 | 0.9821 | 0.0387 | 0.0497 | 0.1437 | < 0.0001 |
| 20:1 <i>n</i> -9/11 | > 0.9999 | 0.0003 | 0.0002 | 0.9711 | 0.9859 | 0.0006 | 0.6977 | 0.6461 | 0.9361 | < 0.0001 | < 0.0001 | 0.0066 | 0.8630 | 0.8031 | 0.0393 |
| 20:1 <i>n</i> -7 | 0.01664 | < 0.0001 | < 0.0001 | 0.0221 | < 0.0001 | 0.9993 | > 0.9999 | 0.3436 | 0.0521 | 0.0513 | 0.9996 | < 0.0001 | 0.9403 | 0.0003 | 0.0026 |
| 20:2 <i>n</i> -6 | 0.2171 | 0.8041 | 0.95739 | 0.9989 | 0.2484 | 0.7105 | > 0.9999 | 0.8894 | 0.9967 | < 0.0001 | < 0.0001 | < 0.0001 | 0.9991 | 0.0703 | 0.4975 |
| 20:3 <i>n</i> -6 | < 0.0001 | > 0.9999 | < 0.0001 | 0.9167 | 0.0004 | 0.8315 | 0.9704 | < 0.0001 | 0.9896 | 0.0081 | 0.0058 | 0.00295 | 0.0002 | 0.1046 | < 0.0001 |
| 20:4 <i>n</i> -6 | 0.5552 | < 0.0001 | 0.0242 | 0.9997 | 0.9622 | 0.0111 | > 0.9999 | 0.9045 | 0.0251 | 0.0007 | < 0.0001 | < 0.0001 | 0.9987 | 0.2459 | < 0.0001 |
| 20:4 <i>n</i> -3 | 0.0007 | 0.0193 | < 0.0001 | 0.9999 | 0.0090 | 0.3382 | > 0.9999 | 0.0818 | 0.5475 | < 0.0001 | 0.1597 | < 0.0001 | 0.9989 | 0.0050 | 0.0033 |
| 20:5 <i>n</i> -3 | < 0.0001 | 0.0016 | < 0.0001 | 0.9429 | < 0.0001 | 0.4619 | 0.9980 | 0.2105 | 0.0464 | < 0.0001 | 0.4538 | < 0.0001 | 0.6174 | 0.0394 | < 0.0001 |
| 22:2 <i>n</i> -9 | 0.8074 | < 0.0001 | < 0.0001 | 0.0173 | 0.0003 | 0.9995 | 0.9743 | 0.5836 | 0.3296 | < 0.0001 | 0.0076 | < 0.0001 | 0.7745 | 0.0726 | 0.0093 |
| 22:2 <i>n</i> -6 | 0.0103 | 0.3711 | 0.7957 | 0.1724 | > 0.9999 | 0.9727 | 0.9974 | 0.7041 | 0.9930 | < 0.0001 | < 0.0001 | < 0.0001 | 0.9975 | 0.0012 | 0.1132 |
| 22:3n-6 | < 0.0001 | 0.0128 | < 0.0001 | 0.9980 | 0.0004 | 0.0309 | > 0.9999 | 0.0037 | 0.2497 | 0.0044 | 0.0975 | < 0.0001 | 0.8929 | < 0.0001 | < 0.0001 |
| 22:4 <i>n</i> -6 | 0.1632 | 0.0002 | < 0.0001 | > 0.9999 | 0.5327 | 0.0118 | 0.9852 | 0.2247 | 0.4713 | 0.7068 | 0.0011 | 0.0667 | 0.0004 | < 0.0001 | > 0.9999 |
| 22:5n-6 | < 0.0001 | < 0.0001 | 0.0860 | 0.0042 | 0.9891 | 0.0612 | 0.9996 | 0.0239 | < 0.0001 | > 0.9999 | < 0.0001 | < 0.0001 | 0.6549 | 0.0006 | < 0.0001 |
| 22:5n-3 | 0.3022 | < 0.0001 | < 0.0001 | 0.7513 | 0.0281 | 0.0761 | 0.9955 | 0.9911 | 0.0007 | < 0.0001 | < 0.0001 | 0.9975 | 0.9997 | 0.1334 | < 0.0001 |
| 22:6n-3 | < 0.0001 | 0.0005 | < 0.0001 | 0.9265 | < 0.0001 | 0.3531 | 0.6376 | 0.7638 | 0.0004 | 0.0008 | 0.9545 | < 0.0001 | 0.2630 | 0.0749 | < 0.0001 |

Table 5. Nemeney test results performed for each fatty acid to assess significant differences between sample groups. Values of p highlighted in light grey are < 0.05. Te: Tagus estuary; RAv: Ria de Aveiro; RV: Ría de Vigo; Rt: Retail; Ws: Wholesaler; DC1: Depuration center tank 1; DC2: Depuration center tank 2.















Highlights (maximum 85 characters, including spaces, per bullet points):

- Fatty acid (FA) profiles of the adductor muscle trace the harvesting site of Manila clams ٠
- The dominant FAs were the 22:6n-3 (DHA), 16:0 (PA) and 20:5n-3 (EPA) •
- Collection site of Manila clams with unknown origin was pinpointed •
- The illegal harvesting of Manila clams from interdicted areas was uncovered ٠

Declaration of interest:

The authors declare that they have no conflict of interest.

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