Influence of aquaculture waste on fatty acid profiles and gonad maturation of wild fish aggregations at fish farms

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1	Influence of aquaculture waste on fatty acid profiles and gonad
2	maturation of wild fish aggregations at fish farms.
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18	

19 ABSTRACT

20 Wild fish belonging to four species belonging to different trophic groups were captured at 21 three distances from fish farm facilities: long distance (>5 Km), medium distance (1.5 Km) and 22 close to sea-cages. Flesh, brain, liver and gonads were sampled for fatty acid analysis. Fish 23 aggregated near sea-cages showed accumulation of fatty acids of vegetable origin in the 24 studied tissues, due to surplus feed consumption or via predation of fish that consumed the 25 feed. Gonads accumulated vegetable fatty acids in different manner in the different species, 26 and the species least and most influenced by fish-feeds were selected for gonad histological 27 examination. Results showed an acceleration of the final stages of the oocyte development in 28 fish aggregated near fish farms compared to fish captured at long distance. Differences in 29 oocyte development were more acute in the species which incorporated higher quantities of 30 vegetable fatty acids.

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33 **Keywords**: Fatty acids, trophic transfer, aquaculture, fish, vegetable oils, oocyte development.

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36 1. Introduction

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The global aquaculture industry has been growing in importance during the last 38 39 decades, reaching a production of 80 million tonnes of edible fish in 2016 (FAO 2018). The consumption of fish have increased worldwide due to general raising awareness and 40 knowledge about the healthy properties of fish and shellfish consumption, mainly due to 41 42 their high content in n-3 long-chain polyunsaturated fatty acids (Simopoulos 1999; 43 Nichols et al. 2010; Tur et al. 2012; Calder 2014; Shahidi and Ambigaipalan 2018). As industry has grown, so too has concern regarding environmental impact, particularly 44 due to the input of high amounts of organic matter in form of lost pellets and faeces into 45 the marine environment. This fact could alter the physicochemical properties of water 46 column and bottom sediments, increasing risk of anoxia due to bacterial activities and 47 thus affecting the local fauna (La Rosa et al. 2001; Maldonado et al. 2005; Sanz-Lázaro 48 and Marín 2011; Fernandez-Gonzalez et al. 2013). At the same time, sea-cage fish 49 farms act as FADs (Fish Aggregation Devices), attracting a large number of different 50 wild fish and macroinvertebrate species which take advantage of the protection 51 52 provided by the submerged structure, as well as by the supply of large quantities of high energy exceed feed and faeces (Sara et al. 2004; Dempster et al. 2009; Sanchez-Jerez et 53 54 al. 2011; Black et al. 2012). Aggregated wild fish can consume up to 80 % of fish-feed in form of lost pellets (Vita et al. 2004), contributing to minimise the environmental 55 56 effect of the discharge of organic matter on the seabed (Katz et al. 2002; Felsing et al. 2005; Fernandez-Jover et al. 2008; Ballester-Moltó et al. 2017). Feeds in aquaculture 57 58 are currently rich in vegetable oils of different origin and lipid composition, characterized to a large extent by the presence of high levels of short/medium-chain 59 60 polyunsaturated fatty acids (PUFA), as linoleic acid (18:2n-6, LA) and α-linolenic acid 61 (18:3n-3, LNA), besides monounsaturated fatty acids (MUFA) like oleic acid (18:1n-9, OA) and saturated fatty acids (SFA) (Watanabe 2002; White et al. 2019). The fatty acid 62 profile of commercial feeds, rich in n-6 short-chain PUFA, are different from the fatty 63 acid profiles of the natural diets of wild fish, rich in long-chain PUFA mainly 64 corresponding to the n-3 series. It is well known that changes in the n-3/n-6 ratio could 65 lead to alterations of the fish immune system, as well as on reproduction and larvae 66 development (Izquierdo et al. 2001; Simopoulos 2002; Tocher 2003; Kiron 2012; 67 Calder 2013). The amount of n-3 fatty acids, especially eicosapentaenoic acid (20:5n-3, 68 EPA) and docosahexaenoic acid (22:6n-3, DHA) in flesh tend to be lower in farmed fish 69

when compared to their wild counterparts (Sprague et al. 2016). Therefore, it is 70 necessary to control the composition of the artificial diets along the life cycle of 71 cultured fish, in order to obtain enough quantities of DHA and EPA for human 72 consumption via farmed fish. A good example would be the use of finishing diets rich 73 74 in n-3 fatty acids before sale, resulting in a final product as similar as possible to a wild fish in terms of flesh fatty acid composition (Henriques et al. 2014; Nichols et al. 2014). 75 76 Unfortunately, it is not possible to exercise that kind of control on aggregated wild fish. They can intake fish-feed rich in n-6 fatty acids of vegetable origin during an 77 indeterminate period of time, and thus modifying the fatty acid profiles of different 78 tissues in a different extent. The egg quality is highly influenced by the dietary lipids, 79 which could be the main factors determining a successful reproduction and survival of 80 the progeny in reared fish (Almansa et al. 1999; Izquierdo et al. 2001). DHA, EPA and 81 82 arachidonic acid (20:4n-6, ARA) are essential fatty acids for marine fish (Sargent et al. 1999) as they cannot synthesize them from their precursors, LNA and LA. Essential 83 84 fatty acids are required for the production of vitellogenin, which will be stored in the oocyte in the form of vitello as the only source of nutrients for the embryo (Alvarez-85 86 Lajonchère 2006). Wild fish consume the lost pellets for as long as they remain close to the sea-cages, accumulating fatty acids of vegetable origin with the consequent 87 reduction on the percentages of the essential fatty acids ARA, EPA or DHA, which 88 could have an effect on the oocyte development, and this fact may be investigated. The 89 90 accumulation of fatty acids of vegetable origin may be species-specific, depending on their feeding preferences. Previous works have shown that the uptake of aquaculture 91 wastes by wild fish may be reduced with increasing distance to the fish farms, measured 92 by fatty acid analysis and body condition (Arechavala-Lopez et al. 2011; Dempster et 93 al. 2011; Izquierdo-Gomez et al. 2015; Woodcock et al. 2018;). Nevertheless, the 94 95 accumulation of fatty acids of vegetable origin used to be only analysed in flesh, due to its importance for human nutrition, whereas less attention has been paid to the impact 96 97 on other tissues with a more relevant role in the fish physiology.

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99 The aim of this research was to check the possible effect on different tissues (flesh, 100 brain, liver and gonads) of commercial feed consumption in form of lost pellets by sea-101 cage aggregated wild fish. Four fish species of commercial interest, known to be 102 aggregated near sea-cages, and presenting different feeding behaviour (which may 103 differ in the amount of aquaculture wastes consumed) were captured in the vicinity of

104 fish farms. Their fatty acid profiles were compared to both, control fish captured off-105 shore at long distance from the farm, and specimens captured at an intermediate 106 distance to the fish farm facilities. Histological examination of the gonads of two 107 species was also carried out in order to check for differences in oocyte development 108 between groups. The obtained results complement those previously published on muscle 109 by the authors (Izquierdo-Gomez et al. 2015).

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111 **2. Material and methods**

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113 2.1 Characteristics of the studied species

Because the difficulties of wild fish sampling, just four species were captured in enough 114 number in the different distances studied in this work. The captured species belonged to 115 different trophic niches, and they were red mullet (Mullus barbatus Linnaeus 1758, 116 zoobenthic predator), which inhabit the benthic environment, consuming mainly 117 polychaetes, decapods and small crustaceans (Machias and Labropoulou 2002); round 118 sardinella (Sardinella aurita Valenciennes 1847, zooplanktivorous), which inhabit the 119 120 pelagic environment and predating mainly copepods and cladocerans (Morote et al. 2008); false scad (Caranx rhonchus Geoffroy Saint-Hilaire 1817, mesopredator), which 121 122 also inhabit the pelagic environment and predating mainly teleosts, crustaceans, molluscs and annelids (Sley et al. 2008); and bluefish (Pomatomus saltatrix Linnaeus 123 124 1766, piscivorous), which represents the highest trophic level of this study, teleost being the main prey but also polychaetes, crustaceans and gastropods (Harding and Mann 125 126 2001).

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128 2.2 Experimental design

129 Specimens of *M. barbatus* were sampled from April to September 2011, and *S. aurita*, C. rhonchus and P. saltatrix specimens were sampled from September to December 130 2011. Two types of commercial feeds used at the aquaculture facilities were also 131 sampled as well as a sample of fish faeces. The four fish species were divided into three 132 categories, according to increasing distances to the fish farms: group "farm" or F, 133 composed of fish captured in the vicinity of two fish farms sited in the Bay of Santa 134 Pola (Fig. 1), Alicante (South-east of Spain); group "medium distance" or MD, 135 composed of fish captured by artisanal fisheries at a minimum distance of 1.5 km from 136

the fish farms; and group "long distance" or LD, composed of fish captured off-shore bytrawlers at a minimum distance of 5 km from the fish farms.



Figure 1. Location of the studied farms in Guardamar, Santa Pola Bay, south-east coast
of Spain, in the Western Mediterranean Sea.

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151 **2.3 Sample collection**

The minimum number of captured specimens by treatment was eight for each species. 152 All samples were kept on ice until delivery to the laboratory. Fish total weight and 153 154 length (body length from the snout to the place where the main ray of the tail comes out of the body) were recorded and condition factor (CF) was calculated as CF = (weight 155 156 length-3) \times 100. Liver and gonad weights were measured to obtain the hepatosomatic and gonadosomatic indices (ratio of fish liver or gonad weight to body weight) (Table 157 1). Flesh samples taken from the anterior-dorsal white muscle portion, liver and brain 158 were sampled for fatty acid analysis. Gonad samples were divided in two portions, one 159 ovary for fatty acid analyses and the other for histological examination. Three replicates 160 of each feed were obtained for fatty acid analysis, while just one pool of faeces could be 161 162 analysed because of the difficulty involved in obtaining a big enough sample. Samples for fatty acid determination were frozen at -80 °C until analyses. 163

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165 2.4 Fatty acid analyses

Fatty acids were extracted from 0.3-1.0 g tissue samples by homogenization in 20 ml of
chloroform/methanol (2:1 v/v) in an Ultra Turrax tissue disrupter (IKA ULTRATURRAX T 25 digital, IKA-WERKE). The total lipids were prepared according to the

method of Folch et al. (1957) and non-lipid impurities were removed by washing with 169 170 0.88 % (w/v) KCl. The weight of lipids was determined gravimetrically after evaporation of the solvent and overnight desiccation in vacuum. Fatty acid methyl esters 171 (FAME) were prepared by acid-catalysed transesterification of total lipids according to 172 the method of Christie (2003), and the total lipid samples were transmethylated 173 174 overnight in 2 ml of 1 % sulphuric acid in methanol (plus 1 ml of toluene to dissolve 175 neutral lipids) at 50 °C. The methyl esters were extracted twice in 5 ml hexane-diethyl ether (1:1, v/v) after neutralization with 2 ml of 2 % KHCO₃, dried under nitrogen and 176 redissolved in 0.1 ml of iso-hexane. Methyl esters were purified by TLC (thin layer 177 chromatography) using iso-hexane:diethyl-ether:acetic acid (90:10:1 v/v/v). FAME 178 were separated and quantified by gas-liquid chromatography using an SP^{TM} 2560 179 flexible fused silica capillary column (100 m long, internal diameter of 0.25 mm and 180 181 film thickness of 0.20 mm; SUPELCO) in a Hewlett-Packard 5890 gas chromatograph. The oven temperature of the gas chromatograph was programmed for 5 min at an initial 182 temperature of 140 °C, and increased at a rate of 3 °C/min to 230 °C, further increased at 183 a rate of 2 °C/min to 240 °C and then held at that temperature for 12 min. The injector 184 185 and flame ionization detector were set at 260 °C. Helium was used as carrier gas at a pressure of 300 kPa, and peaks were identified by comparing their retention times with 186 187 appropriate FAME standards purchased from the Sigma Chemical Company (St Louis, MO, USA). Individual fatty acid concentrations were expressed as percentages of the 188 189 total content.

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191 **2.5 Gonad histology**

M. barbatus and S. aurita (6 and 7 replicates respectively) female specimens from 192 193 treatments F and LD were selected for gonad histology examination, due to the 194 availability of individuals captured at the same time in both, around the sea-cages (group farm) and at long distance from fish farms (group long distance, control), in 195 order to avoid differences in gonad maturation by season. M. barbatus specimens were 196 captured on 30th March and S. aurita specimens were captured between 7th and 14th 197 198 October. Gonad samples were processed histologically for the estimation of the 199 oogenesis. Samples from the anterior, central and posterior part of the ovary were fixed in 4 % (v/v) buffered formaldehyde for 24 h. Afterwards, the tissue samples were 200 washed in phosphate buffer and kept in 70 % ethanol. Fixed pieces were processed in an 201 automatic tissue processor (MYR, Spain), and embedded in paraffin wax. For 202

histological and morphometrical study, dewaxed serial sections (5µm) were rehydrated,
routinely stained with haematoxylin-eosin. Samples were analysed in the "Servicio de
Análisis de Imagen, University of Murcia" using appropriate equipment for
stereological analysis.

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208 2.6 Stereological analysis

209 Stereological analysis was performed using Visiopharm NewCAST Stereology software, an Olympus BX61 microscope, and a Pixelink (1.9 Mpx) digital camera. Six 210 different fields were randomly selected from each histological slide. Oocyte sizes were 211 determined by the superposition of two dotted grid of different size, and by counting the 212 number of marks in each cell category (Oogonia, oocyte in nucleolus stage, oocyte in 213 transition stage, oocyte in perinuclear stage, oocyte in early vitellogenesis stage, oocyte 214 215 in late vitellogenesis stage and mature oocyte). Cell volume was determined by the use of nucleators, by pointing the centre of the nucleus and estimating oocyte area by the 216 217 intersection of six random lines which crosses the oocyte membrane (Bucholtz et al. 2013). 218

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220 2.7 Statistical analysis

221 The results are expressed as mean \pm standard error. Individual fatty acids data were statistically analysed by two-way analysis of variance (ANOVA) to determine 222 223 differences between distance treatments. Multidimensional scaling (MDS), SIMPER (similarity percentages) procedure (Warwick et al. 1990; Clarke 1993) and a 224 permutation test (PERMANOVA) (Clarke 1993; Anderson 2004) comprising 4999 225 permutations were carried out to assess the significance of the overall fatty acid 226 composition among distance treatments for each sampled tissue. SIMPER analyses were 227 228 performed using the Bray-Curtis dissimilarity index (Bray and Curtis 1957). Statistical analyses were conducted using SPSS Statistical Software System version 15.0 (SPSS 229 Inc., Chicago, IL) and Primer (Plymouth Routines In Multivariate Ecological Research; 230 v.6.1.13) and its complementary statistical package PERMANOVA+ (v.1.0.3). As fatty 231 acid data were percentages, they were transformed with arcosen (x + 1), and all 232 statistical tests were performed with a significance level of $\alpha = 0.05$. 233

234

236 **3. Results**

237

238 **3.1 Body condition**

All fish specimens from the three distance treatments were adult fish, with no apparent signs of disease or infestation by parasites. Most of the specimens were female. There were some differences in size and weight, hepatosomatic index and the condition factor between distance treatments (Table 1). Even though all specimens were adults, we could not differentiate them by age, and a link between age and the significances found for weight, length, HSI and body condition cannot be discarded.

- 245
- 246 Table 1. Body condition and number of replicates. Significant differences among distance
- treatments are shown in bold and italic. Results are expressed as mean \pm S.E. HSI:
- 248 Hepatosomatic index; GSI: Gonadosomatic index; CF: Condition factor. The number of

249 replicates is shown differentiating between females and males.

	S. aurita	P. saltatrix	C. rhonchus	M. barbatus
Standard Length				
A	23.17 ± 0.81 ab	46.44 ± 2.03 a	28.44 ± 0.42 a	15.82 ± 0.43 a
В	21.14 ± 0.54 a	33.88 ± 2.55 b	27.38 ± 1.54 ab	14.67 ± 0.34 a
С	23.31 ± 0.41 b	29.83 ± 1.66 b	23.67 ± 0.26 b	13.12 ± 0.38 b
Weight				
		1,437.88 ± 178.32		
А	196.30 ± 17.26 a	a	397.38 ± 14.42 a	75.26 ± 5.60 a
В	137.10 ± 11.26 b	688.42 ± 111.64 b	378.77 ± 63.78 ab	60.00 ± 4.07 ab
С	165.57 ± 7.79 ab	419.22 ± 94.82 b	209.05 ± 5.78 b	45.32 ± 4.90 b
HSI				
A	0.62 ± 0.08	1.25 ± 0.23	1.71 ± 0.10 a	1.76 ± 0.26
В	0.54 ± 0.09	1.30 ± 0.08	1.34 ± 0.06 b	1.44 ± 0.10
С	0.59 ± 0.06	1.15 ± 0.22	1.04 ± 0.05 c	1.60 ± 0.33
GSI (♀)				
Α	0.57 ± 0.04	0.96 ± 0.40	0.66 ± 0.13	0.97 ± 0.19
В	0.73 ± 0.09	1.01 ± 0.21	0.53 ± 0.05	1.34 ± 0.21
С	0.60 ± 0.03	0.64 ± 0.15	0.55 ± 0.12	1.14 ± 0.29
CF				
A	1.56 ± 0.06 a	1.40 ± 0.05	1.72 ± 0.02 a	1.86 ± 0.04
В	1.44 ± 0.09 ab	1.49 ± 0.08	1.67 ± 0.03 ab	1.85 ± 0.03
С	1.30 ± 0.03 b	1.45 ± 0.03	1.58 ± 0.03 b	1.90 ± 0.05
Number of replicates				
Α	10 (7♀ & 3♂)	8 (5♀ & 3♂)	8 (7♀ & 1♂)	13 (13♀ & 0♂)
В	10 (10♀ & 0♂)	19 (18♀ & 1♂)	13 (12♀ & 1♂)	20 (16♀ & 4♂)
С	14 (11♀ & 3♂)	9 (9♀ & 0♂)	10 (7♀ & 3♂)	19 (17♀ & 2♂)

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251

252 **3.2 Fatty acid profile of fish-feeds and faeces**

SFA and MUFA were present in high percentages in both types of feeds (55–59 %).
PUFA content was approximately 41 % in feed A and 45 % in feed B, where OA was

the major fatty acid in feed A (19%) and 16:0 and LA were the major fatty acids in feed

B (18 % and 15 % respectively). The LNA content was 0.27 % and 2 % and the DHA
content was 12 % and 9 % in A and B feeds respectively (Supplementary material,
Table S1).

The sample of faeces showed a high content of SFA (32 %) and MUFA (48 %), OA present in a 28 % and a PUFA percentage of 19% of the total lipid sample, LA being the major PUFA (9 %). Low values were obtained for ARA (0.34 %), LNA (0.32 %), EPA (2.76 %) and DHA (3.36 %).

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3.3 Fatty acid profile of the different tissues

Significant differences in individual main fatty acids among the three distance 265 treatments are shown in Tables 2, 3, 4 and 5 for S. aurita, P. saltatrix, C. rhonchus and 266 *M. barbatus* respectively. In general, when significant differences occur, they follow the 267 same trend in the four tissues studied in all species: the group F showed high levels of 268 OA, total MUFA, LA, total n-6 content and LNA, and low levels of total SFA, ARA, 269 270 EPA, DHA, total n-3 content and n-3/n-6 ratio, in comparison with group MD, group LD, or both. There were some exceptions, like EPA in brain of C. rhonchus, which 271 272 percentage was higher in fish from group F than fish from group LD; total MUFA in 273 brain and gonad of *M. barbatus*, which showed the lowest levels in fish from group F; and ARA in brain of *M. barbatus*, showing higher percentages in group F compared to 274 MD and LD. 275

PERMANOVA pointed to significant differences of the complete fatty acid profile, 276 generally between group F and group MD, or group F and group LD, while *M. barbatus* 277 showed significant differences among the three distance treatments (Table 6). SIMPER 278 analysis showed that the fatty acids with more influence on the dissimilarities among 279 distance treatments were OA, LA and DHA (Supplementary material, Table S2). 280 Samples in the MDS plot are identified by increasing distance to the fish farm (groups 281 F, MD and LD respectively) (Figure 2), where samples showing similar fatty acid 282 283 profiles are placed closer.

Table 2. Fatty acids, n-3/n-6 index, sum of LA and LNA (commercial feed consumption index) and total lipid percentages of flesh (data from Izquierdo-Gomez 285

et al. 2015), brain, liver and gonad samples of S. aurita (mean values ± S.E.). Significant differences among distance treatments are represented in bold and 286 italic. 287

		Flesh			Brain			Liver			Gonad	
	Group F	Group MD	Group LD	Group F	Group MD	Group LD	Group F	Group MD	Group LD	Group F	Group MD	Group LD
SFA^1	30.62 ± 0.87 a	34.31 ± 1.12 a	38.04 ± 0.99 b	28.83 ± 1.17	25.14 ± 1.75	26.87 ± 1.22	36.87 ± 1.25 a	51.41 ± 3.04 b	50.82 ± 1.77 b	31.65 ± 0.71 a	49.00 ± 2.49 b	55.72 ± 3.56 b
OA	22.08 ± 0.48 a	8.84 ± 2.41 b	4.97 ± 0.46 b	34.97 ± 2.44	35.07 ± 1.33	35.34 ± 0.62	27.11 ± 1.79 a	11.43 ± 2.42 b	9.51 ± 1.17 b	21.25 ± 0.65 a	10.51 ± 0.96 b	9.20 ± 0.42 b
MUFA ²	32.04 ± 0.85 a	14.34 ± 3.45 b	8.88 ± 0.87 b	47.94 ± 3.26	48.72 ± 1.53	50.26 ± 0.95	35.72 ± 1.49 a	18.85 ± 3.06 b	15.95 ± 1.60 b	31.22 ± 1.03 a	19.60 ± 1.09 b	17.08 ± 0.55 b
LA	16.58 ± 1.60 a	5.52 ± 2.10 b	1.79 ± 0.14 b	2.79 ± 0.65 a	1.16 ± 0.45 ab	0.20 ± 0.04 b	8.23 ± 1.13 a	2.94 ± 0.89 b	1.81 ± 0.10 b	14.63 ± 1.37 a	2.92 ± 0.50 b	1.96 ± 0.13 b
ARA	0.62 ± 0.03 a	1.50 ± 0.17 b	1.64 ± 0.07 b	2.59 ± 0.17	2.96 ± 0.13	2.62 ± 0.23	0.87 ± 0.12 a	2.24 ± 0.30 b	2.63 ± 0.31 b	0.94 ± 0.11 a	2.65 ± 0.54 b	3.41 ± 0.59 b
n-6 PUFA ³	18.93 ± 1.65 a	8.36 ± 1.99 b	4.33 ± 0.14 b	6.33 ± 0.67 a	5.36 ± 0.53 ab	4.27 ± 0.38 b	11.17 ± 1.28 a	6.14 ± 0.75 b	5.58 ± 0.40 b	17.24 ± 1.41 a	6.41 ± 0.80 b	6.48 ± 0.78 b
LNA	2.11 ± 0.09 a	1.78 ± 0.58 ab	0.80 ± 0.21 b	0.41 ± 0.15	1.07 ± 0.64	0.69 ± 0.45	0.92 ± 0.15 a	0.58 ± 0.12 ab	0.45 ± 0.05 b	1.90 ± 0.09 a	0.64 ± 0.11 b	0.38 ± 0.04 c
EPA	5.82 ± 0.50	5.41 ± 0.41	5.13 ± 0.31	2.31 ± 0.47	2.25 ± 0.28	1.77 ± 0.27	4.17 ± 0.49 a	5.28 ± 0.38 ab	6.04 ± 0.51 b	6.53 ± 0.47	6.15 ± 0.93	4.69 ± 0.67
DHA	8.58 ± 0.83 a	34.49 ± 5.47 b	41.75 ± 1.82 b	13.35 ± 1.56	16.91 ± 1.31	15.70 ± 1.44	9.44 ± 0.94 a	16.50 ± 1.56 b	19.73 ± 1.65 b	9.50 ± 1.15	16.80 ± 2.65	14.42 ± 2.40
n-3 PUFA ⁴	18.41 ± 1.24 a	43.00 ± 5.31 b	48.75 ± 1.66 b	16.90 ± 2.12	20.77 ± 1.75	18.60 ± 1.38	16.24 ± 1.64 a	23.60 ± 1.67 b	27.64 ± 2.18 b	19.89 ± 1.48	24.99 ± 3.39	20.73 ± 3.19
Total PUFA	37.34 ± 1.57 a	51.36 ± 3.69 b	53.08 ± 1.68 b	23.23 ± 2.63	26.13 ± 2.00	22.87 ± 1.49	27.41 ± 2.54	29.74 ± 1.55	33.23 ± 2.50	37.13 ± 1.63	31.39 ± 3.20	27.20 ± 3.82
n-3/n-6	1.09 ± 0.18 a	8.03 ± 1.68 b	11.40 ± 0.54 b	2.70 ± 0.17	4.06 ± 0.39	4.40 ± 0.36	1.60 ± 0.23 a	4.12 ± 0.45 b	5.03 ± 0.26 b	1.25 ± 0.15 a	4.31 ± 0.77 b	3.11 ± 0.38 b
∑(LA; LNA)	18.69 ± 1.68 a	7.30 ± 2.17 b	2.58 ± 0.18 b	3.20 ± 0.70	2.22 ± 0.78	1.16 ± 0.45	9.15 ± 1.27 a	3.51 ± 0.99 b	2.26 ± 0.13 b	16.53 ± 1.45 a	3.56 ± 0.50 b	2.35 ± 0.14 b
TL	9.90 ± 1.55 a	2.70 ± 1.38 b	0.99 ± 0.14 b	13.89 ± 0.65	15.18 ± 0.69	13.63 ± 0.72	14.52 ± 2.34 a	4.51 ± 1.03 b	5.96 ± 1.23 b	11.25 ± 2.69 a	2.34 ± 0.82 b	2.66 ± 0.64 b
1: includes 14:0, 15:0, 16:0, 18:0, 20:0, and 22:0 2: includes 16:1n-7, 18:1n-9, 18:1n-7, 20:1n-9, 22:1n-9 and 24:1n-9 3: includes 18:2n-6, 18:3n-6, 20:2n-6, 20:3n-6, 20:4n-6, 22:2n-6 and 22:4n-6 4: includes 18:3n-3, 18:4n-3, 20:3n-3, 20:5n-3, 22:5n-3 and 22:6n-3												

288

1: includes 14:0, 15:0, 16:0, 18:0, 20:0, and 22:0

289 290 291 292 2: includes 16:1n-7, 18:1n-9, 18:1n-7, 20:1n-9, 22:1n-9 and 24:1n-9

3: includes 18:2n-6, 18:3n-6, 20:2n-6, 20:3n-6, 20:4n-6, 22:2n-6 and 22:4n-6

4: includes 18:3n-3, 18:4n-3, 20:3n-3, 20:5n-3, 22:5n-3 and 22:6n-3

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Table 3. Fatty acids, n-3/n-6 index, sum of LA and LNA (commercial feed consumption index) and total lipid percentages of flesh (data from Izquierdo-Gomez 295

et al. 2015), brain, liver and gonad samples of *P. saltatrix* (mean values ± S.E.). Significant differences among distance treatments are represented in bold and 296

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		Flesh			Brain			Liver			Gonad	
	Group F	Group MD	Group LD	Group F	Group MD	Group LD	Group F	Group MD	Group LD	Group F	Group MD	Group LD
SFA^1	31.58 ± 0.76 a	32.98 ± 0.62 a	36.34 ± 1.19 b	32.06 ± 0.85 a	35.12 ± 0.87 ab	36.41 ± 0.92 b	35.62 ± 1.42	38.81 ± 1.65	40.20 ± 1.88	35.81 ± 1.74	44.13 ± 2.50	42.26 ± 2.49
OA	19.27 ± 1.67	18.93 ± 1.93	19.29 ± 1.87	30.26 ± 1.33 a	27.67 ± 0.74 ab	25.69 ± 0.44 b	26.62 ± 1.58	24.43 ± 2.40	27.79 ± 1.69	18.12 ± 0.71	15.52 ± 0.87	15.22 ± 1.01
MUFA ²	27.77 ± 2.41	26.52 ± 2.48	27.59 ± 2.62	41.73 ± 1.52 a	37.48 ± 0.85 a	34.92 ± 0.25 b	38.25 ± 1.44	35.42 ± 2.87	40.13 ± 1.52	27.49 ± 1.00	24.49 ± 1.27	23.66 ± 1.55
LA	7.25 ± 1.87 a	3.29 ± 1.14 ab	0.83 ± 0.12 b	3.38 ± 1.17 a	1.52 ± 0.33 a	0.49 ± 0.12 b	6.01 ± 1.29 a	2.92 ± 0.92 ab	0.97 ± 0.17 b	6.01 ± 1.38 a	2.61 ± 0.58 ab	1.70 ± 0.25 b
ARA	2.46 ± 0.43	2.75 ± 0.21	3.04 ± 0.23	2.24 ± 0.16	2.47 ± 0.14	2.88 ± 0.23	1.73 ± 0.39	2.35 ± 0.39	2.47 ± 0.40	5.18 ± 0.91	5.53 ± 0.66	7.54 ± 1.06
n-6 PUFA ³	11.15 ± 1.70 a	7.21 ± 1.09 ab	5.00 ± 0.17 b	6.83 ± 1.24	4.77 ± 0.38	4.22 ± 0.28	9.81 ± 1.32 a	6.65 ± 1.02 ab	4.63 ± 0.81 b	12.70 ± 1.06	9.24 ± 0.89	10.58 ± 1.17
LNA	1.35 ± 0.19 a	0.72 ± 0.13 b	0.73 ± 0.22 ab	0.38 ± 0.15	0.15 ± 0.04	0.13 ± 0.10	0.62 ± 0.12	0.35 ± 0.08	0.48 ± 0.18	0.65 ± 0.14 a	0.24 ± 0.06 b	0.36 ± 0.08 ab
EPA	4.74 ± 0.35	4.03 ± 0.21	4.09 ± 0.27	3.33 ± 0.13	3.01 ± 0.15	3.14 ± 0.23	2.35 ± 0.12	2.19 ± 0.19	2.04 ± 0.34	4.46 ± 0.34	3.54 ± 0.35	4.04 ± 0.48
DHA	20.98 ± 2.86	26.89 ± 2.75	24.17 ± 2.68	14.45 ± 0.91 a	18.40 ± 0.92 b	19.93 ± 0.75 b	10.95 ± 1.14	14.85 ± 1.90	10.51 ± 1.24	16.73 ± 2.11	16.81 ± 2.24	16.99 ± 2.33
n-3 PUFA ⁴	29.50 ± 2.85	33.29 ± 2.86	31.08 ± 2.75	19.39 ± 0.68 a	22.63 ± 0.98 b	24.44 ± 0.73 b	16.32 ± 0.97	19.13 ± 2.08	15.04 ± 1.91	24.00 ± 2.37	22.14 ± 2.63	23.49 ± 2.85
Total PUFA	40.65 ± 2.32	40.49 ± 2.77	36.08 ± 2.83	26.21 ± 1.40	27.40 ± 1.05	28.66 ± 0.87	26.13 ± 1.16	25.78 ± 2.49	19.67 ± 2.64	36.71 ± 2.24	31.38 ± 3.19	34.07 ± 3.74
n-3/n-6	3.39 ± 0.80	5.93 ± 0.72	6.21 ± 0.48	3.46 ± 0.53 a	5.25 ± 0.41 b	5.91 ± 0.31 b	2.09 ± 0.51	3.61 ± 0.44	3.50 ± 0.29	2.02 ± 0.32	2.26 ± 0.28	2.27 ± 0.21
∑(LA; LNA)	8.60 ± 1.96 a	4.01 ± 1.23 b	1.56 ± 0.21 b	3.76 ± 1.31 a	1.67 ± 0.37 a	0.62 ± 0.22 b	6.63 ± 1.40 a	3.27 ± 0.99 ab	1.45 ± 0.35 b	6.66 ± 1.51 a	3.22 ± 0.63 b	2.11 ± 0.29 b
TL	1.97 ± 0.64	2.06 ± 0.62	1.69 ± 0.48	12.10 ± 1.34	9.54 ± 1.74	9.16 ± 0.45	10.19 ± 2.12	7.84 ± 1.07	6.61 ± 0.57	3.21 ± 0.26	2.84 ± 0.51	1.86 ± 0.14
1: includes 14:0, 15:0, 16:0, 18:0, 20:0, and 22:0 2: includes 16:1n-7, 18:1n-9, 18:1n-7, 20:1n-9, 22:1n-9 and 24:1n-9 3: includes 18:2n-6, 18:3n-6, 20:2n-6, 20:3n-6, 20:4n-6, 22:2n-6 and 22:4n-6 4: includes 18:4n 3, 20:3n 3, 20:3n 3, 20:5n 3, 20												

298

299 1: includes 14:0, 15:0, 16:0, 18:0, 20:0, and 22:0

300 301 302 2: includes 16:1n-7, 18:1n-9, 18:1n-7, 20:1n-9, 22:1n-9 and 24:1n-9

3: includes 18:2n-6, 18:3n-6, 20:2n-6, 20:3n-6, 20:4n-6, 22:2n-6 and 22:4n-6

4: includes 18:3n-3, 18:4n-3, 20:3n-3, 20:5n-3, 22:5n-3 and 22:6n-3

Table 4. Fatty acids, n-3/n-6 index, sum of LA and LNA (commercial feed consumption index) and total lipid percentages of flesh (data from Izquierdo-Gomez 304 et al. 2015), brain, liver and gonad samples of C. rhonchus (mean values \pm S.E.). Significant differences among distance treatments are represented in bold and 305 italic. 306

	-	Flesh			Brain		-	Liver			Gonad	
	Group F	Group MD	Group LD	Group F	Group MD	Group LD	Group F	Group MD	Group LD	Group F	Group MD	Group LD
SFA ¹	29.01 ± 0.75 a	35.84 ± 0.99 b	35.04 ± 1.13 b	28.11 ± 1.00 a	30.76 ± 0.83 ab	33.30 ± 1.46 b	32.18 ± 0.78 a	39.88 ± 1.31 b	43.73 ± 1.56 b	34.77 ± 1.65 a	43.45 ± 1.73 b	51.17 ± 3.32 b
OA	23.46 ± 0.45 a	16.00 ± 1.65 b	11.96 ± 0.89 b	30.40 ± 0.56	27.67 ± 0.47	28.93 ± 1.07	27.64 ± 0.92	26.57 ± 2.13	26.09 ± 2.21	22.69 ± 0.69 a	19.23 ± 0.97 b	15.71 ± 0.68 c
MUFA ²	35.03 ± 0.77 a	23.25 ± 2.28 b	19.55 ± 1.69 b	43.25 ± 1.04	40.03 ± 0.55	41.25 ± 1.42	39.99 ± 0.97	37.33 ± 2.57	37.71 ± 2.80	35.10 ± 1.09 a	29.13 ± 1.15 b	25.69 ± 1.11 b
LA	11.92 ± 0.89 a	2.38 ± 0.75 b	1.24 ± 0.10 b	3.41 ± 0.55 a	0.63 ± 0.11 b	0.55 ± 0.07 b	10.63 ± 0.83 a	2.33 ± 0.74 b	0.79 ± 0.15 b	10.27 ± 0.73 a	3.02 ± 0.82 b	1.61 ± 0.39 b
ARA	0.89 ± 0.11 a	2.46 ± 0.27 b	2.92 ± 0.27 b	2.24 ± 0.18 a	2.92 ± 0.16 b	2.46 ± 0.13 ab	0.80 ± 0.07 a	2.17 ± 0.33 b	1.96 ± 0.30 b	0.92 ± 0.09 a	2.93 ± 0.48 b	3.33 ± 0.71 b
n-6 PUFA ³	14.34 ± 0.83 a	5.91 ± 0.74 b	5.16 ± 0.27 b	6.60 ± 0.48 a	4.41 ± 0.16 b	3.77 ± 0.07 c	12.91 ± 0.89 a	5.65 ± 0.87 b	3.62 ± 0.50 b	12.51 ± 0.77 a	7.23 ± 0.91 b	6.11 ± 0.79 b
LNA	1.58 ± 0.12 a	0.43 ± 0.11 b	0.33 ± 0.06 b	0.13 ± 0.05	0.00 ± 0.00	0.06 ± 0.04	1.20 ± 0.08 a	0.32 ± 0.08 b	0.09 ± 0.04 c	1.49 ± 0.15 a	0.53 ± 0.11 b	0.25 ± 0.05 b
EPA	5.84 ± 0.37	4.43 ± 0.32	6.21 ± 0.81	3.71 ± 0.24 a	3.20 ± 0.21 ab	2.91 ± 0.16 b	4.16 ± 0.32	3.15 ± 0.35	2.93 ± 0.31	5.80 ± 0.97	4.35 ± 0.41	3.73 ± 0.48
DHA	11.29 ± 1.37 a	28.41 ± 2.97 b	31.54 ± 3.45 b	16.72 ± 0.78	20.23 ± 0.66	17.40 ± 1.08	7.03 ± 0.76 a	11.99 ± 1.53 b	10.37 ± 1.27 ab	7.90 ± 0.83 a	13.48 ± 0.96 b	11.66 ± 1.88 ab
n-3 PUFA ⁴	21.62 ± 1.11 a	35.00 ± 2.76 b	40.25 ± 2.64 b	22.03 ± 1.01	24.80 ± 0.68	21.69 ± 1.16	15.03 ± 0.95	17.14 ± 1.82	14.94 ± 1.67	17.62 ± 1.98	20.18 ± 1.10	17.03 ± 2.43
Total PUFA	35.95 ± 0.87	40.91 ± 2.83	45.41 ± 2.77	28.63 ± 1.12 ab	29.20 ± 0.77 a	25.46 ± 1.19 b	27.92 ± 1.44 a	22.79 ± 2.29 ab	18.56 ± 2.13 b	30.13 ± 2.40	27.42 ± 1.74	23.14 ± 3.04
n-3/n-6	1.59 ± 0.21 a	6.61 ± 0.63 b	7.85 ± 0.51 b	3.40 ± 0.27 a	5.66 ± 0.19 b	5.75 ± 0.29 b	1.19 ± 0.09 a	3.64 ± 0.45 b	4.26 ± 0.25 b	1.42 ± 0.16 a	3.25 ± 0.40 b	2.81 ± 0.37 b
∑(LA; LNA)	13.50 ± 0.99 a	2.81 ± 0.85 b	1.57 ± 0.14 b	3.54 ± 0.59 a	0.63 ± 0.11 b	0.60 ± 0.10 b	11.83 ± 0.91 a	2.66 ± 0.81 b	0.88 ± 0.18 b	11.76 ± 0.85 a	3.55 ± 0.92 b	1.86 ± 0.43 b
TL	6.35 ± 1.21 a	2.26 ± 0.41 b	1.98 ± 0.66 b	12.85 ± 0.94	11.81 ± 0.49	11.00 ± 0.33	17.01 ± 1.45 a	9.52 ± 1.59 b	9.79 ± 1.56 ab	11.68 ± 1.80 a	4.83 ± 1.06 b	2.88 ± 0.65 b
1: includes 14:0, 15:0, 16:0, 18:0, 20:0, and 22:0 2: includes 16:1n-7, 18:1n-9, 18:1n-7, 20:1n-9 and 24:1n-9 3: includes 18:2n-6, 18:3n-6, 20:2n-6, 20:3n-6, 20:4n-6, 22:2n-6 and 22:4n-6 4: includes 18:3n-3, 18:4n-3, 20:5n-3, 20:5n-3, 22:5n-3 and 22:6n-3												

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1: includes 14:0, 15:0, 16:0, 18:0, 20:0, and 22:0

308 309 310 311 2: includes 16:1n-7, 18:1n-9, 18:1n-7, 20:1n-9, 22:1n-9 and 24:1n-9

3: includes 18:2n-6, 18:3n-6, 20:2n-6, 20:3n-6, 20:4n-6, 22:2n-6 and 22:4n-6

4: includes 18:3n-3, 18:4n-3, 20:3n-3, 20:5n-3, 22:5n-3 and 22:6n-3

Table 5. Fatty acids, n-3/n-6 index, sum of LA and LNA (commercial feed consumption index) and total lipid percentages of flesh (data from Izquierdo-Gomez 313

et al. 2015), brain, liver and gonad samples of *M. barbatus* (mean values \pm S.E.). Significant differences among distance treatments are represented in bold and 314

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		Flesh			Brain			Liver			Gonad	
	Group F	Group MD	Group LD	Group F	Group MD	Group LD	Group F	Group MD	Group LD	Group F	Group MD	Group LD
SFA^1	36.19 ± 0.80	36.10 ± 0.80	36.38 ± 0.62	32.27 ± 0.86	31.98 ± 0.95	34.98 ± 1.02	36.66 ± 0.84 a	37.27 ± 1.62 a	44.42 ± 2.09 b	34.17 ± 3.32	33.29 ± 1.42	41.31 ± 3.05
OA	17.12 ± 0.87 a	14.51 ± 1.03 a	8.99 ± 0.83 b	21.50 ± 0.63	24.22 ± 0.64	23.06 ± 1.02	23.53 ± 1.31	19.90 ± 1.46	17.34 ± 1.65	8.53 ± 0.55	8.73 ± 0.77	11.19 ± 1.16
MUFA ²	31.23 ± 1.34 a	29.95 ± 1.49 a	18.39 ± 1.57 b	32.69 ± 0.87 a	36.96 ± 0.67 b	34.34 ± 0.89 ab	42.02 ± 1.28 a	37.69 ± 2.11 a	29.60 ± 2.14 b	15.81 ± 1.08 a	19.87 ± 0.94 ab	21.27 ± 1.83 b
LA	4.71 ± 0.81 a	1.14 ± 0.09 b	0.96 ± 0.04 b	1.12 ± 0.18 a	0.31 ± 0.07 b	0.59 ± 0.08 a	2.89 ± 0.43 a	0.67 ± 0.08 b	0.64 ± 0.05 b	2.74 ± 0.28 a	0.78 ± 0.11 b	1.05 ± 0.10 b
ARA	4.04 ± 0.30 a	3.62 ± 0.49 a	6.52 ± 0.66 b	5.36 ± 0.25 a	4.25 ± 0.18 b	3.89 ± 0.17 b	2.56 ± 0.23	2.81 ± 0.43	3.71 ± 0.47	10.00 ± 0.75	6.88 ± 0.68	6.82 ± 1.11
n-6 PUFA ³	12.17 ± 0.91 a	6.76 ± 0.63 b	9.04 ± 0.67 c	7.57 ± 0.48 a	5.24 ± 0.22 b	5.65 ± 0.31 b	7.45 ± 0.69 a	4.46 ± 0.55 b	5.56 ± 0.60 ab	15.51 ± 1.10 a	9.67 ± 0.58 b	9.44 ± 1.18 b
LNA	0.86 ± 0.16 a	0.42 ± 0.06 a	0.24 ± 0.02 b	0.34 ± 0.22	0.04 ± 0.02	0.14 ± 0.06	0.35 ± 0.07 a	0.15 ± 0.03 b	0.11 ± 0.05 b	0.20 ± 0.05	0.28 ± 0.13	0.30 ± 0.13
EPA	7.89 ± 0.38 a	9.89 ± 0.47 b	11.57 ± 0.36 c	3.71 ± 0.27	4.48 ± 0.35	4.69 ± 0.37	5.10 ± 0.43	5.64 ± 0.50	6.13 ± 0.88	9.76 ± 0.63	10.38 ± 0.49	8.49 ± 1.24
DHA	9.00 ± 1.33 a	14.40 ± 0.96 b	21.76 ± 1.51 c	22.20 ± 1.06	20.15 ± 0.78	18.76 ± 1.48	6.53 ± 0.67	13.23 ± 2.05	12.19 ± 1.73	21.33 ± 1.41	24.26 ± 2.00	16.83 ± 2.33
n-3 PUFA ⁴	20.42 ± 1.60 a	27.19 ± 1.24 b	36.19 ± 1.70 c	27.48 ± 0.96	25.83 ± 0.99	25.03 ± 1.43	13.87 ± 1.15	20.57 ± 2.63	20.42 ± 2.75	34.52 ± 1.80	37.13 ± 2.28	27.98 ± 3.63
Total PUFA	32.59 ± 1.74 a	33.95 ± 1.35 a	45.23 ± 1.94 b	35.05 ± 1.26	31.07 ± 1.13	30.68 ± 1.27	21.32 ± 1.48	25.04 ± 2.97	25.98 ± 3.15	50.02 ± 2.69	46.80 ± 2.23	37.42 ± 4.27
n-3/n-6	1.78 ± 0.22 a	4.50 ± 0.41 b	4.43 ± 0.41 b	3.75 ± 0.20 a	4.99 ± 0.18 b	4.81 ± 0.47 ab	1.94 ± 0.17 a	4.91 ± 0.46 b	3.75 ± 0.46 b	2.28 ± 0.13 a	4.03 ± 0.31 b	3.16 ± 0.45 ab
∑(LA; LNA)	5.57 ± 0.88 a	1.56 ± 0.10 b	1.20 ± 0.05 c	1.46 ± 0.25 a	0.34 ± 0.08 b	0.74 ± 0.13 ab	3.24 ± 0.50 a	0.82 ± 0.10 b	0.75 ± 0.08 b	2.94 ± 0.31 a	1.06 ± 0.18 b	1.35 ± 0.21 b
TL	4.13 ± 0.76 a	3.44 ± 0.48 a	0.92 ± 0.13 b	10.00 ± 0.27	10.06 ± 0.39	9.24 ± 0.33	11.80 ± 0.96 a	7.79 ± 0.84 b	6.02 ± 0.81 b	2.24 ± 0.60	2.89 ± 0.43	4.74 ± 1.01
1: includes 14:0, 15:0, 16:0, 18:0, 20:0, and 22:0												
2: includes 13: includes 14: includes 1	1: includes 14:0, 15:0, 10:0, 18:0, 20:0, and 22:0 1: includes 16:1n-7, 18:1n-9, 18:1n-7, 20:1n-9, 22:1n-9 and 24:1n-9 1: includes 18:2n-6, 18:3n-6, 20:2n-6, 20:3n-6, 20:4n-6, 22:2n-6 and 22:4n-6 1: includes 18:3n-3, 18:4n-3, 20:3n-3, 20:5n-3, 22:5n-3 and 22:6n-3											

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1: includes 14:0, 15:0, 16:0, 18:0, 20:0, and 22:0

317 318 319 320 2: includes 16:1n-7, 18:1n-9, 18:1n-7, 20:1n-9, 22:1n-9 and 24:1n-9

3: includes 18:2n-6, 18:3n-6, 20:2n-6, 20:3n-6, 20:4n-6, 22:2n-6 and 22:4n-6

4: includes 18:3n-3, 18:4n-3, 20:3n-3, 20:5n-3, 22:5n-3 and 22:6n-3

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Table 6. PERMANOVA results for each species and the four tissues studied. Significant P-values are shown in both bold and italic. Journal Pre-proof

in both bold and italic.

		Source	df	SS	MS	Pseudo-F	P(perm)	F - MD	F - LD	MD - LD
		Fatty acid profile	2	3638.9	1819.4	26.41	0.0002	0.0002	0.0002	0.054
	lest	Res	30	2066.8	68,893					
	ш	Total	32	5705.7						
	c	Fatty acid profile	2	659.6	329.8	17,622	0.0872	-	-	-
a	rai	Res	30	5614.6	187.15					
urit	æ	Total	32	6274.2						
ю. а	5	Fatty acid profile	2	2139.6	1069.8	14,395	0.0002	0.0004	0.0002	0.4822
0,	Live	Res	27	2006.6	74,318					
		Total	29	4146.2						
	ad	Fatty acid profile	2	2866.3	1433.1	18,809	0.0002	0.0002	0.0002	0.1306
	Jor	Res	28	2133.5	76,196					
		Total	30	4999.7						
	Ч	Fatty acid profile	2	382.53	191.27	18,369	0.09	-	-	-
	rles	Res	32	3332	104.12					
	-	Total	34	3714.5						
	Ŀ.	Fatty acid profile	2	278.77	139.39	3,125	0.0122	0.0636	0.015	0.1128
trix	Bra	Res	31	1382.7	44,603					
P. saltai		Total	33	1661.5	476.00	10 112	0.004			
	er	Fatty acia profile	2	352.18	176.09	19,112	0.084	- ()	-	-
	Ľ	Res	33	3040.4 2202.6	92,134					
	_	Fatty acid profile	35	5592.0 117 27	222 62	20 122	0.0582			
	nac	Res	2	3611.8	109 45	20,433	0.0382		-	-
	ē	Total	35	4059	105.45					
		10101		1035						
	ų	Fatty acid profile	2	1638.6	819.31	15,575	0.0002	0.0002	0.0002	0.4288
	<u>Fle</u>	Res	23	1209.9	52,604					
		Total	25	2848.5						
S	in'	Fatty acid profile	2	276.61	138.31	36,121	0.0002	0.0006	0.0044	0.1158
chu	Bra	Kes Tatal	25	957.25 1222 0	38.29					
oue		10tui Eattu acid profilo	27	1233.9	E96 07	10 192	0 0002	0 0002	0 0002	0 2414
£	/er	Ράτιν άτια μισμιέ Βρο	2	1553.0	57 553	10,165	0.0002	0.0002	0.0002	0.2414
0	Ŀ	Total	29	2726.1	57,555					
	-	Fatty acid profile	2	890.31	445.16	48.574	0.0022	0.0002	0.0292	0.0676
	nac	Res	34	3115.9	91.645					
	ğ	Total	36	4006.3						
		Fatty acid profile	2	1565.2	782.6	16 591	0 0002	0 0002	0 0002	0 0002
	sh	Pac	42	1003.4	102.0	10,301	0.0002	0.0002	0.0002	0.0002
	Fle	nes Tatal	42	1982.4	47.2					
			44	3547.6	000.07					
	.⊑	Fatty acid profile -	2	404.14	202.07	35,278	0.0268	0.0032	0.003	0.0342
tus	Bra	Res	45	2577.6	57.28					
rba	-	Total	47	2981.8						
þa	_	Fatty acid profile	2	1016.5	508.23	54,061	0.0002	0.004	0.0002	0.0114
N.	ive.	Res	40	3760.4	94.01					
	_	Total	42	4776.9						
	σ	Fatty acid profile	2	1068.1	534.06	43,085	0.0006	0.0002	0.0068	0.0166
	nai	Res	36	4462.4	123.96					
	G	Total	38	5530.5						
			55	00000						



Figure 2. MDS plots of the fatty acid percentages from the different tissues studied in
each species. Data from both types of fish-feed and faeces are also included, in order to
check aquaculture waste influence in wild fish fatty acid profiles.

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345 **3.4 Gonad histology**

346 Two species were selected for gonad study according to their gonad fatty acid content: M. barbatus, which showed minimal variations in gonad fatty acids among distance 347 treatments; and S. aurita, which showed a high number of significant differences among 348 distance treatments in fatty acids. The histological and morphometrical analysis of the 349 ovaries of M. barbatus and S. aurita revealed the presence of oocytes in different 350 maturation stages, which indicates that these species present an asynchronous ovary. 351 352 The usual maturation stages of teleost were observed: oogonia, oocyte in chromatin nucleolus stage, oocyte in perinucleolar stage, oocyte in early vitellogenic stage, and 353 oocyte in late vitellogenic stage, as well as mature oocytes (Figure 3). M. barbatus 354 oocytes in late vitellogenic stage were only found occasionally in fish from group F, and 355 356 S. aurita late vitellogenic oocytes and mature oocytes were also only found in group F.

The percentage of oocytes which have started the oogenesis (oocytes in early 357 358 vitellogenic stage) was significantly higher in S. aurita from group F, and a similar tendency was found in *M. barbatus* from group F. The oocytes in perinuclear stage were 359 significantly lower, in gonads of both species captured close to the fish farm (group F) 360 compared with control fish (group LD) (Figure 4A and 5A). There were no volume 361 differences at any stages of development (Figure 4B and 5B) for both species. The 362 363 studied histological sections did not show abnormalities, degradation or malformations 364 in the gonads.

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Figure 3. Haematoxylin-eosin light micrograph of ovary section in *M. barbatus* (100x),
showing different oocyte development stages.

- **382** A- Oocyte in chromatin nucleolus stage.
- **383** B- Oocyte in perinuclear stage.
- 384 C- Oocyte in early vitellogenic stage.
- **385** D- Oocyte in late vitellogenic stage.
- 386
- 387
- 388

389 4. Discussion

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391 This work demonstrates, by using fatty acids as biomarkers of waste feed consumption, 392 that farm-associated wild fish have an altered fatty acid profile in several tissues, and this effect attenuates with increasing distance to the aquaculture facilities. Aquaculture 393 394 sites attract and concentrate large quantities of wild fish from contiguous areas (Dempster et al. 2009; Callier et al. 2017), being the main attracting factor the 395 396 availability of high energy feed in form of lost pellets that directly feeds the aggregated wild fish (Tuya et al. 2006; Fernandez-Jover et al. 2008). Predators are also attracted to 397 398 fish farms, where some species modify their feeding behaviour consuming lost pellets, 399 while other species are attracted by the high density of potential prey in the area, as it is 400 the case of P. saltatrix (Fernandez-Jover et al. 2008; Sanchez-Jerez et al. 2008; 401 Izquierdo-Gomez et al. 2015). The levels of particulate organic matter also increase in 402 the vicinity of sea cages (Sara et al. 2004; White et al. 2017), and it is used as a trophic resource by planktivorous species like S. aurita (Sanchez-Jerez et al. 2011) as well as 403 404 macroinvertebrate species (Gonzalez-Silvera et al. 2015).

405 The input of organic matter from fish farms to the marine environment is mainly due to 406 lost pellets and faeces. Previous research showed that not only pellets but also faeces 407 could be used as a trophic resource by aggregated fauna (Johansson et al. 1998; Madin 408 et al. 2009; Gonzalez-Silvera et al. 2015), so even with the lack of enough number of 409 replicates, faeces data were used in this work together with aquafeeds data to perform 410 the MDS plots. MUFA represented the major component of the faeces total lipids (48.01 %) while PUFA levels were low (19.65 %). These results agree with those found 411 by Van Biesen and Parrish (2005), being the high proportion of MUFA due to the 412 former's poor digestibility by fish. 413

414 Benthic (M. barbatus) and pelagic (S. aurita and C. rhonchus) fish species showed a similar response to the fish farm influence in terms of individual fatty acid percentages. 415 416 The fatty acid profile of flesh and liver reflected the fatty acid composition of the commercial diets, showing higher percentages of OA and LA and lower percentages of 417 DHA in group F compared to groups MD and LD. OA and LA were the major fatty 418 419 acids in fish-feeds and faeces, and were also pointed by SIMPER as the fatty acids with more influence on the differences observed in this work. Therefore, they are good 420 421 candidates as tracers of aquaculture waste consumption in the studied area, especially 422 LA which was the only fatty acid present at significant higher levels in group F

compared with fish captured at longer distances from the fish farm, in the four analysed 423 tissues from the four studied species. These results about the suitability of the fatty acid 424 listed above confirm those previously found by other authors in flesh of farm-associated 425 wild fish species (Fernandez-Jover et al. 2011) and by our research group in golden 426 mullet under laboratory conditions (Gonzalez-Silvera et al. 2016). Significant 427 428 differences in individual fatty acid percentages were found between fish captured in the 429 vicinity of the fish farm and fish captured by trawlers at long distance from the fish farm, which are supposed to have had limited or null contact with aquaculture facilities. 430

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There are several studies, which similarly to our results, highlight the differences found 432 433 in flesh and liver fatty acids between wild and reared fish. Alasalvar et al. (2002) and Fuentes et al. (2010) reported differences in flesh fatty acids between wild and reared 434 sea bass (Dicentrarchus labrax), the last showing higher levels of OA and LA and 435 436 lower levels of ARA, EPA and DHA. Arechavala-Lopez et al. (2011) found differences in flesh fatty acid profile of bogue (Boops boops) aggregated near sea-cages and bogue 437 caught by fishermen using trammel nets in comparison with individuals caught by 438 trawlers at long distance. Bogue specimens captured by trammel nets presented a 439 similar fatty acid profile to fish farm associated bogue, and both showed presence of 440 feed pellets in their gut content, while bogue captured by trawlers at long distance from 441 farms consumed natural trophic items. Changes in fatty acids followed the same trend 442 443 than in our results, where bogue captured around the fish farm presented higher levels 444 of LA, LNA and OA and lower levels of ARA and DHA, although EPA levels where higher in bogue captured at farms and by trammel nets. Ramírez et al. (2013) obtained 445 446 similar results, in bogue captured within a radius of 3 km from a fish farm. Fernandez-Jover et al. (2007) found that wild horse mackerel (Trachurus mediterraneus) were 447 aggregated around fish farms throughout the year, and their flesh showed a different 448 fatty acid profile than individuals captured at control sites. High percentages of LA, 449 LNA and OA, and lower percentages of ARA and DHA were found in aggregated 450 specimens, compared to control counterparts. Similar results were found in other marine 451 452 fish species, like gilthead sea bream (Sparus aurata) (Grigorakis et al. 2002), aggregated golden mullet (Liza aurata) and saddled sea bream (Oblada melanura) 453 (Fernandez-Jover et al. 2009), and also in Atlantic cod (Gadus morhua) and saithe 454 (Pollachius virens) (Fernandez-Jover et al. 2011) which was also reported to have 455

differences in fillet taste (Skog et al. 2003). Few studies reported the opposite result, as the work of Rueda et al. (2001), who found higher levels of LA, EPA and DHA in flesh of reared sharpsnout sea bream (*Diplodus puntazzo*), in comparison with flesh from wild specimens; and the work of Mnari et al. (2007), who also found higher values of DHA and EPA in reared compared to wild *S. aurata*. In any case, LA levels in those studies were higher in cultured fish.

Irrespectively of their habitat and feeding regimes, the four studied species showed 462 differences in their fatty acid profile, where fish captured around the sea cages had a 463 464 fatty acid profile more similar to fish-feed and faeces, as showed by the MDS plots. The predator P. saltatrix has been previously reported to feed on species aggregated near 465 fish farms, and even on reared fish (Sanchez-Jerez et al. 2008; Arechavala-Lopez et al. 466 2014) instead of lost pellets. The fatty acids analysis of brain, liver and gonads of this 467 468 species reasserted the results previously published by Izquierdo-Gomez et al. (2015) based only in flesh fatty acid composition. The accumulation of LA in the four studied 469 470 tissues of *P. saltatrix* demonstrates the transfer of fatty acids of vegetable origin through different trophic levels. Potential preys aggregated near fish farms, as S. aurita, may 471 472 have been consuming lost pellets and therefore, present a modified fatty acid profile with high inclusion of LA. P. saltatrix prey on those wild fish in the vicinity of fish 473 474 farms, and LA is assimilated and accumulated in flesh, liver, brain and gonads, the latter also showing higher levels of LNA compared to controls. The obtained results 475 demonstrate the capacity of fatty acids of vegetable origin to accumulate along the food 476 chain, and the consequences for human consumption would be a higher intake of short 477 478 chain n-6 fatty acids at the expense of essential long-chain polyunsaturated fatty acids from the n-3 family (EPA and DHA) and n-6 (ARA). Fish consumption is the main 479 480 source of EPA and DHA for human nutrition, and depletion of these fatty acids in 481 aggregated wild fish may affect the recommendations of human fish consumption to achieve an optimal health status. 482

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We have demonstrated that the impact of aquaculture waste consumption differs from one species to another, probably depending on their preferred habitat and feeding behaviour, and the effect on fatty acid percentages attenuates with increasing distances to the fish farms. Migration to remote areas may revert these changes, but our group has already demonstrated that only 2 weeks of commercial feed consumption can be enough to modify the fatty acid profile of flesh in *Liza aurata*, together with a modulation of the

490 immune responses (Gonzalez-Silvera et al. 2017). We also demonstrated in other study 491 that a shift from a commercial diet to a natural diet consumption for a minimum of two 492 months is not a guaranty of recovering a natural fatty acid profile, as LA levels will 493 remain at high percentages (Gonzalez-Silvera et al. 2016). Those results lead us to 494 hypothesize that the fatty acid profile will remain modified, with high percentages of 495 LA, even in the case of migration to areas none influenced by aquaculture.

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Due to aquafeeds composition, wild fish aggregated near fish farms use to show higher 497 fat content and hepatosomatic index than controls (Dempster et al. 2009; Arechavala-498 Lopez et al. 2011), which, together with a decrease in the n-3/n-6 ratio, represent an 499 important physiological change. In any case, it has been reported that increases in the fat 500 content and condition factor result in an increase in fecundity and hatching success, 501 although egg quality and larvae survival rate could be affected by the low levels of 502 DHA and n-3 fatty acids in general, provided by artificial diets (Fernández-Palacios et 503 504 al. 1995; Adams 1999; Almansa et al. 1999; Izquierdo et al. 2001; White et al. 2016). 505 During the vitellogenesis, fish need high fat and protein feeds in order to produce 506 vitellogenin, a phospholipoprotein precursor of lipovitellin and phosphovitellin which are stored in the oocytes in the form of vitello. The amount and quality of the vitello are 507 508 key factors for a successful reproduction, as the vitello is the unique food source for the embryo and the first larvae stages (Alvarez-Lajonchère 2006). 509

510 Hauville et al. (2015) suggested that, despite the high fat levels found in reared common snook (Centropomus undecimalis), cholesterol and ARA levels were lower than their 511 512 wild counterparts, which would have a negative effect in reproductive success and gametogenesis, as ARA has been reported to have an important role in gonadal 513 514 maturation (Pérez et al. 2007; Norberg et al. 2017). Nevertheless, Cejas et al. (2003) 515 reported no differences in gonad total lipids between reared and wild white sea bream (Diplodus sargus), and unlike our results in M. barbatus, but similarly to the results on 516 517 the other three species, cultured fish showed lower gonad ARA levels than wild fish.

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Figure 4. Mean proportions (A) and volumes (B) of the different oocyte development
stages on *M. barbatus* for groups F and LD. Volumes are represented in logarithmic
scale. The "*" indicates significant differences between distance treatments.

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Figure 5. Mean proportions (A) and volumes (B) of the different oocyte development
stages on *S. aurita* for groups F and LD. Volumes are represented in logarithmic scale.
The "*" indicates significant differences between distance treatments.

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587 Our results showed, in *S. aurita* and *M. barbatus* specimens, higher total lipid 588 percentage and lower n-3/n-6 ratio in liver, which is supposed to have a direct influence 589 on eggs production (Marshall et al. 1999; Salze et al. 2005). The gonad fatty acid profile 590 was clearly influenced by the composition of aquafeeds in *S. aurita* specimens, whereas 591 there was just little influence in gonads of *M. barbatus* specimens. Therefore, these two

species were selected for gonad histological examinations, as examples of high and low 592 593 aquafeed impact, with the aim of checking for differences in oocyte maturation between aggregated fish (group F) and non-influenced fish (group LD). The gonad of the two 594 studied species showed higher percentages of LA, lower percentages of DHA and lower 595 596 n-3/n-6 ratio in aggregated fish compared with LD fish. In addition, S. aurita specimens 597 also showed higher percentages of OA and lower percentages of ARA in group F compared to group LD. Fish from group F in both species showed oocytes in 598 perinuclear stage in higher number than group LD, and oocytes in early vitellogenic 599 stage were found in lower number in aggregated S. aurita specimens compared to non-600 aggregated specimens. The proportions of the oocyte stages in gonads of S. aurita were 601 different between LD and F groups, the last showing presence of late vitellogenic and 602 mature oocytes that were not found in LD specimens. Therefore, it is likely that M. 603 barbatus associated to fish farms, ingesting aquaculture wastes, have a slightly faster 604 605 development of the oogenesis, while S. aurita specimens captured in the vicinity of fish 606 farms and reflecting the fatty acid composition of fish-feeds showed an accelerated 607 development compared to controls, and it may be caused by the higher ingest of fat 608 and/or vegetable fatty acids in the diet. The cell volumes of the different stages were the same in both distance treatments, which is indicative of a lack of differences in the 609 610 amount of vitello accumulated. In any case, fatty acids and stereological results in M. barbatus specimens did not shed light on the possibility of negative effects derived of 611 such shift in diet, while other species more influenced by the consumption of lost pellets 612 such as S. aurita should be studied in greater depth. Other factors may be considered in 613 614 future studies, such as the influence of the altered fatty acid profiles on the immune system, or the ecological impact derived from behavioural modifications due to the 615 616 access to large quantities of waste feed.

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619 **5. Conclusion**

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Different species of wild fish aggregated near fish farms, with different feeding behaviour, showed alterations of their fatty acid profile in different degrees in the four tissues studied, pelagic species showing the most modified profiles in flesh and liver. We confirmed a trophic transfer of fatty acids of vegetable origin, mainly LA, from surplus feeds to aggregated wild fish, and from those to predators in the vicinity of fish

farms. These effects attenuate at a distance of more than 1.5 km from fish farm, and totally disappear in fish captured at long distances (minimum of 5 km from farms). We encouraged the use of fish caught as far away as possible from fish farms in studies which require obtaining natural fatty acid profiles as controls, in order to avoid the possibility of aquaculture influence.

Fatty acid transfer to gonads may be well regulated in *M. barbatus*, as just few differences were found in farm-associated fish compared to controls. *S. aurita* aggregated specimens showed huge accumulation of vegetable fatty acids in gonads, which may be related to an accelerated oocyte development compared to nonaggregated fish. We can therefore conclude that uncontrolled consumption of surplus feed rich in vegetable fatty acids can produce modifications in the development of the gonads, the extent of these depending on the feeding behaviour of the species studied.

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640 Supplementary material

641 The fatty acid profile of fish feeds, the complete fatty acid profile for each tissue and 642 species, a table with dates of capture, and the results of the SIMPER analysis can be 643 found in the supplementary material to this work.

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917

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Highlights

Sea-cage aggregated wild fish consume lost pellets rich in terrestrial fatty acids.

Fatty acid profiles of four fish of different trophic level were analysed.

Flesh, brain, liver and gonad fatty acids reflect the composition of surplus feed.

Gonad development is accelerated in fish species aggregated at farms.

Consumption of lost pellets modulates fatty acid composition and gonad maturation.

Declaration of interests

 \boxtimes The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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