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1	Impact of dietary starch on extrahepatic tissue lipid metabolism in farmed
2	European (Dicentrarchus labrax) and Asian seabass (Lates calcarifer)
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26	Abbreviation list
27	<sup>2</sup> H deuterium; <sup>2</sup> H <sub>2</sub> O deuterated water; ACLY, ATP citrate lyase; ACO, acyl-CoA

oxidase; CHO carbohydrates; CPT1, carnitine palmitoyl transferase I; DHAP, 28 dihydroxyacetone phosphate; DNL, de novo lipogenesis; FA, fatty acids; FAS, fatty 29 30 acid synthase; G3P, glyceraldehyde 3-phosphate; G6PDH, glucose-6-phosphate 31 dehydrogenase; DNL, de novo lipogenesis; HOAD, 3-hydroxyacyl-CoA dehydrogenase; LPL, lipoprotein lipase; NMR, nuclear magnetic resonance; PFK, 6-32 33 phosphofructokinase; PK, pyruvate kinase; TAG, triacylglycerol; VAT, visceral 34 adipose tissue

#### 35 Abstract

36 In aquaculture, there is high interest in substituting marine-derived with vegetable-37 based ingredients as energy source. Farmed carnivorous fish under high carbohydrate 38 diets tend to increase adiposity but it remains unclear if this happens by increased 39 lipid retention/accumulation, promotion of lipogenic pathways, or both. In order to 40 determine the response of extrahepatic tissue to dietary starch, European 41 (Dicentrarchus labrax) and Asian (Lates calcarifer) seabass were fed a control (low 42 starch; LS) or experimental (high starch; HS) diet, for at least 21 days and then transferred for 6 days to saltwater enriched with deuterated water <sup>2</sup>H<sub>2</sub>O. Incorporation 43 of <sup>2</sup>H-labelling follows well-defined metabolic steps, and analysis of triacylglycerols 44 (TAG) <sup>2</sup>H-enrichment by <sup>2</sup>H-NMR allowed evaluation of *de novo* lipogenesis (DNL) 45 46 in muscle and visceral adipose tissue (VAT). Fractional synthetic rates for TAG-47 bound fatty acids and glycerol were quantified separately providing a detailed 48 lipogenic profile. The FA profile differed substantially between muscle and VAT in 49 both species, but their lipogenic fluxes revealed even greater differences. In European 50 seabass, HS promoted DNL of TAG-bound FA, in muscle and VAT. High <sup>2</sup>H-51 enrichment also found in muscle TAG-bound glycerol was indicative of its role on 52 lipid cycling. In Asian seabass, HS had no effect on muscle FA composition and lipogenic flux, with no <sup>2</sup>H-enriched TAG being detected. VAT on the other hand 53 54 revealed a strong enhancement of DNL in HS-fed fish along with high TAG-bound 55 glycerol cycling. This study consolidated the use of <sup>2</sup>H<sub>2</sub>O as tracer for fish lipid 56 metabolism in different tissues, under different dietary conditions and suitable to use 57 in different fish models.

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59 Key words: seabass, barramundi, muscle, visceral adipose tissue, NMR,
60 triacylglycerol, fatty acids, glycerol.

### 61 Introduction

62 As the farming of carnivorous fish species such as seabass continues to grow 63 worldwide, the industry struggles to find affordable source ingredients that are able to 64 provide a balanced fatty acid (FA) profile. This should preferably occur while 65 reducing overall dependence on fishmeal with plant-based ingredients, and as 66 consequence, increasing dietary carbohydrates (CHO) such as starch. This has been 67 the case for European seabass Dicentrarchus labrax (Messina et al., 2013; Moreira et 68 al., 2008; Viegas et al., 2016) and Asian seabass (also known as, and hereafter 69 referred to as barramundi) Lates calcarifer (Glencross et al., 2016; Glencross et al., 70 2012; Salini et al., 2016). In this context, balanced formulations should be able to 71 maintain growth performances and yields on the one hand, and provide a final product 72 that delivers optimal levels of critical nutrients for human consumption on the other.

73 From tissue composition, somatic indices and circulating lipids, feed formulations 74 with higher CHO content have been considered responsible for an overall increase in 75 adiposity (Dias et al., 1998; Glencross et al., 2014; Nankervis et al., 2000; Peres and 76 Oliva-Teles, 2002). However, based on studies addressing the regulation and 77 transcription of hepatic enzymes (Castro et al., 2015a; Castro et al., 2015b; Dias et al., 78 1998; Enes et al., 2006; Glencross et al., 2016), it remains unclear if this happens by increased lipid retention/accumulation, promotion of lipogenic pathways, or by their 79 80 combined effects. Moreover, muscle and visceral adipose tissue (VAT) metabolism, 81 regarded as preferential lipid storage sites in teleost fish (Weil et al., 2013), are often 82 overlooked in relation to the liver, as are the factors that control lipid deposition in 83 these locations. The whole-body fatty acid balance method (Turchini et al., 2008), 84 already applied in barramundi (Salini et al., 2015) but, to our knowledge not under 85 high CHO dietary treatments, may be considered as a more holistic analysis. 86 Nonetheless, this method is still blind to lipid compartmentalization in tissues, both in 87 terms of content (Castro et al., 2015a; Messina et al., 2013) but also distribution (Wu 88 et al., 2015).

In aquaculture, excess fat deposition in the muscle has been mainly attributed to environmental and/or nutritional factors that promote lipid retention, such as temperature (Cordier et al., 2002; Ibarz et al., 2007; Moreira et al., 2008), unbalanced FA profiles in fish feed (Izquierdo et al., 2003), and starch (Alvarez et al., 1999; Castro et al., 2015b; Dias et al., 1998; Lanari et al., 1999; Messina et al., 2013), respectively. As the edible fraction of the fish, this tissue is also under permanent

95 scrutiny by the consumer who associates visible fat depots with fish of "inferior" 96 quality, especially if compared with wild fish (Grigorakis, 2007; Manthey-Karl et al., 97 2016; Vidal et al., 2012). Excess fat deposition around the viscera decreases yields for 98 producers and appeal for consumers. However, VAT is no longer regarded as a 99 metabolically inert sink for excess (dietary or synthesized) fat after being associated 100 in mammalian models with endocrine action, energy homeostasis and metabolic 101 interplay in several conditions such as obesity and cardiovascular disease (Ronti et al., 102 2006). This has spurred recent efforts to study fish adipocyte metabolism and its 103 response to dietary CHO (Bou et al., 2016) and hormonal treatments, particularly 104 those closely related to high CHO intake like insulin (Caruso and Sheridan, 2011).

105 Overall, the capacity of fish to endogenously utilize, accumulate or modify FA, and 106 then compartmentalize excess fat is still far from being understood. This has been 107 mostly assessed by tissue composition and indirect interpretation from mRNA 108 abundance of the enzymatic machinery and transporters involved. In this context the 109 use of isotopes, both stable and radioactive, has been a useful tool to directly follow 110 the location and metabolic transformation of dietary substrates. Interesting data on 111 how extrahepatic tissues handle high CHO levels and its consequences on lipid 112 metabolism by in vivo studies: injection (Brauge et al., 1995) or forced feeding (Hemre and Storebakken, 2000) of <sup>14</sup>C-glucose; dietary incorporation of <sup>13</sup>C-starch 113 114 and subsequent recovery in different tissues (Felip et al., 2012); whole body 115 conversion to lipids (Ekmann et al., 2013). In vitro studies, namely the infusion of adipocytes with <sup>14</sup>C-glucose (Bou et al., 2016) have also contributed to a better 116 117 understanding this subject. Instead of following the metabolic fate of a single labeled 118 substrate, the stable isotope deuterium  $(^{2}H)$ , presented as deuterated water  $(^{2}H_{2}O)$  in 119 fish tanks, rapidly equilibrates with fish body water (Viegas et al., 2011) and gets 120 widely incorporated in newly synthesized metabolites such as alanine (Marques et al., 121 2016), glucose or glycogen (Viegas et al., 2015). Similarly, <sup>2</sup>H gets incorporated into 122 different sites of the triacylglycerol (TAG) molecule following well-defined 123 metabolic steps from which estimations for *de novo* lipogenesis (DNL) and glycerol 124 turnover can be derived (Viegas et al., 2016). In order to determine the response of 125 extrahepatic tissues to dietary starch in terms of lipid metabolism we measured 126 incorporation of <sup>2</sup>H into muscle and VAT TAG, in seabass and barramundi farmed in 127 similar settings and fed a control (low starch) or an experimental (high starch) diet.

128

#### 129 Material and Methods

130 *Diet formulation* 

131 For this study two diets were formulated to fulfill the energetic requirements of each 132 species: one low- (LS) and one high-starch (HS) diet (Table 1). For seabass, HS was 133 formulated by replacing an inert filler of cellulose without nutritional value for 17.8% 134 starch from gelatinized pea. For barramundi, HS was formulated by replacing protein 135 and fat for 32.5% starch from gelatinized wheat. Further details on the formulations 136 may be found in (Viegas et al., 2015) and (Glencross et al., 2014) for seabass and 137 barramundi, respectively. Fish of both experiments were acclimated to the diets and 138 experimental conditions for one week.

139

## 140 Fish handling

141 For European seabass, experimental protocol was the same as described previously 142 (Viegas et al., 2015). Briefly, European seabass (D. labrax) from Tinamenor 143 (Cantabria, Spain) were transported to the lab (Coimbra, Portugal) and randomly 144 assigned to 2 different 200 L tanks (32 fish per tank; initial mean body weight of 145  $21.9\pm0.3$  g) of a recirculated system supplied with well-aerated seawater ( $20\pm1^{\circ}C$ ; 146 30±1‰ salinity). Fish were fed twice daily to satiety for more than 21 days the 147 correspondent diet. Experimental procedures complied with the Guidelines of the 148 European Union Council (86/609/EU). Similarly, barramundi (L. calcarifer) from 149 Betta Barra fish hatchery (Atherton, QLD, Australia) were transported to the lab 150 (Bribie Island, QLD, Australia) and randomly assigned to 2 different 200 L tanks (30 151 fish per tank; initial mean body weight of 51.4±0.5 g) of a recirculated system 152 supplied with well-aerated seawater ( $28\pm1^{\circ}$ C;  $35\pm1^{\circ}$ M salinity). Fish were fed once 153 daily to satiety for 21 days the correspondent diet. All experiments were performed in 154 accordance with the Australian code of practice for the care and use of animals for 155 scientific purposes and were approval by the CSIRO Animal Ethics Committee 156 (approval numbers: A8-2010 and A8-2016). No mortality was registered.

157

# 158 Fish residence in ${}^{2}H_{2}O$ and sampling

Following the feeding period each group of fish from each species was transferred to
 a separate tank of <sup>2</sup>H-enriched seawater for 6 days. Approximate 3.5-5.0% <sup>2</sup>H-

161 enrichement was achieved by the addition of 99%-enriched  ${}^{2}H_{2}O$  (seabass: Eurisotop,

162 France; barramundi: Sigma cat. #151882) and tank water <sup>2</sup>H enrichment was assessed

163 at the beginning and end of the trials (Viegas et al., 2011). This tank was maintained 164 with an independent closed filtering system but with similar characteristics to the 165 tanks used during the feeding period in terms of size, volume of water (200 L), 166 opacity, filtering material and water parameters. During the 6-day residence in <sup>2</sup>H-167 enriched saltwater, fish were fed once a day (ad libitum) and sacrificed 24 h after last meal on day 5. Fish were anesthetized in a 30 L tank of <sup>2</sup>H-enriched seawater 168 (seabass: 0.1 g L<sup>-1</sup> of MS-222; barramundi: 0.02 mL L<sup>-1</sup> of Aqui-S<sup>®</sup>), measured, 169 weighed and blood was drawn from the caudal vein with heparinized syringes. A 170 171 ~100 µL aliquot was centrifuged (3000xg, 10 min), and plasma was stored at -20°C 172 for quantification of body water <sup>2</sup>H enrichments. Fish were sacrificed (seabass: by 173 cervical section; barramundi: overdose of Aqui-S<sup>®</sup>); muscle tissue was dissected from the epaxial quadrant (seabass: n=8, 1.6±0.1 g; barramundi: n=5, 1.1±0.1 g) and 174 175 visceral adipose tissue (VAT) (seabass: n=8,  $0.5\pm0.1$  g; barramundi: n=6,  $0.5\pm0.1$  g) 176 was carefully stripped from the peritoneal cavity. Both tissues were weighed, freeze-177 clamped with aluminum tongs cooled in liquid nitrogen, pulverized with chilled pestle 178 and mortar and stored at -80°C until further analysis.

179

### 180 Sample treatment

181 Muscle and VAT lipids were extracted from pulverized tissue according to Matyash et al. 182 (2008) using methyl tert-butyl ether, methanol and water mixture (MTBE:MeOH:H<sub>2</sub>O, 10:3:2.5; 20 mL g<sup>-1</sup> of tissue) transferred to glass amber vials, 183 dried under N<sub>2</sub> stream and stored at -20°C. Triacylglycerols (TAG) were purified by 184 solid phase extraction with prepacked 2 g cartridges (Discovery® DSC-NH<sub>2</sub> 52641-U, 185 Supelco) according to Ruiz et al. (2004). Muscle TAG quantifications were performed 186 187 in a fully-automated analyzer Miura 200 (I.S.E. S.r.l.; Guidonia, Italy) using its 188 dedicated reagent kit (ref. A-R0100000901; seabass: n=7, barramundi: n=5).

189

## 190 NMR analysis

191 Tank water (TW) and fish body water (BW) <sup>2</sup>H enrichments were determined by <sup>2</sup>H 192 NMR using calibrated acetone and analyzed in duplicates as previously described 193 (Jones et al., 2001). Tank and plasma water content was assumed to be 96,5% and 194 92% of total sample, respectively. NMR spectra of TAG samples were obtained at 195 25°C with a Bruker Avance III HD system with an UltraShield Plus magnet (11.7 T, 196 <sup>1</sup>H operating frequency 500 MHz) equipped with a 5-mm <sup>2</sup>H-selective probe with <sup>19</sup>F 197 lock and <sup>1</sup>H-decoupling coil. TAG were reconstituted in chloroform containing a pyrazine standard as previously described (Viegas et al., 2016) - representative TAG 198 <sup>1</sup>H and <sup>2</sup>H NMR spectra are provided as supplementary material (Figure S1). As <sup>1</sup>H 199 and <sup>2</sup>H signals are essentially isochronous, the identity of the <sup>2</sup>H signals can be 200 confirmed by matching their chemical shifts with their <sup>1</sup>H counterparts, meaning that 201 202 the respective signal assignments apply to both nuclei (Table S1). As control for the 203 TAG extraction, a FA/glycerol ratio (should be ~3) was calculated from the area of all 204 α protons times 2, divided by TAG-bound glycerol sn1,3 protons (Duarte et al., 2014). 205 The FA profile (in percentage) for saturated (SFA) and unsaturated fatty acids (UFA), 206 both poly- (PUFA) and monounsaturated fatty acids (MUFA) were estimated from <sup>1</sup>H NMR spectra according to Viegas et al., (2016). Positional <sup>2</sup>H-enrichments were 207 quantified from the <sup>1</sup>H and <sup>2</sup>H NMR spectra by measuring the <sup>1</sup>H and <sup>2</sup>H intensities 208 209 (areas) of selected signals relative to the <sup>1</sup>H and <sup>2</sup>H intensities of a pyrazine standard, 210 after correction for linoleic acid contribution according to Duarte et al. (2014). 211 Briefly, during their residence in <sup>2</sup>H-enriched seawater, newly synthesized FA from 212 de novo lipogenesis incorporate <sup>2</sup>H-enrichment in the FA terminal methyl group 213 (signal at 0.80 ppm). The same principle applies to for newly synthesized glycerol, 214 incorporating <sup>2</sup>H-enrichment in the sn-1,3 glyceryl site (signals at 4.15 ppm). Fractional synthetic rates (FSR; in  $\% d^{-1}$ ) of newly synthesized TAG-bound FA and 215 TAG-bound glycerol were estimated by dividing the respective positional <sup>2</sup>H-216 217 enrichment by the BW. <sup>2</sup>H-enrichments were calculated after systematic subtraction 218 of 0.015%, taken as the mean background <sup>2</sup>H-enrichment. If the values were below 219 zero, these were considered as 0.0 for FSR calculation purposes. Spectra were 220 processed by applying exponential multiplication to the free-induction decay (<sup>1</sup>H: 0.1 221 Hz; <sup>2</sup>H: 1.0 Hz). Spectra processing and peak integration was performed using 222 ACD/NMR Processor Academic Edition from ACD\Labs 12.0 software (Advanced 223 Chemistry Development, Inc.).

224

# 225 Statistical analysis

226 Data are presented as mean  $\pm$  S.E.M. Whenever possible, two-way ANOVA was used 227 to test main effects of, and interactions between, diet and tissue. In the case of 228 statistically significant interactions, or in the impossibility to perform a two-way 229 ANOVA, differences between diets were tested using a Student's two-tailed unpaired 230 t-test. Analyses were performed in GraphPad Prism® software (GraphPad Software,

Inc.). Differences were considered statistically significant at P < 0.05.

232

# 233 Results

234 Following extraction and subsequent isolation from other lipid classes by solid phase 235 extraction, TAG gave well-resolved <sup>1</sup>H NMR spectra. The FA/glycerol ratio was not 236 affected by diet for any tissue of both species, and was overall consistent with a 237 successful TAG separation (seabass: n=32, 2.96±0.03; barramundi: n=22, 3.03±0.04; 238 t-test, P > 0.05). Signals from PUFA and MUFA moieties dominated the spectra, 239 while contributions from SFA were relatively minor. In seabass, TAG-bound FA 240 composition as categorized by <sup>1</sup>H NMR spectra was tested for effects of diet (LS vs. 241 HS) and tissue distribution (muscle vs. VAT) (Table 2). All were significant for the 242 latter, symptomatic of a differential profile where SFA were stored to a higher degree 243 in VAT than in muscle while the opposite trend was observed regarding UFA. Within 244 UFA, more PUFA, and consequently also more n-3 were found in muscle than in 245 VAT. In the case of PUFA and MUFA effects were also observed due to dietary 246 treatment, with PUFA decreasing, and MUFA increasing with elevated dietary starch. 247 No interactions between dietary treatment and the analyzed tissues were observed, as 248 summarized in Table 2. For barramundi, the same lipid composition analysis from  ${}^{1}\text{H}$ 249 NMR spectra was performed as shown in Table 3. Due to poor signal-to-noise ratio, 250 probably resulting from technical problems associated with the lipid extraction and 251 not to low lipid concentration per se, two muscle samples (one per diet) were 252 considered unsuited for spectral analysis. As in seabass, barramundi lipid composition 253 revealed differential tissue distribution, with the exception of PUFA. As previously 254 observed, SFA were stored to a higher degree in VAT, while UFA, mainly driven by 255 MUFA, were preferentially stored in muscle. None of the lipid species were affected 256 by the dietary treatment even if PUFA mean values seemed to indicate otherwise. 257 Again, no interactions between variables were observed (Table 3).

As equivalent <sup>1</sup>H and <sup>2</sup>H signals resonate at approximately the same chemical shift, the observed <sup>2</sup>H NMR signals correspond to specific enriched sites in the TAG molecule. This enrichment is derived from ~0.015% <sup>2</sup>H natural abundance (mean background <sup>2</sup>H-enrichment) plus excess enrichment from the metabolic incorporation of <sup>2</sup>H from the 6-day residence in <sup>2</sup>H<sub>2</sub>O-enriched seawater. Specifically, this incorporation resulted in peaks corresponding to FA terminal methyl group site (non n-3) (signal at 0.80 ppm) revealing TAG-bound FA synthesized *de novo*, and to the
sn1,3 glyceryl site, revealing newly synthesized or cycled TAG-bound glycerol.
Labeling was not detected in glycerol of seabass VAT (Fig. 1), and in both FA and
glycerol of muscle of barramundi (Fig. 2). For both species, glyceryl FSR were
substantially higher than for FA; ~20-80 times higher in the case of seabass muscle,
and ~2-20 times higher in the case of barramundi VAT.

270 In seabass (Fig. 1), differences in FA FSR were attributable to both tissue distribution 271 and diet, being significantly higher in muscle in regard to VAT, and HS in regard to 272 LS. Glycerol revealed higher FSR when compared to FA FSR and was also 273 statistically lower in the HS when compared with LS. In barramundi VAT, FA FSR 274 was significantly higher in fish fed the HS diet while glyceryl FSR on the other hand 275 was unaffected by diet. Muscle TAG levels did not differ between diets for both 276 species (seabass: LS 8.4±1.2 vs. HS 7.4±0.6; barramundi LS 1.0±0.2 vs. HS 0.7±0.1, in g  $100g^{-1}$  of tissue; t-test P > 0.05). 277

278

# 279 Discussion

280 In vertebrates the liver is the centerpiece for metabolic regulation and in teleost fish it 281 is the main lipogenic organ where key endocrine and nutrient sensing mechanisms 282 intersect (Conde-Sieira and Soengas, 2017). In similar feeding trials, hepatic TAG 283 content and FA composition was sensitive to high CHO diets (Castro et al., 2015a; 284 Lanari et al., 1999; Messina et al., 2013; Peres and Oliva-Teles, 2002; Viegas et al., 285 2016). In the present study, muscle and VAT from both species presented different 286 FA profiles, but only in seabass these profiles were responsive to HS diet, particularly 287 PUFA and MUFA. CHO-stimulated accumulation of muscle lipids has been 288 associated with transcriptional response of hepatic FA desaturation and elongation 289 enzymes in rainbow trout (Oncorhynchus mykiss) (Kamalam et al., 2012), and 290 enhanced metabolic elongation rates in the same seabass analyzed in the present study 291 (Viegas et al., 2016). Interestingly in barramundi muscle, lack of CHO-stimulated FA 292 profile alterations may relate to absolute lack of <sup>2</sup>H-enriched TAG, either in the FA or 293 glycerol moieties. This suggests that this pool had very limited turnover, either in 294 terms of net FA replacement, or FA-TAG cycling (this latter process accounting for 295 the higher enrichment of glycerol compared to FA in other tissues as discussed 296 ahead). Muscle FA profile in this species has proven to be sensitive to dietary lipid 297 manipulations (Alhazzaa et al., 2011), but as regard to CHO, further studies should be 298 conducted. Notwithstanding, potential muscle FA profile alterations were often 299 accompanied by little or no variation in muscle lipid content as verified in seabass 300 (Boujard et al., 2004; Castro et al., 2015a; Dias et al., 1998; Messina et al., 2013; 301 Peres and Oliva-Teles, 2002). The same could be indirectly inferred in barramundi by 302 the fact that head-on-gutted lipid composition, mainly composed by muscle tissue, 303 was unaffected by HS (Glencross et al., 2014). This is most likely associated with the 304 poor capacity of muscular tissue, which represents about 50-60% of the whole-body 305 mass, to effectively clear excess CHO. Rainbow trout is one of the most intensely 306 studied fish species, and under high CHO diets muscle mRNA levels for GLUT4 307 remained unaltered (Kamalam et al., 2012; Panserat et al., 2009). After a short-term 308 administration of insulin, muscle GLUT4 (Polakof et al., 2010b), along with muscle 309 FAS (Polakof et al., 2010a) mRNA levels decreased. A long-term (chronic) insulin 310 administration reverted these effects, but regardless of the duration of the insulin 311 treatment, muscle glycogen always increased significantly (Polakof et al., 2010b). In 312 the seabass from the present study, incorporation of <sup>2</sup>H into glycosyl units revealed 313 that hepatic glycogen synthesis via direct pathway was significantly augmented in 314 HS-fed fish (Viegas et al., 2015), so the same could be expected in muscle tissue. It is worth noting that in rainbow trout fed with <sup>13</sup>C-labelled dietary starch, the fraction 315 316 recovered in muscle tissue was for the most part present in lipids and glycogen. 317 Interestingly, no differences we observed for both parameters between fish fed 318 digestible and raw starch (Felip et al., 2012). Regardless of its lipogenic action in the 319 liver, under normal feeding the effects of insulin in fish muscle seem to ineffectively 320 regulate CHO disposal, particularly in a species where insulin release was poorly 321 stimulated by dietary CHO (Enes et al., 2010) like the seabass. There is however 322 margin for improvement and revision of these metabolic models, particularly in the context of aquaculture, as incredibly versatile trait-selected fish (e.g. Fat and Lean 323 324 lines of rainbow trout) unveiled the combined effects of i) modulation of lipogenesis 325 in the liver by the mTOR pathway (Skiba-Cassy et al., 2009), ii) modulation of 326 muscle glycolytic (PK and PFK) (Song et al., 2018) and fatty acid oxidation enzymes 327 (CPT1, HOAD and ACO) (Jin et al., 2014a), and finally iii) improved response to 328 insulin (Jin et al., 2014b) to achieve fish able to display higher muscle lipid content. 329 Contrary to barramundi, considerable levels of <sup>2</sup>H-enriched TAG were detected in 330 seabass muscle. When compared with the liver (Viegas et al., 2016), CHO-stimulated 331 DNL and/or incorporation of starch into body lipid (muscle and VAT) was lower.

332 Despite the fact that the labeling was recovered from a single type of lipid, the synthesis, and therefore the <sup>2</sup>H-enrichment of the TAG glyceryl backbone and its 333 334 three esterified FA, happens independently. FA terminal methyls hydrogens become 335 enriched in <sup>2</sup>H by DNL (other TAG fatty acyl hydrogens may also become enriched 336 by elongation reactions). TAG glyceryl hydrogens become enriched via de novo 337 glycerol-3-phosphate synthesis from glyceraldehyde-3-phosphate (G3P) and exchange 338 between glycerol-3-phosphate and G3P. Their enrichment is suitably discriminated by 339 <sup>2</sup>H NMR, a feature that mass-based technologies are unable to do unless additional 340 sample treatment was performed. Regardless of the dietary treatment and species, TAG-bound glycerol revealed considerably higher <sup>2</sup>H-enrichment when compared to 341 342 TAG-bound FA. It has been hypothesized that fish maintain high glycerol rates of 343 appearance by constantly cycling (reesterifying) up to two-thirds of circulating TAG 344 to free FA (Bernard et al., 1999; Magnoni et al., 2008). During exercise, fish muscle 345 augments lipoprotein lipase (LPL), critical for lipid mobilization (Magnoni et al., 346 2013) but TAG-FA turnover rates were maintained unalterably high. In the absence of 347 glycerol kinase in muscle, this glycerol cannot be recycled to glycerol-3-phosphate 348 and reused in TAG cycling, being instead shuttled to the liver. Alternatively, de novo 349 synthesis of glycerol-3-phosphate must occur and as consequence, enrichment of the 350 triglyceride glyceryl moiety is typically much higher than that of the FA, which also 351 include FA from dietary (unlabeled) origin. Glucose can be a contributing precursor 352 to glycerol synthesis (through dihydroxyacetone phosphate; DHAP) via an 353 abbreviated pathway of glycolysis as confirmed by <sup>13</sup>C- (Rito et al., 2018) and <sup>14</sup>C-354 glucose (Walter et al., 2006) tracer studies. Higher levels of circulating (unlabeled) 355 glucose may putatively explain why, glyceryl FSR was lower in the muscle of seabass 356 fed with HS diet, as already observed in the liver if these fish (Viegas et al., 2016). 357 This same study also revealed that despite elevated hepatic TAG levels (LS: 11.1±0.2 and HS: 35.4±0.7 g 100 g<sup>-1</sup> liver; t-test P < 0.001), this was not attributable to 358 359 increased hepatic DNL. So, it was particularly intriguing to find that in muscle, TAG-360 bound FA from DNL were significantly increased in the HS diet, even if muscle TAG levels remained unaltered (LS: 8.4±1.2 vs. HS: 7.4±0.6 g 100 g<sup>-1</sup> muscle; t-test P >361 362 0.05). This indicates an independent regulation of muscle TAG synthesis activity 363 during starch feeding, previously observed for rainbow trout (Brauge et al., 1995) but 364 whose mechanisms are yet to be addressed.

365 In seabass, CHO-derived overall increased adiposity is driven not only by increased 366 liver lipid content but also by VAT accumulation (Castro et al., 2015a; Dias et al., 367 1998; Peres and Oliva-Teles, 2002). This was not observed in the present experiment, 368 as perivisceral fat index remained unaltered (LS: 4.9±0.2 vs. HS: 5.1±0.2) (Viegas et 369 al., 2016). In rainbow trout, contrary to documented for muscle, in VAT insulin is 370 regarded as an important hormone for lipid deposition: i) via its anti-lipolytic effects 371 (Albalat et al., 2006); ii) through upregulation of ACLY and FAS and iii) by 372 production of NADPH for lipogenesis (Polakof et al., 2010b). In a species from the 373 same genus, coho salmon (O. kisutch), adipocyte GLUT4 transporter was sensitive to 374 insulin notwithstanding a lower affinity for glucose compared to the mammalian 375 homolog (Capilla et al., 2004). In another salmonid species, in vitro studies revealed 376 even though the DNL pathway is active in Atlantic salmon (Salmo salar) adipocytes, 377 rates of conversion of glucose into lipids were relatively low (Bou et al., 2016). It is 378 worth noting that in salmonids, adjpocytes were not nutritionally regulated by CHO 379 (Figueiredo-Silva et al., 2012; Kamalam et al., 2013), but displayed elevated G6PDH 380 activity and NADPH levels even in the absence of CHO (Barroso et al., 2001). This 381 seems not to be the case for seabass and barramundi VAT where TAG-bound FA 382 synthesis via DNL was significantly higher for HS diet. This was also described in 383 gilthead seabream (Sparus aurata) adipocytes which under high CHO diets, up-384 regulated G6PDH expression and FAS also tended to increase (Bou et al., 2014). 385 Besides a stronger response to insulin (Albalat et al., 2007) through LPL activation, 386 CHO utilization in this species' VAT was also favored over FA oxidation by 387 modulation of the PPARs transcription factors (peroxisome proliferator-activated 388 receptors) (Bou et al., 2014).

389 In seabass, FA FSR was significantly lower in VAT than in muscle but was 390 nevertheless influenced by diet. Contrary to observed in muscle, TAG-FA cycling did not occur in VAT as interpreted by the lack of <sup>2</sup>H-enrichment in TAG-bound glycerol. 391 392 In barramundi the opposite seemed to take place; on the one hand, no <sup>2</sup>H-enrichment 393 was detected in muscle TAG, and on the other, not only VAT FA were extremely 394 stimulated by the HS diet, but also high FSR for glycerol were estimated. Similar 395 findings were obtained from Atlantic salmon (Salmo salar) adipocytes incubated with <sup>14</sup>C-glucose. Analysis of TAG revealed 16-fold more <sup>14</sup>C incorporation into glycerol 396 397 than FA (Bou et al., 2016). This is well within the range observed in the present study 398 for barramundi VAT TAG with 19-fold excess <sup>2</sup>H-enrichment of glycerol over FA

399 during HS feeding. Bou and colleagues proposed that the way glucose stimulates 400 lipogenesis was by stimulating the pentose phosphate pathway, which in turn 401 generates G3P precursors for TAG glycerol as well as providing NADPH for 402 sustaining FA synthesis. Our study provides further evidence for this mechanism, not 403 only in barramundi adipose tissue but also seabass muscle. It should be noted that 404 despite our best efforts to provide a framework for comparing both species by using 405 isoenergetic diets, certain parameters differed. Particularly, the diets for barramundi 406 were not isoproteic but none was protein limiting as it was ensured that the DP:DE 407 ratio exceeded the established requirements for this species (Glencross, 2008). The 408 fact that these were not isolipidic may have alone interfered with overall lipid 409 metabolism, perhaps with stronger effects in the liver rather than in muscle or VAT. 410 Nonetheless, the present study has provided further insight into the impact and fate of 411 dietary starch in extrahepatic tissues of two carnivorous seabass species. The FA 412 profile differed substantially between muscle and VAT, but their lipogenic fluxes 413 revealed even greater differences. In seabass, HS promoted DNL of TAG-bound FA, 414 in muscle and VAT. High <sup>2</sup>H-enrichment found in muscle TAG-bound glycerol was 415 indicative of its role on lipid cycling. In barramundi, HS had no effect on muscle FA composition and lipogenic flux, with no <sup>2</sup>H-enriched TAG being detected. VAT on 416 the other hand revealed a strong enhancement of DNL in HS-fed fish along with high 417 418 TAG-bound glycerol cycling.

419 Overall, while the aquaculture industry seeks to further stretch the optimization of fish 420 feed production, the administration of isotopes will provide deeper insights into the 421 regulation of lipid storage and oxidation in fish species in response to different 422 combination of macronutrients. This may be particularly interesting in the 423 procurement of new species to farm or in the optimization and selection of existing 424 ones, currently happening by trait preference (Jin et al., 2014b; Song et al., 2018) or 425 by recurring to the wide spectrum of metabolic responses occurring in nature 426 (Betancor et al., 2016; Marandel et al., 2018).

427

### 428 Disclosures

429 No conflicts of interest, financial or otherwise, are declared by the authors.

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Figure 1: Fractional synthetic rate for TAG-bound fatty acids (fatty acyls; FA FSR) and TG-bound glycerol (Glyceryl FSR) expressed as percent of newly synthesized TAG from *de novo* lipogenesis per day in muscle and visceral adipose tissue (VAT) of seabass (*D. labrax*) fed with low starch (LS) and high starch (HS) diets, after a 6day residence in <sup>2</sup>H-enriched seawater. Mean values  $\pm$  S.E.M. (n=8) are presented. When not applicable a two-way ANOVA, significant differences between diets are tested (t-test) and indicated by asterisks (\**P* < 0.05, \*\**P* < 0.01, \*\*\**P* < 0.001).



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Figure 2: Fractional synthetic rate for TAG-bound fatty acids (fatty acyls; FA FSR) and TG-bound glycerol (Glyceryl FSR) expressed as percent of newly synthesized TAG from *de novo* lipogenesis per day in muscle and visceral adipose tissue (VAT) of barramundi (*L. calcarifer*) fed with low starch (LS) and high starch (HS) diets, after a 6-day residence <sup>2</sup>H-enriched seawater. Mean values  $\pm$  S.E.M. (n=5 for muscle; n=6 for VAT) are presented. Significant differences between diets are tested (t-test) and indicated by asterisks (\**P* < 0.05, \*\**P* < 0.01, \*\*\**P* < 0.001).

- **Table 1.** Ingredients and proximate composition of the experimental diets provided to
- 693 European seabass (*D. labrax*) and barramundi (*L. calcarifer*)

	Seabass		Barramundi	
Proximate composition (% dry weight)	LS	HS	LS	HS
Dry matter	96.0	95.6	93.0	89.0
Crude protein	50.2	50.2	63.3	50.2
Crude fat	16.1	16.1	11.7	6.6
Starch	0.2	17.8	1.6	32.5
Ash	11.5	9.3	9.0	11.5
Gross Energy (kJ g <sup>-1</sup> dry weight)	22.66	22.03	21.3	20.8

**Table 2.** Percentage of lipid species in triacylglycerol of muscle and visceral adipose
tissue (VAT) of European seabass (*D. labrax*) fed with a low starch (LS) and high
starch (HS) diet as determined from <sup>1</sup>H NMR spectra.

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PUFA MUFA UFA SFA n-3 Muscle (n=8) LS 27.6±0.3 46.7±0.9 82.3±1.7 17.7±1.7  $36.5 \pm 1.0$ HS 27.2±0.3  $45.1 \pm 0.4$  $37.3\pm0.6$  $82.5\pm0.6$  $17.5\pm0.6$ VAT (n=8) LS  $40.6 \pm 1.1$  $38.4\pm0.6$  $25.5\pm0.2$ 79.1±1.1  $21.0{\pm}1.1$ HS 24.6±0.5  $35.5 \pm 2.4$  $41.8 \pm 0.4$  $77.3 \pm 2.2$  $22.7 \pm 2.2$ 2-way ANOVA \*\* Diet \* ns ns ns \*\*\* \* \* Tissue \*\*\* \*\*\* Interactions ns ns ns ns ns

700 Mean values±S.E.M are presented. Two-way ANOVA; sources of variations: diet (LS vs. HS) and

701 tissue (muscle vs. visceral adipose tissue) (\*P < 0.05, \*\*P < 0.01, \*\*\*P < 0.001; ns: not significant).

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703 **Table 3.** Percentage of lipid species in triacylglycerol of muscle and visceral adipose

tissue (VAT) of Asian seabass (barramundi *L. calcarifer*) fed with a low starch (LS)

and high starch (HS) diet as determined from  ${}^{1}H$  NMR spectra.

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		n-3	PUFA	MUFA	UFA	SFA
Muscle (n=5)	LS	$7.8 \pm 0.9$	26.4±3.7	54.2±3.9	80.7±7.0	19.4±7.0
	HS	$10.8 \pm 1.8$	29.4±3.4	51.5±4.1	73.6±5.8	26.4±5.8
VAT (n=6)	LS	15.1±1.2	26.5±2.5	37.4±0.9	64.0±2.1	36.1±2.1
	HS	16.6±0.2	30.2±0.8	34.4±0.9	63.3±1.1	36.7±1.1
2-way ANOVA	Diet	ns	ns	ns	ns	ns
	Tissue	***	ns	***	**	**
	Interactions	ns	ns	ns	ns	ns

707 Mean values±S.E.M are presented. Two-way ANOVA; sources of variations: diet (LS vs. HS) and

708 tissue (muscle vs. visceral adipose tissue) (\*P < 0.05, \*\*P < 0.01, \*\*\*P < 0.001; ns: not significant).