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## Different particle sources in a bivalve species of a coastal lagoon: evidence from stable isotopes, fatty acids, and compound-specific stable isotopes

Mathieu-Resuge Margaux <sup>1, 4, \*</sup>, Schaal Gauthier <sup>1</sup>, Kraffe Edouard <sup>1</sup>, Corvaisier Rudolph <sup>1</sup>, Lebeau Oanez <sup>2</sup>, Lluch-Cota Salvador E. <sup>3</sup>, Salgado García Rosa L. <sup>3</sup>, Kainz Martin J. <sup>4</sup>, Le Grand Fabienne <sup>1</sup>

<sup>1</sup> Univ Brest, CNRS, IRD, Ifremer, LEMAR, IUEMPlouzané, France

<sup>2</sup> Univ Brest, CNRS, UMS3113, IUEMPlouzané, France

<sup>3</sup> Centro de Investigaciones Biológicas del Noroeste (CIBNOR)La Paz, Mexico

<sup>4</sup> WasserCluster Lunz-Inter-University Centre for Aquatic Ecosystem ResearchLunz am See,Austria

\* Corresponding author : Margaux Mathieu-Resuge, email address : m.mathieuresuge@gmail.com

#### Abstract :

The trophic fate of various food sources is of central interest for ecologists, yet not well understood in coastal lagoon food webs. In this field study, fatty acids (FA), stable isotopes (SI), and compound-specific isotopic analysis (CSIA) on FA were used to investigate how diets from oceanic and local sources are retained in a bivalve species (Spondylus crassisguama; Lamarck 1819) along a transect in the Ojo de Liebre Jagoon (BCS, Mexico). Results from SI and FA indicated the contribution of oceanic diatoms at the entrance of the lagoon, through 15N enrichment, and higher proportions of 16:1n-7 and 20:5n-3 in digestive glands. In the inner bay, higher abundance of 18-carbon FA (18:1n-9, 18:3n-3, 18:4n-3) suggested a higher contribution of microheterotrophs, including (dino)flagellates and ciliates, to the diet of this bivalve derived from local production. Significant spatial differences for the  $\delta$ 13C of FA highlighted changes in the origin of food sources. Indeed, a 13C depletion was observed in the δ13C of heterotrophic flagellates biomarkers in individuals from the innermost station, revealing that their origin in the diet of bivalves differs within the lagoon, highlighting the importance of local processes (sediment resuspension, remineralization) in the trophic functioning of the lagoon. The  $\delta$ 13C values of FA considered as diatoms biomarkers (16:1n-7 and 20:5n-3) were consistent, which suggests that diatoms assimilated have very similar origins throughout the lagoon. The complementary of the tracers used here allowed for a better understanding of the trophic functioning of this coastal lagoon submitted to oceanic influences.

#### 45 Introduction

46 Coastal lagoons are complex and productive ecosystems, and their primary production is 47 supported by a highly diverse origin of nutrients (Nixon 1982). At the interface between land 48 and ocean, lagoons are characterized by shallow water and a large diversity of potential food 49 sources, including continental inputs, salt marsh, seagrass, macroalgae, and phytoplankton, 50 and resulting in marked spatial patterns in food web interactions (Carlier et al. 2008; Clavier 51 et al. 2014). In coastal lagoons, benthic assemblages are largely dominated by suspension-52 feeding bivalves (Bachelet et al. 2000). Because these organisms are sedentary primary 53 consumers, they are good indicators of processes occurring at the base of the food web 54 (Marchais et al. 2013). Therefore, studying the nature and the origin of food sources 55 involved in their diet provides a spatially and temporally integrated overview of organic 56 matter transfer between benthic and pelagic systems, and across ecosystem boundaries 57 (i.e., between lagoons and the nearby coastal ocean). 58 The trophic ecology of suspension-feeding invertebrates inhabiting coastal environments has 59 been extensively investigated over the last 20 years using indirect biomarker-based 60 approaches. Among the most common, the analysis of bulk carbon and nitrogen stable 61 isotopes (SI) has provided valuable insights into the origin and nature of bivalve food sources

62 (Riera 2007; Marchais et al. 2013). Because primary producers typically display contrasted SI

63 composition according to their benthic *vs* pelagic (France 1995) or freshwater *vs* marine

64 (Riera and Richard 1996) origin, and because the SI composition of consumers are indicative

of their source, this approach is currently widely used to address questions in trophic

- 66 ecology (Fry 1988; Layman et al. 2012). However, to be efficient, this method requires
- 67 primary producers displaying contrasted SI composition. Although different species of
- 68 planktonic microalgae can vary in their SI values (Falkowski 1991; Vuorio et al. 2006), it is

69 generally difficult to differentiate between potential diet sources that share the same 70 habitat (Kharlamenko et al. 2001). Therefore, it remains a challenge for bulk SI ecology to 71 assess the dietary contribution of different primary producers to consumers. 72 The analysis of fatty acids (FA) is a powerful and complementary approach, which is based 73 on the assumption that most animals have limited ability to biosynthesize polyunsaturated 74 FA (PUFA) or FA of bacterial origin de novo (Budge et al. 2006), and thus the FA composition of a consumer resembles that of its food source (Dalsgaard et al. 2003). Among the different 75 76 FA synthesized by primary producers, some of them are considered as trophic biomarkers 77 because they characterize specific food sources; for example, palmitoleic acid (16:1n-7) and 78 eicosapentaenoic acid (20:5n-3) are used as biomarkers of diatoms, and stearidonic acid 79 (18:4n-3) and docosahexaenoic acid (22:6n-3) are abundant in (dino)flagellates (Parrish et al. 80 2000; Kharlamenko et al. 2001; Alfaro et al. 2006). Therefore, it is possible to assess the 81 contribution of specific taxonomic groups (e.g. diatoms, dinoflagellates, marine plants) in the 82 diet of primary consumers (Kelly and Scheibling 2012); by paying attention when analyzing 83 bivalve tissues presenting different turnover rates resulting in diverse integrating dietary 84 information over time (e.g. the digestive gland (DG), has faster turnover rates than muscle 85 tissues) (Lorrain et al. 2002; Dalsgaard et al. 2003; Nerot et al. 2015). Because SI can be 86 useful in assessing food sources, in particular when using stable C and N isotopes in 87 combination (Lorrain et al. 2002; Schaal et al. 2016) and FA can differentiate between algal, 88 bacterial or even terrestrial sources (Kainz et al. 2002), these two approaches have been 89 successfully used in combination to unravel trophodynamic trajectories in a variety of 90 coastal environments (Alfaro et al. 2006; Jaschinski et al. 2008; Allan et al. 2010). The 91 combined use of SI and FA is based on the assumption that specific SI values or FA molecules 92 are attributed to distinct sources, which is unlikely in complex ecosystems (Kharlamenko et

al. 2001). For instance, it would be impossible to characterize the precise origin (i.e. oceanic

94 or coastal) of the diet of a suspension feeder assimilating planktonic dinoflagellates and

95 benthic diatoms using only bulk SI and FA approaches.

96 Compound-specific isotope analysis (CSIA) represents an ecologically complementary

97 approach, through which the identification of the SI composition of source-specific

98 compounds can characterise their origin. For example, CSIA has been successfully used in

99 trophic ecology to highlight the contribution of ice algae to the diet of bivalves (Gaillard et al.

100 2017), or dietary shifts in benthic invertebrates at the vicinity of finfish farming (Colombo et

101 al. 2016).

102 Lagoon, such as the Ojo de Liebre lagoon (Baja California Sur, Mexico), are of particular

103 interest for trophic ecology as they rely on a wide diversity of both local sources

104 (autochthonous) such as local phytoplankton or resuspended benthic sources, including

105 eelgrass detritus (Zostera marina; Linnaeus, 1753), and allochthonous sources, such as

106 oceanic phytoplankton supplied to the lagoon by tide current, especially during important

107 oceanic events occurring from April to June in this region (Du et al. 2015)..

108 In this context, the aim of this study was to apply three trophic biomarker-based approaches

to examine spatial patterns of organic matter sources and their biochemical composition

assimilated by *S. crassisquama*. It was hypothesized that lower oceanic phytoplankton

availability in the inner part of the lagoon, which is less connected to the ocean, would result

in higher reliance on local food sources. Stable isotope, FA, and CSIA values in consumers

113 located close the ocean were thus expected to resembled those of the ocean, testing the

- effect of spatial diet proximity to the ocean and how far its impact is perceived inside the
- 115 lagoon; by contrast, consumers furthest away from the ocean were isotopically and in their

- 116 FA composition expected to be closer to the autochthonous diet sources highlighting the
- 117 effect of local diet incorporation.

#### 119 Material and methods

#### 120 Sampling

121 The Ojo de Liebre lagoon is a 446 km<sup>2</sup> lagoon situated on the Pacific coast of Baja California 122 hosting one of the most important bivalve fishery (in particular Spondylus crassiquama; 123 Lamarck 1819) of western Mexico, was sampled in June 2017 at three stations along a 124 transect (Fig. 1); Station 1: located 3.5 km outside the bay; Station 2: at 6.1 km from the 125 mouth, inside the lagoon; and Station 3: 15.5 km inside the lagoon. Sampling depths ranged 126 from 7 to 10 m. Stations 1 and 3 corresponded to the most outer and inner sites, respectively, where the target species, Spondylus crassisquama, could be found. At each 127 128 station, 10 individuals of S. crassisquama of similar size (~12 cm of length), and potential 129 food sources (particulate organic matter; POM, and, sediment-water interface organic 130 matter; SOM) were collected by scuba divers. The Zostera marina fragments, at two 131 different degradation stages (later called fresh and detrital), were also collected from the 132 shore at the eastern part of the sampling area. Bivalves were placed in cooler boxes with 133 water from sampling sites at ambient temperature, while collected surface water and 134 sediment cores and eelgrass detritus were protected from light using black plastic bags until 135 transportation (within 3 hours) to the lab facilities at the Northwestern Center for Biological 136 Research (CIBNOR, Guerrero Negro, BCS). Once in the laboratory, bivalve DG and adductor 137 muscles were dissected, packed and stored in liquid nitrogen. 138 Food sources (POM, SOM, and eelgrass fragments) were prepared for analysis by the 139 following methods; a) sediment-water interface were soaked in filtered sea water (GF/F 0.7

- 140  $\mu$ m), and allowed to settle. The supernatant containing fine organic particles (SOM),
- 141 potentially affected by resuspension events and therefore available to benthic suspension-

142 feeders, was filtered on pre-combusted (6 h, 450°C) GF/F filters. Four subsamples of SOM 143 (two for SI, and two for FA analyses) were prepared for each sampling station, packed and 144 frozen in liquid nitrogen; b) particles from surface water were filtered on pre-combusted (6 145 h, 450°C) GF/F filters until clogging. Immediately after filtration, filters subsamples of POM (n 146 = 2 for SI, and n = 2 for FA analyses) were packed and frozen in liquid nitrogen immediately 147 after filtration, and; c) large epiphytes were first removed from eelgrass fragments, which 148 were then packed and stored in liquid nitrogen. Once at the main laboratory (CIBNOR, La Paz), all samples were stored at -80°C until further analysis. 149

#### 150 Stable isotopes analysis

Muscles and eelgrass samples were freeze-dried (24 h) and homogenized using a ball mill. Because bivalve muscles are generally poor in lipids, lipids were not removed from muscle tissues prior to SI analysis (Lorrain et al. 2002). Indeed, the measured C:N ratios did not exceed 3.5, rendering lipid removal unnecessary for SI analysis (Post et al. 2007). Muscle tissues (~25 mg dry weight) and particles of SOM and POM (scraped off from the freezedried filters; ~1.5 mg dry weight) were packed in tin capsules (8x5 mm) for subsequent bulk SI analysis.

All samples were analyzed by continuous flow on a Flash EA 2000 IRMS elemental analyzer coupled to a isotope ratio mass spectrometer (IRMS; Thermo Fisher Scientific Delta V Plus). Isotopic calibration was done using international standards (IAEA-600 Caffeine, IAEA-CH-6 Sucrose and IAEA-N-2 Ammonium Sulphate). The standard deviation calculated with the acetanilide working standard (Thermo Scientific), repeatedly measured after 7 samples, was ± 0.1 ‰ (n = 19) for both  $\delta^{13}$ C and  $\delta^{15}$ N. Results were expressed in delta ( $\delta$ ) units with respect to international standards (Vienna Pee Dee Belemnite for  $\delta^{13}$ C and atmospheric

- 165 nitrogen for  $\delta^{15}$ N), following the equation:  $\delta^{13}$ C or  $\delta^{15}$ N = [(R<sub>sample</sub>/R<sub>standard</sub>)-1] x 10<sup>3</sup>
- 166 (expressed in ‰), where R is  ${}^{13}C/{}^{12}C$  or  ${}^{15}N/{}^{14}N$ .
- 167 Fatty acid analysis
- 168 Lipid extraction
- 169 Total lipids of freeze-dried and homogenized bivalve DG and eelgrass fragments (between
- 170 0.2 and 0.4 g), and POM and SOM filter samples were extracted using chloroform/methanol
- 171 (6mL; 2:1; v/v) applying a modified method of Folch et al. (1957). Samples were then
- sonicated at 4°C during 5 min, to ensure complete extraction of lipids. Until further analysis,
- all lipid extracts were stored at -20°C under nitrogen atmosphere to avoid oxidation.

### 174 Separation of neutral lipids

- 175 DG lipids were separated into neutral and polar lipids (the latter was not analyzed in the
- present study) following the method described elsewhere (Le Grand et al. 2014). In brief, an
- aliquot (1/6) of the total lipid extract was evaporated under nitrogen, recovered with 3
- 178 washes using chloroform/methanol (0.5 mL; 98:2; v/v) and spotted at the top of a silica gel
- 179 column (40 mm x 4 mm, silica gel 60A 63-200  $\mu$ m rehydrated with 6% H<sub>2</sub>O; 70-230 mesh).
- 180 Neutral lipids (NL) were eluted using chloroform/methanol (10 mL; 98:2; v/v) and collected
- 181 in glass vials containing an internal standard (2.3 µg of tricosanoic acid; C23:0). Lipid
- 182 fractions were then stored at -20°C until further analyses.
- 183 Fatty acid analysis by gas chromatography

184 The NL fraction of DG as well as aliquots of POM, SOM and eelgrass total lipid extracts were

- 185 evaporated to dryness under nitrogen. Fatty acids methyl esters (FAME) were obtained by
- an acidic transesterification following a modified method by (Le Grand et al. 2014). In brief,

187 transesterification was performed by the addition of 0.8 mL of a H<sub>2</sub>SO<sub>4</sub>/methanol mixture 188 (3.4 %; v/v) to the dried extracts containing NL and heated at 100°C for 10 min. After cooling, 189 hexane (0.8 mL) and distilled water saturated in hexane (1.5 mL) were added. Vials were 190 then homogenized and centrifuged (at 738 g for 1 min at 20°C). Only the organic phase-191 containing FAME was kept and washed two more times with distilled water saturated in 192 hexane (1.5 mL). At each step, the aqueous phase was discarded. 193 Analyses of FAME were conducted on a Varian CP8400 gas chromatograph (GC), by 194 simultaneous separation on two columns with two different phase polarities: one polar 195 (ZBWAX: 30 m x 0.25 mm ID x 0.2  $\mu$ m, Phenomenex) and another apolar column (ZB5HT: 30 196 m x 0.25 mm ID x 0.2 µm, Phenomenex). The GC runs followed these temperature programs: 197 the GC oven temperature was raised to 150°C at 50°C min<sup>-1</sup>, then to 170°C at 3.5°C min<sup>-1</sup>, to 198 185°C at 1.5°C min<sup>-1</sup>, to 225°C at 2.4°C min<sup>-1</sup>, and finally to 250°C at 5.5°C min<sup>-1</sup> and 199 maintained for 15 min) and equipped of two splitless injectors regulated at 220°C, and two 200 flame-ionization detectors (280°C), using hydrogen as vector gas. Identification of FAME was 201 realized by comparison of their retention times with those of commercial standards from 202 Sigma (Supelco 37 Component FAME Mix, the PUFA No.1 and No.3, and the Bacterial Acid 203 Methyl Ester Mix) and an in-house standard mix from marine bivalves and microalgae. The 204 FA content (%) was expressed as the mass percentage of the total FA content.

205

Compound-specific isotopic analysis on fatty acids

206 Five bivalve samples previously analyzed for FA composition were randomly selected for

207 compound-specific isotopic analysis. The utilization of GC (Thermo Fisher Scientific GC

208 ISOLINK TRACE ULTRA) allowed the separation of FAME using the same apolar phase (Agilent

209 DB5) and the same analytical program as for GC-FID analysis (see above). Each of the FA was

210 converted into CO<sub>2</sub> by combustion in the ISOLINK furnace and transferred to the CONFLO IV 211 interface and then introduced to the IRMS (Delta V Plus; Thermo Fisher Scientific). As above, 212 FAME were identified by comparison of their retention time with those of commercial 213 standards and in-house standard mixtures as described above. 18:1n-9 and 18:3n-3 did 214 coelute on the apolar column used in GC-C-IRMS analysis, and were therefore analyzed 215 simultaneously. Fatty acids kept for  $\delta^{13}$ C analyses were selected based on their abundance 216 and detection in CSIA (i.e., with amplitudes > 800 mV). Calibration of  $\delta^{13}C$  values 217 218 The  $\delta^{13}$ C values were calibrated using the F8-3 standard mixture of eight acid ethyl and methyl esters (14:0, 16:0, 18:0, and 20:0, with  $\delta^{13}$ C values ranging from -26.98±0.02‰ to -219 220 30.38±0.02‰) supplied by Indiana University Stable Isotope Reference Materials, inserted 221 before and after every 3 analytical replicates of each sample. 222 Correction of the  $\delta^{13}$ C contribution of the carbon added by trans-esterification 223 Because of the addition of a methyl group derived from the methanol used in the 224 transesterification reaction,  $\delta^{13}$ C of FAME analyzed here differed from the original  $\delta^{13}$ C of FA 225 present in source material. To correct the contribution of the carbon from this additional 226 methyl group, several free FA (14:0, 16:0, 16:1n-7, 17:0, 18:0, 18:1n-9, 18:2n-6, 18:3n-3, 227 18:3n-6, 20:0, 20:4n-6, 20:5n-3, 22:0, 23:0, and 24:0; Sigma), were trans-esterified with the 228 same methanol as the one used for samples. Prior to trans-esterification, the  $\delta^{13}$ C values of 229 each of those free FA were determined by using continuous flow on a Flash EA2000 230 elemental analyzer coupled to a Delta V Plus mass spectrometer (Thermo Fisher scientific). After trans-esterification of free FA, the  $\delta^{13}$ C values of the resulting FAME were measured 231 232 using the GC-C-IRMS system. Then, an average correction was calculated using the following

| 233  | equation: $\delta^{13}C$ Methanol = $-n * \delta^{13}C_{FA} + (n + 1) * \delta^{13}C_{FAME}$ , where n is the number of   |
|--|---|
| 234  | carbon atoms in the free FA (Abrajano et al. 1994). The average $\delta^{13}$ C value (-39.6‰) was  |
| 235  | calculated for the methyl-derived carbon based on the difference between the $\delta^{13}\text{C}$ values of  |
| 236  | the corresponding free FA and their respective FAME and this value was used to correct the  |
| 237  | FAME $\delta^{13}$ C by rearranging the above equation. Further studies found no kinetic isotope  |
| 238  | effect associated to trans-esterification (Budge et al. 2008; Graham et al. 2014), thus this  |
| 239  | aspect was not considered for $\delta^{13}$ C analysis.   |
| 240  | Analytical error  |
| 241  | The analytical error (consisting of the SD of 10 analyses of the C16:0 FA laboratory standard   |
| 242  | interspersed during the samples run) was 0.2 ‰. Therefore the analytical precision was  |
| 243  | estimated to be $\leq 0.2\%$ .  |
|  |   |
| 244  | Statistical Analysis  |
| 244<br>245   | Statistical Analysis<br>Normality (Shapiro-Wilks test) and homoscedasticity (Bartlett-test) were tested prior to  |
| 244<br>245<br>246  | <i>Statistical Analysis</i><br>Normality (Shapiro-Wilks test) and homoscedasticity (Bartlett-test) were tested prior to<br>parametric or non-parametric tests. Parametric tests were applied when conditions of   |
| 244<br>245<br>246<br>247   | Statistical Analysis<br>Normality (Shapiro-Wilks test) and homoscedasticity (Bartlett-test) were tested prior to<br>parametric or non-parametric tests. Parametric tests were applied when conditions of<br>normally distributed data and homoscedasticity were satisfied, otherwise non-parametric   |
| 244<br>245<br>246<br>247<br>248                                    | Statistical Analysis<br>Normality (Shapiro-Wilks test) and homoscedasticity (Bartlett-test) were tested prior to<br>parametric or non-parametric tests. Parametric tests were applied when conditions of<br>normally distributed data and homoscedasticity were satisfied, otherwise non-parametric<br>tests with Bonferroni's adjustment method were performed. The isotopic variation in bivalve  |
| 244<br>245<br>246<br>247<br>248<br>249                             | Statistical Analysis<br>Normality (Shapiro-Wilks test) and homoscedasticity (Bartlett-test) were tested prior to<br>parametric or non-parametric tests. Parametric tests were applied when conditions of<br>normally distributed data and homoscedasticity were satisfied, otherwise non-parametric<br>tests with Bonferroni's adjustment method were performed. The isotopic variation in bivalve<br>muscles was compared among stations by Kruskal-Wallis (KW) tests followed by Conover-   |
| 244<br>245<br>246<br>247<br>248<br>249<br>250                      | Statistical Analysis Normality (Shapiro-Wilks test) and homoscedasticity (Bartlett-test) were tested prior to parametric or non-parametric tests. Parametric tests were applied when conditions of normally distributed data and homoscedasticity were satisfied, otherwise non-parametric tests with Bonferroni's adjustment method were performed. The isotopic variation in bivalve muscles was compared among stations by Kruskal-Wallis (KW) tests followed by Conover- Iman multiple comparisons. Only the FA >0.5% of total FA were considered to compare the  |
| 244<br>245<br>246<br>247<br>248<br>249<br>250<br>251               | Statistical Analysis Normality (Shapiro-Wilks test) and homoscedasticity (Bartlett-test) were tested prior to parametric or non-parametric tests. Parametric tests were applied when conditions of normally distributed data and homoscedasticity were satisfied, otherwise non-parametric tests with Bonferroni's adjustment method were performed. The isotopic variation in bivalve muscles was compared among stations by Kruskal-Wallis (KW) tests followed by Conover- Iman multiple comparisons. Only the FA >0.5% of total FA were considered to compare the dissimilarity among stations, by a permutational variance analyses (PERMANOVA).  |
| 244<br>245<br>246<br>247<br>248<br>249<br>250<br>251<br>252        | Statistical Analysis Normality (Shapiro-Wilks test) and homoscedasticity (Bartlett-test) were tested prior to parametric or non-parametric tests. Parametric tests were applied when conditions of normally distributed data and homoscedasticity were satisfied, otherwise non-parametric tests with Bonferroni's adjustment method were performed. The isotopic variation in bivalve muscles was compared among stations by Kruskal-Wallis (KW) tests followed by Conover- Iman multiple comparisons. Only the FA >0.5% of total FA were considered to compare the dissimilarity among stations, by a permutational variance analyses (PERMANOVA). Subsequently, a test of similarity percentages analyses (SIMPER) was carried out to assess   |
| 244<br>245<br>246<br>247<br>248<br>249<br>250<br>251<br>252<br>253 | Statistical Analysis Normality (Shapiro-Wilks test) and homoscedasticity (Bartlett-test) were tested prior to parametric or non-parametric tests. Parametric tests were applied when conditions of normally distributed data and homoscedasticity were satisfied, otherwise non-parametric tests with Bonferroni's adjustment method were performed. The isotopic variation in bivalve muscles was compared among stations by Kruskal-Wallis (KW) tests followed by Conover- Iman multiple comparisons. Only the FA >0.5% of total FA were considered to compare the dissimilarity among stations, by a permutational variance analyses (PERMANOVA). Subsequently, a test of similarity percentages analyses (SIMPER) was carried out to assess the most discriminant FA responsible of the difference among stations (>80%). Each FA |

- 255 permitting its detection in CSIA in all DG samples, was accounted. For that, one-way analysis
- of variance (ANOVA) followed by Tukey's HSD, or KW tests followed by Conover-Iman
- 257 multiple comparison were carried out to compare the difference of their percentage of
- 258 neutral lipids, and their respective  $\delta^{13}$ C values, between the individuals from the three
- 259 stations. All statistical analyses and graphics were performed with the free software R (Core
- 260 Team 2017), with R Version 3.4.1 (2017 06 30).

262 Results

#### 263 Stable isotopes analyses

No significant differences in bulk  $\delta^{13}$ C values were observed in bivalve muscles between the 264 different stations (KW test, H25 = 2.12, P = 0.35). In contrast, a significant  $\delta^{15}$ N difference 265 266 was observed (KW test, H25 = 17.71, P < 0.001) (Fig. 2). Individuals from stations 1 and 2 displayed similar  $\delta^{15}N$  (8.3‰ and 8.5‰, respectively) (Fig. 2), while station 3 was  $^{15}N$ 267 268 depleted (7.2‰). For logistical reasons, only two replicates of POM and SOM could be 269 sampled per site, which could not allow to statistically compare the results for these 270 potential food sources. The pattern observed in POM was the same as observed for bivalve muscles with stations 1 and 2 being <sup>15</sup>N enriched compared to station 3 (from 6.5‰ and 271 272 6.9‰ for stations 1 and 2 respectively, to 4‰ at station 3) (Fig. 2). The POM  $\delta^{13}$ C value 273 sampled outside the lagoon (-22.8‰) was slightly lower than at stations 2 and 3 (-21.1‰ 274 and -20.9‰, respectively). SOM displayed quite a different spatial pattern than the one observed for POM, with station 1 being <sup>15</sup>N enriched and <sup>13</sup>C depleted ( $\delta^{15}N = 7.3\%$ ,  $\delta^{13}C = -$ 275 14.5‰) compared to the two inner stations 2 and 3 ( $\delta^{15}N = 5.2\%$  and 4.6‰,  $\delta^{13}C = -10.2\%$ 276 277 and -13‰, respectively). Both samples of Zostera marina were <sup>13</sup>C enriched (-10.0‰ for 278 fresh eelgrass and -11.2‰ for detrital eelgrass) compared to other samples. Fresh eelgrass 279 displayed higher  $\delta^{15}$ N than detrital eelgrass (5.6‰ and 1.8‰, respectively) (Fig. 2).

280

#### 281 Fatty acids composition

The FA composition of neutral lipids of DG varied significantly among stations (PERMANOVA, F = 48.76, P < 0.001). Individuals from stations 1 and 2, the closest to the mouth of the bay, were characterized by higher contents of 14:0, 20:4n-6, and the diatom biomarkers 16:1n-7 and 20:5n-3 than individuals from station 3 (ANOVA or KW tests followed by post-hoc; Table

| 286 | 1). The PUFA 22:6n-3 was slightly more abundant in individuals from station 1 (12.1%) than   |
|-----|--|
| 287 | in those from station 2 (11.4%) and station 3 (10.5%) (Table 1). The DG of individuals from  |
| 288 | the most inner station in the lagoon (station 3) had significantly higher contents of C18-FA |
| 289 | (18:0, 18:1n-9, 18:3n-3, and 18:4n-3) and C16-FA (ANOVA or KW tests followed by post-hoc;    |
| 290 | Table1).   |
| 291 | Some FA in POM samples presented the same spatial variations than in bivalve DG, in          |
| 292 | particular 16:1n-7 that presented higher proportions at the external station (Table 2), and  |
| 293 | 18:4n-3 that showed higher values at the inner station (Table 2). When compared to bivalve   |
| 294 | DG, the PUFA 18:4n-3 and 20:5n-3 in POM were similar along the sampled transect (Table 2),   |
| 295 | and the 18:1n-9 content was lower at station 2 and 3 (3% and 2.8%, respectively) compared    |
| 296 | to station 1 (5.2%) (Table 2).   |
|     |  |

- 297
- 298 Compound-specific isotopic analyses

299 The  $\delta^{13}$ C values of almost all selected FA of bivalve DG differed significantly among 300 stations (ANOVA or KW tests followed by post-hoc; Table 1), with station 3 being different 301 from stations 1 and 2, except for 20:4n-6, 20:5n-3 and 18:1n-7 (Table 1, Fig. 3). The 302 differences among stations were significant for most FA, however, the range of variation did 303 not exceed 1‰ for some FA, such as 16:1n-7 (from -27‰ at the external station, to -25.9‰ 304 at the inner station; Table 1), and 20:5n-3 at station 2 (-26.9‰) differed significantly from 305 station 3 (-27.6‰; Table 1) (Fig. 3). The variability of  $\delta^{13}$ C values of 18:1n-9+18:3n-3 was 306 1.9‰ (Fig. 3), ranging from -29.7‰ (station 1) to -29.1‰ (station 2), and finally to -31.0‰ 307 (station 3; Table 1). Because these FA coeluted on the apolar column used for GC-C-IRMS 308 analysis, they were reported jointly. The  $\delta^{13}$ C values of 18:4n-3 displayed the highest range 309 of variability (2.3‰) (Fig. 3), ranging from -29.2‰ at stations 1 and 2 to -31.5‰ at station 3

310 (Table 1). Finally, 22:6n-3 varied in its  $\delta^{13}$ C values among the stations (1.8‰; Fig. 3) with 311 higher  $\delta^{13}$ C values at the external stations 1 and 2 (-26.1‰ and -26.9‰, respectively) 312 compared to lower  $\delta^{13}$ C values at the inner station 3 (-27.5‰) (Table 1). For C18 FA (18:1n-9, 313 18:3n-3, 18:4n-3) and 22:6n-3 of bivalve DG, samples from station 3 were always more 314 depleted in <sup>13</sup>C compared to other stations (Table 1 and Fig. 3). 315 Similar trends in isotopic variability of FA were found in POM samples than in bivalve DG, 316 with 18C and 22:6n-3 always more depleted in <sup>13</sup>C with increasing distance from the mouth 317 of the lagoon (Table 2). For example, the  $\delta^{13}$ C values of 18:4n-3 were similar at station 1 (-318 31.6‰) and 2 (-31.4‰) and more depleted at station 3 (-32.3‰; Table 2), and the 22:6n-3 319 showed  $\delta^{13}$ C depleted values along the transect (from -25.6‰ and -27.5‰ at stations 1 and 320 2 to -34.9‰ at station 3; Table 2). Like in DG samples, both FA, 16:1n-7 and 20:5n-3 were  $^{13}$ C 321 enriched at the internal station (Table 2) in POM samples. Indeed, 16:1n-7 and 20:5n-3 322 showed respectively  $\delta^{13}$ C from -26.7‰ and -29.5‰ at the external station, to -25.8‰ and -323 28.7‰ at the station near to the mouth, and to -25.7‰ and -27.5‰ at the inner station 324 (Table 2).

326 Discussion

345

327 Results from this study suggest that organic matter from the ocean is transported into the 328 lagoon, contributing to the primary production and to the diet of benthic filter feeders. The 329 CSIA on FA data indicate that diatoms (indicated by 16:1n-7 and 20:5n-3) assimilated by 330 bivalves have a very similar marine origin throughout the lagoon, according to their 331 comparable  $\delta^{13}$ C values among stations. Moreover, results also demonstrate that a diversity 332 of heterotrophic flagellates, characterized by higher contents of 18 carbon FA, and 22:6n-3 may also enter the diet of bivalves. The variable  $\delta^{13}$ C values of these FA among stations 333 334 suggest that their origin varies according to the location within the lagoon, and depleted 335 values at the inner station indicate an influence of local processes in the diet of these 336 consumers. 337 The most striking result from bulk SI analysis of bivalve muscles and POM was the significant 338 <sup>15</sup>N enrichment observed near the entrance of the lagoon, with individuals from stations 1 and 2 displaying similar  $\delta^{15}$ N values that were higher than in the inner bay. This reveals an 339 oceanic influence, and particularly the contribution of <sup>15</sup>N oceanic inputs to the diet of 340

bivalves near the entrance of the lagoon, but also that such dietary influence of the ocean

did not extend to the innermost part of the lagoon. This oceanic influence may be explained

by active wind-driven seasonal upwelling occurring outside the lagoon from April to June

344 (Ibarra-Obando et al. 2001; Du et al. 2015). It has been suggested that water masses

346 Pacific coast of Baja California (Zaytsev 2003), promoting primary production and potentially

containing upwelled biological material could be transported into coastal lagoons of the

347 affecting their trophic functioning. The hypothesis that upwelled waters affect the diet of

bivalves inside the lagoon is based on the fact that during upwelling conditions, the biomass

of large phytoplankton increases (Taylor and Landry 2018), and as upwelled nitrate is rapidly

consumed by phytoplankton (O'Reilly et al. 2002), its  $\delta^{15}$ N increases. Although coastal 350 351 upwelling influence on the studied lagoon was not supported by chlorophyll *a* or 352 temperature data, such high  $\delta^{15}$ N with no changes in  $\delta^{13}$ C have been reported in various 353 systems under upwelling influence worldwide (O'Reilly et al. 2002; Hill and McQuaid 2008; 354 Reddin et al. 2015). 355 The spatial differences found in the FA composition of neutral lipids in the DG of bivalves 356 indicates a change in the proportion and possibly in the nature of food sources with 357 increasing distance from the mouth of the lagoon. The DG at the entrance of the lagoon 358 (stations 1 and 2) had higher 16:1n-7 and 20:5n-3 contents when compared to individuals 359 from the inner station (station 3), indicating a higher contribution of diatoms in their diet 360 (Parrish et al. 2000; Alfaro et al. 2006). A previous study revealed that during the late spring, 361 diatoms are the dominant phytoplankton taxa found in the Northern California current (Du 362 et al. 2015). The higher importance of diatoms in the diet of bivalves near the entrance of 363 the lagoon therefore supports the influence of oceanic primary production. Individuals from 364 the inner station had lower contents of these two FA, suggesting a dilution of oceanic inputs further into the lagoon. The importance of 22:6n-3 in DG of individuals at the external 365 366 station suggests that dinoflagellates also represent an important dietary contribution of 367 Spondylus crassisquama (Parrish et al. 2000). This contribution decreases slightly with 368 increasing distance from the mouth of the lagoon, being the lowest at the internal station, 369 suggesting a decreasing contribution of dinoflagellates to this station. However, the high 370 abundance of 18:4n-3, another dinoflagellate marker (Kharlamenko et al. 2001; Bachok et al. 371 2003; Nerot et al. 2015), at the inner station (station 3) suggests the opposite. Such 372 conflicting information by these two dinoflagellate markers may indicate different 373 assemblages being assimilated by bivalves in the lagoon, but such change in dietary

374 biomarkers does not necessarily suggest any shift in contribution of dinoflagellates to the 375 diets of these consumers. Bivalves from the inner bay were also characterized by higher C18-376 FA contents (18:1n-9, 18:3n-3). These FA can be characteristic of different dietary sources, 377 such as seagrass (Kharlamenko et al. 2001) or heterotrophic flagellates constituting microbial 378 food webs (Zhukova 1991). Although seagrass beds are known to be a source of dissolved 379 organic matter (DOM; Fenton and Ritz 1988), bivalve muscles were too <sup>13</sup>C depleted as 380 compared to seagrass  $\delta^{13}$ C to be in accordance with a significant trophic contribution of 381 Zostera marina. Consequently, the abundance of these FA likely reflects the contribution of 382 heterotrophic microorganisms (i.e. bacteria, ciliates, flagellates, dinoflagellates), relying on 383 locally produced DOM, to the diet of bivalves. This highlights a higher diversity of food 384 sources for bivalves at the internal station than for those submitted to oceanic influences 385 and shows that diet source variation within this and possibly other lagoons is based on 386 allochthonous and autochthonous contribution. Such various diet sources could also present 387 differences in terms of quality and quantity, which consequently impact bivalve stocks and 388 consequently fisheries. More detailed understanding of spatio-temporal dynamics of these 389 food resources would lead to a better management of bivalve stocks in the Ojo de Liebre 390 lagoon and elsewhere.

Inferring diet composition based on CSIA requires FA-specific fractionation coefficients, which are not available for our species, and would require extensive laboratory experiments (Ruess and Chamberlain 2010; Bec et al. 2011). Consequently, our approach did not aim to characterize the accuracy of food sources retention by bivalves, but to scrutinize the trophic spatial variability in an effort to provide evidence of a different spatial origin of the diets for this consumer (Ramos et al. 2003; Van den Meersche et al. 2004). Although no difference in bulk  $\delta^{13}$ C values was observed in muscles of individuals from the different stations, CSIA

398 detect the isotopic composition of FA that may indicate source-specific differences of FA 399 (Budge et al. 2008; Colombo et al. 2016). Some differences were observed in the range of 400 variation in FA  $\delta^{13}$ C along the transect depending on biomarkers considered (diatoms vs 401 heterotrophic flagellates). In DG neutral lipids, diatom biomarkers (16:1n-7 and 20:5n-3) 402 displayed the smallest range of variation among the three stations ( $\leq 1$ %), which is of little 403 ecological value. The spatial consistency in the  $\delta^{13}$ C values of these diatom biomarkers 404 suggests that diatoms assimilated by bivalves have all oceanic origin throughout the bay. 405 Therefore, it seems that phytoplankton of local origin (produced within the lagoon) is of 406 relatively little dietary importance for S. crassisquama. The C18-FA 18:1n-9 and 18:3n-3 were 407 both considered to reveal the contribution of microheterotrophs (flagellates, ciliates, see 408 above). Even if the three stations presented significant differences in their  $\delta^{13}$ C for 18:1n-9 409 and 18:3n-3, stations 1 and 2 displayed very similar  $\delta^{13}$ C values (only differed by 0.6‰), 410 while station 3 was depleted in <sup>13</sup>C by 1.9‰ compare to the other stations. This difference 411 suggests that the origin of these microheterotrophs differed within the lagoon. 412 Microheterotrophs are central elements of microbial food webs, feeding on bacteria and 413 other small unicellular organisms, and ultimately relying on DOM (Azam et al. 1983). The <sup>13</sup>C 414 depletion observed at the inner station suggests a local source of DOM, which is of primary 415 importance for bivalves in the lagoon. Although the lagoon of Ojo de Liebre hosts one of the 416 largest eelgrass bed of the Northern Pacific (Cabello-Pasini et al. 2003), a seagrass-derived 417 DOM seems unlikely because seagrass is usually <sup>13</sup>C enriched compared to other marine 418 primary producers (Hemminga and Mateo 1996), which was also observed in the present 419 study. The possible DOM release from the sediment is also not in agreement with  $\delta^{13}C$ 420 measured for these FA (around -24.5‰ in SOM). In fact, such <sup>13</sup>C-depleted values in coastal 421 environments are usually associated with red algae, which can be extremely low in  $\delta^{13}$ C

422 (Raven et al. 2002). Although no extensive population of such algae was observed during 423 sampling, it is possible that such populations exist in the inner bay, supplying a pool of 424 dissolved organic carbon that is subsequently trophically transferred to bivalves. 425 Dinoflagellate FA biomarkers (18:4n-3 and 22:6n-3) had a very similar spatial distribution 426 pattern as observed for biomarkers of other microheterotrophs (18:1n-9 and 18:3n-3), with 427 a marked <sup>13</sup>C depletion at the inner station. Therefore, in contrast to diatoms, dinoflagellates 428 entering the diet of bivalves do not seem to be of marine origin throughout the lagoon. The 429 similarity observed between the CSIA in microheterotrophs and dinoflagellates might 430 suggest that the same factors affect the SI composition of these two possible food sources. 431 In fact, although dinoflagellates are usually described as primary producers, heterotrophy is 432 a widespread pattern in this group (Jeong et al. 2010). Based on these results, it is possible 433 that dinoflagellates assimilated by *S. crassisquama* in the inner part of the lagoon may rely 434 on heterotrophy, emphasizing a potentially important role of the microbial food web in this 435 enclosed ecosystem.

436

#### 437 Conclusion

The use of CSIA provided a new scale of complexity in the diet of *Spondylus crassisquama* in the Ojo de Liebre lagoon. Although dietary diatoms retained in bivalves appeared to have the same oceanic origin throughout the lagoon, this study indicates that the heterotrophic component of bivalve diet varies spatially in the lagoon, highlighting an influence of local processes in the diet of these consumers. The combination of the three methods used here showed to be complementary, resulting in a more informative analysis of spatial feeding ecology of this and likely also other lagoons. The lower  $\delta^{13}$ C observed at the most inner

- station could not be explained in this study, although any potential role of seagrass in
- 446 providing DOM for the associated microbial food web could be discarded based on different
- 447 SI data. Further research is warranted to identify how the origin of basal resources vary and
- 448 support food webs in lagoons and to better understand the quantitative importance of
- dietary sources for bivalves.

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463

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- 470 **Compliance with Ethical Standards**
- 471 **Conflict of interest**

472 The authors declare that they have no conflict of interest.

## 473 Ethical approval

- 474 All applicable international, national and/or institutional guidelines for the care and use of
- 475 bivalves *Spondylus crassisquama* were followed. The individuals of *S. crassisquama* have
- 476 been sampled under the permit PRMN/DGOPA-011/2017, delivered by the Mexican
- 477 government.

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- 623

## 624 Table captions

| 625 | Table 1 – Neutral lipid fatty acid (FA) composition (mean ± SD; mass % of total FA; n = 10)                  |
|-----|--|
| 626 | and Compound Specific Isotopic analysis (CSIA) of neutral lipid FA (mean $\pm$ SD; $\delta^{13}$ C ‰; n = 5) |
| 627 | of Spondylus crassisquama digestive gland in June 2017, for the 3 stations (1, 2, and 3). Only               |
| 628 | the FA accounting for more than 80 % of dissimilarity between stations (SIMPER test) and                     |
| 629 | presenting the greatest abundance permitting their good detection in CSIA are shown.                         |
| 630 | Different letters indicate significant difference between the stations (ANOVA or KW tests                    |
| 631 | followed by multiple comparison tests, at the significant level $\alpha$ < 0.05). *In CSIA, 18:1n-9          |
| 632 | and 18:1n-3 are coeluted and $\delta^{13}\text{C}$ value is presented in the same line.                      |
| 633 |  |
| 634 | Table 2 – Total fatty acid (FA) composition (mean; mass % of total FA; n = 2) and Compound                   |
| 635 | Specific Isotopic analysis (CSIA) of FA (mean; $\delta^{13}$ C ‰; n = 2) of potential food sources, for the  |
| 636 | 3 stations (1, 2, and 3). Only the FA accounting for more than 80 % of dissimilarity between                 |
| 637 | stations (SIMPER test) and presenting the greatest abundance permitting their good                           |
| 638 | detection in CSIA are shown. NA: Not analyzed. *In CSIA, 18:1n-9 and 18:1n-3 are coeluted                    |
| 639 | and $\delta^{13}$ C value is presented in the same line.   |
| 640 |  |

641

## 642 Figure captions

Fig. 1 Location of the 3 sampling stations in the Ojo de Liebre lagoon (Baja California Sur,
Mexico). Station 1 is located at 3.5 km outside the bay. Station 2 and 3 are located inside the

lagoon, respectively at 6.1 km and 15.5 km from the mouth of the lagoon. (Map modifiedfrom Google earth).

647

| 648 | <b>Fig. 2</b> Stable Isotope (SI) bi-plot ( $\delta^{13}$ C and $\delta^{15}$ N, mean values ±SD when n > 2) of the adductor |
|-----|--|
| 649 | muscles of Spondylus crassisquama and of its potential food sources, in June 2017, at the 3                                  |
| 650 | sampled stations. Samples from station 1 are shown in dark blue, 2 in light blue, and 3 in                                   |
| 651 | green. Bivalves are represented by squares, POM by circles, SOM by triangles, and eelgrass                                   |
| 652 | by crosses (* fresh; x detrital).  |

653

654Fig. 3 Box plot of  $\delta^{13}$ C values (‰; n = 5) of some selected neutral lipid fatty acid (FA) of655Spondylus crassisquama digestive gland in June 2017 at each stations (1, 2, and 3). Only the656FA accounting for more than 80 % of dissimilarity between stations, presented the greatest657abundance permitting their good detection in CSIA, and present in all samples are shown.658Different letters indicate significant difference between the stations (ANOVA or KW tests659followed by multiple comparison tests, at the significant level α < 0.05). Samples from</td>660station 1 are shown in dark blue, 2 in light blue, and 3 in green.

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662

### Table 1

|          | Fatty Ac            | ids | (mass % of l | neut      | ral lipid FA) |   | Compound Specific Isotopic Analysis ( $\delta^{13}$ C ‰) |    |             |   |             |   |  |
|----------|---------------------|-----|--------------|-----------|---------------|---|--|----|-------------|---|-------------|---|--|
|          | Station 1 Station 2 |     |              | Station 3 |               |   | Station 1  |    | Station 2   |   | Station 3   |   |  |
| 14:0     | 5.8 ± 0.6           | A   | 6.1 ± 0.5    | A         | 4.2 ± 0.3     | В | -28.2 ± 0.2  | а  | -28.3 ± 0.2 | а | -29.7 ± 0.3 | b |  |
| 16:0     | 21.6 ±0.4           | В   | 21.9 ± 0.9   | В         | 23.9 ± 0.9    | A | -27.5 ± 0.3  | а  | -27.1 ± 0.1 | а | -29.9 ± 0.6 | b |  |
| 18:0     | 4.1 ± 0.5           | В   | 3.9 ± 0.4    | В         | 5.6 ± 0.5     | A | -26.8 ± 0.3  | а  | -26.4 ± 0.2 | а | -28.3 ± 0.4 | b |  |
| 16:1n-7  | 10.1 ± 0.8          | A   | 10.5 ± 0.8   | A         | 5.0 ± 0.2     | В | -27.0 ± 0.2  | b  | -26.6 ± 0.1 | b | -25.9 ± 0.4 | а |  |
| 18:1n-7  | 2.8 ± 0.1           |     | 2.8 ± 0.2    |           | 2.8 ± 0.1     |   | -27.5 ± 0.5  |    | -27.2 ± 0.6 |   | -27.8 ± 0.4 |   |  |
| 18:1n-9* | 3.4 ± 0.1           | В   | 3.3 ± 0.3    | В         | 4.8 ± 0.4     | A | -29.7 ± 0.3  | а  | -29.1 ± 0.2 | b | -31.0 ± 0.2 | с |  |
| 18:3n-3* | $3.4 \pm 0.1$       | В   | 3.3 ± 0.1    | В         | 5.3 ± 0.2     | A |  |    |             |   |             |   |  |
| 18:4n-3  | 5.1 ± 0.4           | В   | 5.4 ± 0.5    | В         | 6.6 ± 0.4     | A | -29.2 ± 0.9  | а  | -29.2 ± 0.6 | а | -31.5 ± 1.1 | b |  |
| 20:4n-6  | 1.7 ± 0.1           | A   | 1.6 ± 0.1    | A         | $1.0 \pm 0.1$ | В | -26.7 ± 0.4  |    | -26.8 ± 0.6 |   | -26.3 ± 1.5 |   |  |
| 20:5n-3  | 12.0 ± 0.3          | A   | 11.4 ± 0.8   | A         | 8.6 ± 1.2     | В | -27.1 ± 0.3  | ab | -26.9 ± 0.4 | а | -27.6 ± 0.5 | b |  |
| 22:6n-3  | 12.1 ± 1.0          | A   | 11.4 ± 0.8   | AB        | 10.5 ± 0.9    | В | -26.1 ± 0.2  | а  | -25.7 ± 0.4 | а | -27.5 ± 0.8 | b |  |

## Table 2

| Fatty Acids (mass% of total lipid FA) |
|---------------------------------------|
|---------------------------------------|

Compound Specific Isotopic Analysis ( $\delta^{13}$ C ‰)

|          | POM          |              |              | POM SOM      |              |              | Eel   | Eelgrass POM |              |              |              | SOM          | Eelgrass     |              |       |          |
|----------|--------------|--------------|--------------|--------------|--------------|--------------|-------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|-------|----------|
|          | Station<br>1 | Station<br>2 | Station<br>3 | Station<br>1 | Station<br>2 | Station<br>3 | Fresh | Detrital     | Station<br>1 | Station<br>2 | Station<br>3 | Station<br>1 | Station<br>2 | Station<br>3 | Fresh | Detrital |
| 14:0     | 9.7          | 11.4         | 7.2          | 2.6          | 3.8          | 3.2          | 0.8   | 1.9          | -26.7        | -25.9        | -27.7        | NA           | NA           | NA           | -18.9 | -26.4    |
| 16:0     | 21.3         | 25.0         | 26.0         | 16.3         | 22.2         | 20.6         | 21.8  | 25.6         | -30.5        | -31.1        | -34.5        | -27.2        | -23.6        | -23.3        | -17.5 | -22.3    |
| 18:0     | 6.4          | 6.1          | 4.5          | 6.4          | 6.1          | 6.3          | 1.9   | 2.6          | -29.0        | -29.8        | -30.8        | -30.1        | -27.7        | -26.6        | -16.4 | -25.3    |
| 16:1n-7  | 6.1          | 5.4          | 5.1          | 7.3          | 12.0         | 8.3          | 0.4   | 1.0          | -26.7        | -25.8        | -25.7        | -23.5        | -23.4        | -22.2        | -15.8 | -17.2    |
| 18:1n-7  | 3.1          | 2.6          | 3.0          | 6.7          | 3.9          | 5.2          | 0.4   | 1.4          | -23.5        | -23.1        | -20.9        | -21.1        | -20.1        | -19.4        | NA    | NA       |
| 18:1n-9* | 5.2          | 3.0          | 2.8          | 4.1          | 3.0          | 4.3          | 1.4   | 1.9          | 20.4         | 20.0         | 20.0         | 25.0         | 24.0         | 24 5         |       |          |
| 18:3n-3* | 2.2          | 2.5          | 3.3          | 1.8          | 0.9          | 1.2          | 38.3  | 29.7         | -28.4        | -29.9        | -30.8        | -25.8        | -24.0        | -24.5        | NA    | NA       |
| 18:4n-3  | 3.6          | 3.8          | 3.9          | 0.9          | 1.3          | 1.5          | 0.1   | 0.3          | -31.6        | -31.4        | -32.3        | NA           | NA           | NA           | NA    | NA       |
| 20:4n-6  | 0.2          | 0.1          | 0.1          | 0.4          | 0.2          | 0.2          | 0.1   | 0.5          | NA           | NA           | NA           | -26.0        | -23.2        | -23.3        | NA    | NA       |
| 20:5n-3  | 5.5          | 5.3          | 5.3          | 7.4          | 7.2          | 8.8          | 0.2   | 1.5          | -29.5        | -28.7        | -27.5        | -25.4        | -21.2        | -22.8        | NA    | NA       |
| 22:6n-3  | 7.9          | 7.1          | 4.3          | 5.8          | 2.7          | 3.4          | 0.3   | 0.7          | -25.6        | -27.5        | -34.9        | -25.1        | -21.7        | -24.4        | NA    | NA       |

1 Fig. 1



## 4 Fig. 2



## 6

8 Fig. 3

