

1 **The ratio between digestible protein and digestible energy affects accumulation**
2 **and depuration of geosmin and 2-methylisoborneol (2-MIB) in Japanese**
3 **seabass (*Lateolabrax japonicus*) raised in a recirculated aquaculture system**

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17
18 **Abstract**

19 Actinobacteria and cyanobacteria accounted for less than 1% of total of bacteria in water in a
20 recirculated aquaculture system (RAS) during a 15-week feeding trial with 0.11-g Japanese
21 seabass. Resulting concentration of geosmin and 2-methylisoborneol (2-MIB) in RAS water were
22 169 and 45 ng L⁻¹, sufficient to produce strong off-flavor. The seabass were fed diets with 42, 45
23 and 49% protein, and each protein level was supplemented with 15 or 18% lipid. Accumulation
24 of off-flavors was independent of diet in fatty ventral tissue. Dietary protein significantly reduced
25 off-flavors in lean, dorsal tissue. This was mainly rationalized by linear reduction in 2-MIB in
26 response to increasing DP/DE, and a strong, 2nd degree polynomial response in geosmin. The ratio
27 between geosmin and 2-MIB was slightly higher at the beginning of a 10-day period with clean
28 water and fasting, than what was observed throughout depuration. 2-MIB remained between 0.2
29 and 1 µg kg⁻¹ in dorsal tissue throughout depuration. Geosmin in ventral tissue ranged from 10 to
30 more than 30 µg kg⁻¹ at the termination of the feeding period and was reduced to a range from 6 to
31 20 µg kg⁻¹ by depuration.

32

33

34 **KEYWORDS**35 geosmin, 2-methylisoborneol (2-MIB), depuration, *Lateolabrax japonicus*, RAS, DP:DE ratio

36

37 **1 INTRODUCTION**

38 Geosmin and 2-methylisoborneol (2-MIB) are the most widespread sources of muddy flavours in
39 freshwater. Both are secondary metabolites produced by microorganisms (Jiang, He, & Cane,
40 2007). The employment of quantitative real-time PCR (qPCR) analysis allows the identification
41 and quantification of the *geoA* and 2-MIB synthase genes, which encode for geosmin and 2-
42 methylisoborneol (2-MIB) synthesis in bacteria (Lukassen, 2017; Suurnäkki et al., 2015; Wang,
43 Xu, Shao, Wang, & Li, 2011). Previous studies have shown that cyanobacteria (Schrader & Dennis,
44 2005; Wang et al., 2011) and actinobacteria (Lukassen, Saunders, Sindilariu, & Nielsen, 2017;
45 Lylloff, Mogensen, Burford, Schlüter, & Jørgensen, 2012) are primary sources of geosmin and 2-
46 MIB. Myxobacteria from the phylum proteobacteria also produce geosmin and 2-MIB and release
47 them into the water (Jeroen S. Dickschat, Bode, Mahmud, Müller, & Schulz, 2005; Jeroen S
48 Dickschat et al., 2007; Schulz, Fuhlendorff, & Reichenbach, 2004).

49

50 There are some disagreements in the literature about the solubility of Geosmin and 2-MIB, as Ikai
51 et al. (2003) state that they are water soluble, while the general understanding is that they are lipid
52 soluble (Tucker, 2000). They are mainly absorbed via the gills or skin (Tucker, 2000) and
53 accumulate in lipid-rich tissues (Howgate, 2004). High dietary lipid levels or low digestive protein
54 to energy ratios in feed stimulate fat accumulation in fish tissues (Ding et al., 2010; Luo, Xu, Teng,
55 Ding, & Yan, 2010; Santinha, 1999), and are supposed to cause off-flavours in fish. Typically,
56 the 2-MIB levels in channel catfish (*Ictalurus punctatus*) with high tissue fat content (> 2.5%)
57 were three times higher than in lean fish (< 2%) (Peter B. Johnsen & Lloyd, 1992). Recirculated
58 aquaculture systems (RAS) have low water exchange rates, resulting in high abundance of
59 microorganisms, both in the biofilter and in the rearing water. This may produce off-flavours and
60 cause the accumulation of these in fish. Fish with intense muddy flavours have low sale value and
61 are not well received in most markets. Thus, removal of muddy flavour before harvest is necessary.
62 The most efficient method is purging in clean fresh water; however, this is resource demanding
63 and time consuming (Burr, Wolters, Schrader, & Summerfelt, 2012). The depuration efficiency is

64 mainly influenced by the fat content in fish, and fatty fish need more time to be purged in
65 freshwater than lean fish (Peter B. Johnsen & Lloyd, 1992; Peter B Johnsen, Lloyd, Vinyard, &
66 Dionigi, 1996). In addition to purging, oxidants such as ozone, H₂O₂, and ClO₂ have also been
67 extensively used to improve water quality. These strong oxidants can disinfect water by reducing
68 the concentration of microbes (Westerhoff, Nalinakumari, & Pei, 2006), and directly oxidize
69 geosmin or 2-MIB in fish meat (Zhang et al., 2016). However, the low level (0.25-0.28 mg L⁻¹) of
70 ozone used in the RAS was not effective at reducing levels of off-flavours, neither in rearing water,
71 nor in the fish fillets (Schrader, Davidson, Rimando, & Summerfelt, 2010). Lindholm-Lehto and
72 Vielma (2019) recently reviewed the challenges of controlling off-flavours in RAS. They
73 concluded that purging with fresh water is the most effective and economical method to reduce
74 off-flavours in fish, although many methods have been studied and tested for the removal of off-
75 flavours, including biological degradation or physical absorption.

76
77 The aim of this study was to investigate how the accumulation, distribution, and depuration of
78 geosmin and 2-MIB were affected by dietary protein and lipid levels in Japanese seabass
79 (*Lateolabrax japonicus*) raised in a freshwater RAS.

81 2 MATERIALS AND METHODS

82 Healthy Japanese seabass (initial weight, 0.11 kg) were placed into 18 tanks at the beginning of
83 the experiment in RAS (30 fish per tank). Six extruded diets were formulated based on a 3×2
84 factorial design with three crude protein levels (420, 450, and 490 g kg⁻¹) and two crude lipid levels
85 (150 and 180 g kg⁻¹); A constant level of Peruvian fish meal (225 g kg⁻¹) and Soybean meal (203
86 g kg⁻¹) were included in each diet with varied inclusions of soy protein concentrate (110-170 g
87 kg⁻¹), wheat gluten (26-130 g kg⁻¹) and canola meal (79-132 g kg⁻¹) as sources of protein. A varied
88 inclusion of marine fish oil (70-75 g kg⁻¹) and soy oil (31-67 g kg⁻¹) were used to provide the lipid.
89 All the diets were extruded at the Feed Technology Laboratory of the Feed Research Institute,
90 Chinese Academy of Agricultural Sciences in Beijing. All the dry ingredients were ground with a
91 hammer mill through a 0.18-mm screen, mixed, preconditioned and extruded in a twin-screw
92 extruder (MY56X2A, Muyang, Jiangsu, China) with 4.0-mm die plate. The extrusion process was
93 optimized to obtain a bulk density > 420 g L⁻¹ in the pellets before drying, in order to facilitate
94 floating of the feed after drying and coating with lipid. The obtained extruded pellets were forced-

95 air dried to 950 g dry matter kg⁻¹ at ambient temperature and then coated with oils with a ZJB-40
96 vacuum coater.

97

98 Table 1 shows the main chemical composition of these diets. Each diet was randomly assigned to
99 three of eighteen tanks. Fish were hand-fed three times per day for a 15-week accumulation trial,
100 and feed intake and uneaten pellets were recorded daily for the first 12 weeks. Feed intake was not
101 assessed during the last 3 weeks, due to disturbing the fish by repeated stripping of the fish to
102 obtain feces for digestibility assessment. At the beginning of the 16th week, a ten-day depuration
103 period with starvation was initiated. Water and fish tissues were sampled for analysis at the end of
104 the accumulation and depuration periods.

105

106 **2.1 Recirculated aquaculture system, water quality and depuration period**

107 The recirculated aquaculture system comprises 24 culture tanks (1 m³ in volume) and water
108 treatment units, supplied by Goldbill (Ningde, Fujian, China). The rearing water from the tanks
109 was collected in a drum filter for the removal of particles, and water was disinfected by UV light.
110 Water was then pumped from the drum filter into the biofilter. The biofilter provided substrate for
111 nitrobacteria that nitrified ammonia. After bio-filtration, the water was pumped back to the culture
112 tanks. The water flow was 8 to 9 L min⁻¹ in each of the 24 tanks. The total volume of water in the
113 system was approximately 24 m³, and 12.5% of the water was replaced by freshwater every day.

114

115 Water quality was measured in the tanks every day after feeding. Oxygen was assessed using a
116 Dissolved oxygen meter (AZ8401, Az Instrument Corp., Taiwan), and ranged from 5.5 to 6.5 mg
117 l⁻¹ in tank. Water temperature was decreased gradually from 27.5 °C to 22.5 °C, and the pH was
118 maintained above 6.5 by adding lime slurry (pH=10) every day. A “Water quality regulator”
119 (Miracle Animal, FFC research institute, Okayama, Japan) was added into the system weekly for
120 controlling concentrations of total ammonia and nitrite, which were below 5 mg l⁻¹ and 0.25 mg
121 l⁻¹, respectively. Total ammonia and nitrite were assessed using commercial testing kits (Yi'er
122 Biology Engineering Co., Ltd., Guangzhou, Guangdong, China). Seawater, disinfected with
123 sodium hypochlorite, with salinity at 25 ppt, was added twice (on the 7th and 9th weeks, 2 m³ new
124 water each time) into the system. This resulted in salinity in the RAS at 2 ppt. The depuration tank
125 was filled with 22 m³ of freshwater, and this water was partially replaced by 11 m³ tap water on

126 the 5th day of depuration. The clean water was aerated to minimize residual chloride before it was
127 distributed to the fish.

128

129 **2.2 Water sampling and fish tissue preparation**

130 At the end of the accumulation trial, 6 fish with average individual weights of about 0.4 kg, were
131 randomly selected from each tank. Two were slaughtered, and the dorsal and ventral muscle tissues
132 without skin and bone were sampled, sealed in cups, and stored at -80 °C. The remaining fish were
133 injected with PIT tags (Smartrac N.V., Amsterdam, Netherland) after being anesthetized by 0.9 g
134 L⁻¹ of MS-222. All tagged fish were pooled into a 22 m³ holding tank with clean fresh water and
135 starved for 10 days for depuration. After depuration, two fish from the same feeding tank in the
136 accumulation trial were identified using PIT tags and sampled for analysis. Water samples for
137 muddy flavour analysis were collected from different sections of RAS, sealed into bottles, and
138 stored at -80 °C.

139

140 **2.3 Analysis of geosmin and 2-MIB in fish tissues and water**

141 Geosmin and 2-MIB were extracted by headspace solid-phase microextraction (HS-SPME) using
142 a 65 µm DVB/PDMS fibre (57310-U) in a manual holder (57330-U) (Sigma-Aldrich, St. Louis,
143 MO, USA). Approximately 5 g of fish tissue was weighed and homogenized with ultrapure water.
144 The mixture was transferred to a 10 mL glass bottle with 5 µL of internal standard solution (DHN)
145 (10 ng µL⁻¹ Decahydro-1-naphthol in methanol) and heated in a microwave reactor for 3 min. Pure
146 nitrogen (99.999%, 75 mL min⁻¹) was used to carry the stream (steam and off-flavours) to a
147 condenser that held a temperature of 4 °C. Water for the analysis of muddy flavour components
148 was collected in 15 mL extraction bottles with Teflon-faced silicone septa caps (Agilent
149 Technologies, Palo Alto, CA, USA). The solution volume was replenished to 10 mL with ultrapure
150 water, and 3 g of NaCl was added. The extraction bottle was heated in a water bath using a heating
151 magnetic stirrer (IKA RET basic, Staufen, Germany), and the SPME fiber was injected through
152 the septa. The rotation speed was 1100 rpm, temperature was set to 60 °C, and the extraction time
153 was 40 min. After extraction, the SPME fiber was transferred and injected into the operated
154 injector of a gas chromatograph-mass spectrometer (GC-MS, Agilent 7890B-7000C, Agilent
155 Technologies, Palo Alto, CA, USA) for desorption. Desorption was carried out by heating the fiber

156 to 250 °C with a flow of carrier gas (high-pressure He, 0.45 MPa) for 2 min. The temperature
157 program of gas chromatography was 50 °C (2 min), raised at 10 °C min⁻¹ to 200 °C (1 min), and
158 at 50 °C min⁻¹ to 250 °C (2 min). The temperatures of the transfer line and ion source were
159 maintained at 280 °C and 230 °C, respectively. The electron energy was 70 eV, and quantification
160 of geosmin and 2-MIB was performed using the selected ion monitoring mode of the m z⁻¹ 112
161 and 95 fragments, respectively. After 21 min, the relative response ratios of geosmin and 2-MIB
162 to DHN in the tissues were measured.

163
164 To convert the relative response ratios to actual values, the standard curves of geosmin and 2-MIB
165 in tissues were plotted. Mixed standard samples were prepared by blending equal weights of the
166 dorsal tissues and ventral tissues. A standard solution (100 ng μL⁻¹ (+/-)-geosmin and 2-
167 methylisoborneol, Sigma-Aldrich, St. Louis, MO, USA) was diluted to 10 ng μL⁻¹ using methanol
168 in advance, and eight pieces of mixed standard tissues were injected with 0, 0.5, 1, 2.5, 12.5, 25,
169 50, and 75 μL of the diluted standard solution, respectively. The relationships between the response
170 ratio and concentration were linear, and the actual concentrations of geosmin and 2-MIB in tissues
171 were calculated from these curves.

172
173 Fifty mL of water sample were added to a 100 mL extraction bottle with 15 g of NaCl, 5 μL of
174 DHN, and a small magnetic rotor. For the standard curve, each of six 150 mL extraction bottles
175 were filled with 120 mL of ultrapure water, 36 g of NaCl and 5 μL of DHN. Aliquots of 0, 0.3, 0.6,
176 1.2, 3.0, and 4.8 μL of the diluted standard solution were then added to the bottles, which were
177 subjected to the same protocol as the tissues.

178

179 **2.4 Analysis of fat content in fish tissues**

180 The tissues remaining after off-flavour extraction were dried (temperature: -50 °C, pressure:
181 <0.1Pa, duration: 24h) in a vacuum freeze dryer (SJIA-10N-50A, Shuangjia Instrument Co. Ltd.,
182 Ningbo, Zhejiang, China). Dried tissues were ground mildly and analyzed for fat content by
183 SoxROC Extractor (SX-360, OPSIS AB, Furulund, Sweden).

184

185 **2.5 Analysis of microbes in water**

186 For bacterial analysis, water samples (300 mL) were filtered through 0.2 µm polycarbonate
187 membranes. DNA extraction and quality verification, PCR amplification, high-throughput
188 sequencing and bioinformatic analysis were performed refer to the previous study (Li et al., 2020).

190 2.5.1 DNA extraction, amplification, and library construction

191 Total genomic DNA was extracted using DNA PowerSoil Kit following the manufacturer's
192 instructions. Quality and quantity of DNA was verified with NanoDrop 2000 and agarose gel.
193 Extracted DNA was diluted to a concentration of 1 ng/µL and diluted DNA used as template for
194 PCR amplification of bacterial 16S rRNA genes with the barcoded primers and Takara Ex Taq
195 (Takara, Japan). The 16S rRNA genes were amplified using bacterial primer set 343F (5' -
196 TACGGRAGGCAGCAG)/798R (5' - AGGGTATCTAATCCT). An Illumina Sequencer MiSeq
197 (Illumina Inc. San Diego, CA, USA) was used for high-throughput sequencing by OE
198 Biotechnology Company (Shanghai, China).

200 2.5.2 Bioinformatic analysis

201 Raw paired-end reads were subjected to quality control procedures using Trimmomatic software
202 (Bolger et al, 2014). After trimming, paired-end reads were assembled using FLASH software
203 (Reyon et al, 2012). Clean reads were subjected to primer sequences removal and clustering to
204 generate operational taxonomic units (OTUs) using Vsearch software with 97% similarity cutoff
205 (Edgar, 2011), and chimeric sequences identified and removed using UCHIME (Edgar, 2016). The
206 representative read of each OTU was selected using QIIME package. For the observed species,
207 Shannon-Wiener index and Simpson's diversity index were calculated based on the OTUs.

209 **2.6 Analysis of the ratio of digestible protein on digestible energy (DP:DE)**

210 Feces was collected at the end of the study by careful stripping from the pectoral fin towards anus
211 pooled by tank and frozen at - 20 °C until freeze dried to constant weight and homogenized by
212 pestle and mortar. Gross energy in feed and feces was analyzed by bomb calorimeter (Parr-1271,
213 Parr company, USA). Determination of yttrium oxide content in feed using ICP-MS inductively
214 coupled plasma mass spectrometer (7900, Agilent, USA). Crude protein (CP) was assessed by an
215 automated Kjeldahl analyzer (KD-310, OPSIS, Sweden). Gross energy was analyzed by bomb
216 calorimetry (Parr-1271, Parr company, USA). Apparent digestibility coefficients of nitrogen and

217 gross energy were calculated as: $1 - (Y_{2O_3} \text{ in feed} \times \text{nutrient or energy in feces}) / (Y_{2O_3} \text{ in feces} \times$
218 $\text{nutrient or energy in feed})$. DP:DE was calculated as g digestible CP / MJ digestible energy. DP:DE
219 values for each of the 6 diets are shown in Table 1.

220

221 **2.7 Ethics statement**

222 This study did not involve any endangered species. Japanese seabass (*Lateolabrax japonicus*) is
223 not the protected species by Chinese law. It is a commercially harvested and farmed species in
224 China. During the feeding period and sampling procedures, the experimental fish were maintained
225 in compliance with the Laboratory Animal Welfare Guidelines of China (Decree No. 2 of Ministry
226 of Science and Technology, issued in 1988).

227

228 **2.8 Statistical analysis**

229 Statistical analysis, plots, correlation (Spearman's test), regression analysis and curve fitting were
230 carried out in R-studio (Boston, MA, USA). The Shapiro-Wilk normality test and homogeneity
231 test of variances were carried out in advance. Significant differences between dietary treatments
232 and their interactions were tested by one-way and two-way analysis of variance (ANOVA), using
233 a significance (α) of 0.05. Bonferroni's test and Duncan's test were used for multiple comparisons
234 (post hoc tests) when variances were equal, or the Kruskal-Wallis test and Nemenyi test were used.

235

236 **3 RESULTS AND DISCUSSION**

237 **3.1 Occurrence of microbes that synthesize components causing muddy flavour** 238 **and oxidize nitrogen in the RAS water, and concentration of geosmin and 2-MIB in** 239 **the rearing water.**

240 The concentration of geosmin in water from the depuration tank rose from trace amounts (5.1 ng
241 L^{-1}) at the onset of depuration to 45.9 ng L^{-1} at the end of the 10-day period. The water in the RAS
242 tank with fish contained 169 ng geosmin L^{-1} , and the water in the drum filter contained 184 ng
243 geosmin L^{-1} . Corresponding values for 2-MIB were 21.4 ng L^{-1} at the end of depuration, while the
244 concentrations of 2-MIB were 45.4 ng L^{-1} in the RAS tank and 41.3 ng L^{-1} in the drum filter.

245 The diversity indices, as assessed by of high-throughput sequencing, revealed 698 microbial
246 species in rearing tank water, and 729 species in the water of the drum filter. The Shannon-Wiener
247 Index were 6.26 and 6.61, while the Simpson's Diversity Index were 0.94 and 0.95 in tanks and
248 drum filter, respectively. The microbial structures showed that proteobacteria was the predominant
249 phylum both in the rearing tanks and in the drum filter, accounting for 54% of the total bacteria in
250 both (Figure 1 a). Actinobacteria, accounting for 1.0 % of bacteria in the water of the drum filter
251 and 1.2 % in the tanks with fish, as well as Cyanobacteria accounting for 0.03% in the drum filter
252 and 0.05% in the RAS tanks are the most probable sources for geosmin and 2-MIB. These levels
253 are consistent with previous observations that Actinobacteria and Cyanobacteria can cause intense
254 off-flavours, even when these bacteria represent low (0.007-0.9%) proportions of the total bacteria
255 (Lukassen et al., 2017). In Figure 1 (b), nitrobacteria were also assessed. *Nitrosomonas*, which
256 oxidizes ammonia to nitrite, represented 0.7 %, in the drum filter and 1.1 % in the rearing tanks.
257 Corresponding values for *Nitrospira*, which further oxidizes nitrite to nitrate, were 1.0 % in the
258 drum filter and 1.5 % in the tanks with fish. Although the nitrate nitrogen does not directly affect
259 the geosmin and 2-MIB levels in the water (Schrader, Davidson, & Summerfelt, 2013), low
260 nitrogen level in the water might be an efficient way to control the growth of nitrogen-dependent
261 actinobacteria and cyanobacteria (Cottingham, Ewing, Greer, Carey, & Weathers, 2015; Dai et al.,
262 2018; Saadoun, Schrader, & Blevins, 2001). The observed differences indicate that the fish rearing
263 tanks are prioritized water sampling points for controlling off-flavour in RAS.

264

265 3.2 Accumulation of geosmin and 2-MIB in dorsal and ventral tissues

266 At onset of the depuration, the lipid concentration in dorsal tissues was lean, only 19% of the lipid
267 content in ventral tissue. The dorsal tissue also had lower concentration of 2-MIB (31% of that in
268 ventral tissue) and geosmin (19%) (Table 2). Lipid concentration both in dorsal and ventral tissues
269 were significantly related to dietary lipid concentration. No significant correlation between dietary
270 protein or lipid concentrations and 2-MIB or geosmin were seen in ventral tissue, and no significant
271 interactions were evident.

272

273 The main effect of dietary protein level on 2-MIB and geosmin concentration in dorsal tissue,
274 however, was highly significant (Table 2). The concentration of 2-MIB in this tissue decreased
275 from an average of 0.69 to 0.44 $\mu\text{g kg}^{-1}$ when dietary protein level increased from 420 to 490 g

276 kg⁻¹. Similarly, the concentration of geosmin decreased from 5.54 to 2.96 µg kg⁻¹. This significant
277 response to protein, and corresponding lack of response to lipid in the feeds may be due to preferred
278 binding to lean tissues, reflecting the water-soluble features of 2-MIB and geosmin (Ikai et al.,
279 2003).

280

281 A more reasonable explanation is that the various diets provide different amounts of substrate for
282 microbial growth. The two main sources of nutrients for bacterial growth from crude protein are
283 indigestible nitrogenous components and endogenous nitrogen, both being excreted in feces. Also,
284 amino acids are deaminated and ammonia is excreted in situations where the essential amino acid
285 composition is imbalanced, or protein is in excess. The ratio between digestible protein and
286 digestible energy (DP:DE) is a good measure for the latter (Einen and Roem, 1997). DP:DE values
287 ranging from 20.6 to 25.6 g DP (MJ DE)⁻¹ were seen in the diets (Fig. 1).

288

289 The regressions of DP:DE on 2-MIB and geosmin in dorsal tissue are presented in Fig. 3. Only
290 values from this tissue are presented since the ventral tissues were not significantly affected by the
291 DP:DE ratio of the feeds. Increasing DP:DE was accompanied by a linear decrease on 2-MIB, with
292 moderately high determination ($R^2 = 0.55$). The concentration of geosmin also decreased when
293 DP:DE increased, and the response was best described ($R^2 = 0.98$) by a 2nd degree curvilinear
294 regression. The response was steep when increasing DP:DE from 20.6 to 24.3 g MJ⁻¹, while only
295 a marginal response was seen by a further increase in DP:DE to 25.6 g MJ⁻¹.

296

297 The DP:DE ratio was linearly and highly determined ($R^2 = 0.90$) by dietary crude protein
298 concentration (Table 3). Dietary ash and the analytical residue both accounted for an R^2 at 0.48,
299 while the determination of dietary lipid on DP:DE was only $R^2 = 0.37$. This indicates that dietary
300 protein played an important role in limiting accumulation of 2-MIB and geosmin in lean tissues
301 than lipids, minerals and various indigestible organic dietary components contributing to the
302 analytical residues. This finding should be subject to further investigation. The results were in
303 keeping with previous findings of a positive correlation between lipids in feed and tissues, and a
304 negative correlation between dietary protein and tissue lipids (Santinha, 1999). Intake of dietary
305 crude protein during the first 12 weeks of feeding on dorsal tissue 2-MIB was significantly ($R^2 =$
306 0.83) explained by a 2nd degree polynomial regression. Dietary gross energy intake was not

307 significantly ($R^2 = 0.05$) related to tissue 2-MIB concentration. Simultaneously, the determination
308 of crude protein intake on dorsal tissue geosmin was moderate ($R^2 = 0.38$), while that of dietary
309 energy intake was low ($R^2 = 0.23$).

310

311 The ratio of 2-MIB on geosmin was slightly higher at the beginning of the 10-day period with
312 clean water and fasting, than after depuration (Fig. 4). This indicates that 2-MIB was removed
313 from the tissues more efficiently than what was the case with geosmin, in keeping with the
314 hypothesis of a previous review (Rurangwa & Verdegem, 2015).

315

316 As can be seen from Table 2 and the clusters in Fig. 5, the tissue lipid content affected the
317 accumulation of both geosmin and 2-MIB. Prior to depuration, the lean dorsal tissue contained 7.6
318 $\mu\text{g kg}^{-1}$ geosmin and 0.9 $\mu\text{g kg}^{-1}$ 2-MIB, distributed within a narrow range. The concentration of
319 geosmin in the fatty ventral tissue ranged from 11.1 to 35.3 $\mu\text{g kg}^{-1}$, while that of 2-MIB ranged
320 from 0.8 to 2.7 $\mu\text{g kg}^{-1}$. Thus, the results in Table 2 and Fig. 5 (a and c) confirm that the fatty
321 ventral tissue accumulated off-flavour components to a much higher degree than the lean dorsal
322 tissue. ANOVA also revealed a significant ($P < 0.001$) difference in lipid, geosmin, and 2-MIB
323 levels between dorsal and ventral tissues. This higher capacity of storing 2-MIB and geosmin in
324 fatty tissues distribution of lipid and muddy flavours in fish is consistent with previous findings
325 on barramundi (*Lates calcarifer*) (Percival, Drabsch, & Glencross, 2008). Furthermore, Johnsen
326 and Lloyd (1992) found that channel catfish with more than 2.5% accumulated body fat contained
327 3 times as much 2-MIB as leaner fish with less than 2.5% body fat when exposed to water with
328 0.5 $\mu\text{g 2-MIB L}^{-1}$ for eight hours. However, body fat content and dietary composition may not be
329 the only factors controlling the uptake and deposition of components causing off-flavours.
330 Experiments with rainbow trout have shown that there was no significant correlation between
331 tissue lipid (1.9-10.6 %) and geosmin or 2-MIB in rainbow trout (*Oncorhynchus mykiss*) (Mikael
332 A. Petersen, Hyldig, Strobel, Henriksen, & Jørgensen, 2011). The concentrations of geosmin and
333 2-MIB in the rearing water seemed to be a main driving force for accumulation in trout tissues,
334 but Petersen also found a significant positive correlation between fish size and accumulation of 2-
335 MIB and geosmin. Simultaneously, no significant correlation was found between sensory traits
336 and tissue lipid in yellow perch (*Perca flavescens*) (González et al., 2006) or in barramundi (Frank,
337 Poole, Kirchhoff, & Forde, 2009).

338

339 **3.3 Depuration of geosmin and 2-MIB from Japanese seabass**

340 Depuration with freshwater is the most common procedure used to remove muddy flavours, and
341 notable changes can be seen during the first 24 hours of treatment (Peter B. Johnsen & Lloyd,
342 1992; Robertson, Jauncey, Beveridge, & Lawton, 2005; Rohani, Normah, Zahrah, Utama, &
343 Saadiah, 2009). For example, the concentrations of muddy flavours can decrease to below the
344 detection threshold after 7 days (Mikael A. Petersen et al., 2011; Robertson et al., 2005). In this
345 experiment, the effect of depuration was evident. After 10 days of depuration, the concentration
346 of geosmin in the ventral tissue was reduced to less than $18.7 \mu\text{g kg}^{-1}$, while that of the dorsal
347 tissue had values between 0.6 and $7.4 \mu\text{g kg}^{-1}$ (Figure 3 b and d). Simultaneously, the concentration
348 of 2-MIB in ventral tissue was reduced to less than $2.0 \mu\text{g kg}^{-1}$, while the concentration of 2-MIB
349 in the leaner dorsal tissue was between 0.2 and $0.9 \mu\text{g kg}^{-1}$. The clusters of geosmin were clearly
350 separated from those of 2-MIB before depuration. After depuration these clusters were overlapping.
351 This was mainly due to higher concentration of geosmin than that of 2-MIB. Reduction in the
352 ventral clusters was the highest. The concentration of both geosmin and 2-MIB in ventral tissue
353 decreased by nearly 50%). This indicates that rate of depuration may be dose dependent, with
354 higher rate of removal with high tissue concentration. This result is consistent with a previous
355 study that showed the similar depuration rates (approximately 75% removal of geosmin and 2-
356 MIB in 10 days) in Atlantic salmon (*Salmo salar*) (Davidson et al., 2014), although Rurangwa and
357 Verdegem (2015) suggested that the depuration rate of geosmin should be slower than that of 2-
358 MIB. Clearance of both geosmin and 2-MIB during depuration was slower in the lean dorsal than
359 in the fatty ventral tissue. This indicates that the rate of depuration is more efficient from fatty than
360 lean tissues.

361

362 Both geosmin and 2-MIB were initially found at only low levels in the depuration pond water
363 (Figure 2), and the concentrations of both were significantly increased when the depuration period
364 was completed. The combination of fasting fish and adding fresh water into the depuration tank
365 resulted in the removal of geosmin and 2-MIB from fish tissues. However, the current purging
366 procedure was not sufficient to render the fish tissues without muddy flavour. The threshold
367 concentrations for detection are 0.25 - $0.5 \mu\text{g kg}^{-1}$ for geosmin and 0.1 - $0.2 \mu\text{g kg}^{-1}$ for 2-MIB
368 (Grimm, Lloyd, & Zimba, 2004). Previous experiments on fatty fish, such as Arctic charr

12

369 (*Salvelinus alpinus*) (Houle et al., 2011), also indicated that high lipid content in the fish
370 complicates purging if only fresh water is employed. When Davidson (2014) tried disinfecting the
371 depuration tank with hydrogen peroxide (H₂O₂) prior to purging fish, a rapid reduction of geosmin
372 and 2-MIB levels in Atlantic salmon was observed. This indicates that the pre-treatment of
373 depuration tanks or water with environmentally friendly oxidants might be useful to increase the
374 efficiency of purging of fatty fish when by the combined use of fasting and clean freshwater.

375

376 **4 CONCLUSIONS**

377 Japanese seabass, kept in a Recirculated Aquaculture System (RAS) were fed 6 diets with different
378 contents of protein and lipid for 15 weeks. Accumulation of the muddy flavor components geosmin
379 and 2-MIB in was decreased by increasing ratio of digestible protein on digestible energy (DP:DE).
380 The decrease was linear for 2-MIB and curvilinear for geosmin with reduced accumulation by
381 increasing the CP:DE ratio from 20.6 to 24.3 g DP per MJ DE. Understanding the underlying
382 mechanisms for the dependence of high DP:DE to reduce tissue accumulation of geosmin and 2-
383 MIB requires more research. Both geosmin and 2-MIB were accumulated at higher rates in fatty
384 ventral tissues than in lean dorsal tissues. Ten days purging by keeping the fish in freshwater and
385 fasting them resulted in similar rates of removal of geosmin and 2-MIB. This depuration was not
386 sufficient to produce high-quality fish, and this purging procedure should be combined with other
387 means to reduce geosmin and 2-MIB-producing *Actinobacteria* and *Cyanobacteria* in water of the
388 fish rearing tanks of the RAS.

389

390 **ACKNOWLEDGEMENTS**

391 This study was supported by the National Natural Science Foundation of China (Grant No:
392 31502182), National Key R&D Program of China (Grant No:2019YFD0900203), Provincial Key
393 Research and Development Program of Zhejiang (Grant No: 2019C02048), and Public Welfare
394 Technical Applied Research Project of Zhejiang Province (LGN19C190001).

395

396 **CONFLICT OF INTEREST**

397 The authors declare no conflict of interest.

398

399 AUTHOR CONTRIBUTIONS

400 Qiang Lu and Yuan Zou were involved in data analysis, and manuscript writing. Yuexing Zhang
401 designed the experiment, obtained funding and was involved in writing and manuscript revisions.
402 Liying Huang, Haokun Liu and Xiaolong Yin provided essential reagents and materials, and were
403 involved in manuscript revisions. Qiang Lu, Yuan Zou and Zhiyong Dong conducted the
404 experiment. Trond Storebakken was involved in design, manuscript writing and revisions.

405

406 DATA AVAILABILITY STATEMENT

407 The authors confirmed that the data supporting the results in this study are presented in tables and
408 figures in this published article.

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558 TABLE 1 Main chemical compositions of the experimental diets (in dry matter)

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Proximate Composition, kg ⁻¹	Diet no. (Protein/Lipid)					
	D1 42/15	D2 42/18	D3 45/15	D4 45/18	D5 49/15	D6 49/18
Dry matter, g	924	933	934	931	926	928
Crude protein, g	423	411	458	452	494	496
Crude lipid, g	152	185	154	187	141	174
Ash, g	73	71	72	72	74	72
Gross energy, MJ	22.4	23.1	22.5	23.0	22.5	23.2
DP/DE ¹ , g MJ ⁻¹	22.0	20.6	23.7	22.6	25.6	24.3

560 ¹DP/DE is ratio of digestible protein on digestible energy.

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561 TABLE 2 The concentrations (wet weight) of lipid, geosmin and 2-MIB in dorsal and ventral
 562 tissues of Japanese seabass fed diets with different levels of protein and lipid.¹
 563

	Dorsal tissue			Ventral tissue		
	lipid, g kg ⁻¹	2-MIB, µg kg ⁻¹	geosmin, µg kg ⁻¹	lipid, g kg ⁻¹	2-MIB, µg kg ⁻¹	geosmin, µg kg ⁻¹
One-way ANOVA						
D1 (42/15)	13.5 ^{bc}	0.67 ^{ab}	4.76 ^b	70.3	1.71	19.1
D2 (42/18)	20.8 ^a	0.73 ^a	6.58 ^a	72.6	1.70	20.3
D3 (45/15)	12.4 ^{bc}	0.55 ^{bc}	3.03 ^c	55.6	2.45	29.8
D4 (45/18)	14.3 ^b	0.42 ^c	3.47 ^c	80.6	1.76	21.1
D5 (49/15)	10.1 ^c	0.47 ^c	3.08 ^c	46.9	1.84	17.4
D6 (49/18)	11.7 ^{bc}	0.41 ^c	2.85 ^c	78.6	1.21	18.7
Pooled s.e.m. ²	3.42	0.12	1.33	12.21	0.36	4.08
Two-way ANOVA						
<i>P</i> -value						
Protein	< 0.01	< 0.01	< 0.001	0.62	0.49	0.16
Lipid	< 0.05	0.26	0.30	< 0.05	0.30	0.65
Protein * Lipid	0.23	0.46	0.16	0.37	0.74	0.35
Main effect of crude protein ³						
420	16.6 ^a	0.69 ^a	5.54 ^a	71.4	1.70	19.7
450	13.2 ^{ab}	0.50 ^b	3.20 ^b	68.1	2.10	25.4
490	10.9 ^b	0.44 ^b	2.96 ^b	59.6	1.58	17.9
Main effect of lipid ⁴						
150	11.8 ^b	0.55	3.48	56.1 ^b	1.98	21.4
180	14.6 ^a	0.48	3.90	77.2 ^a	1.55	20.0

564 ¹Means of three replicate tanks. Means in each column with different superscripts are significantly
 565 different ($P < 0.05$). ²s.e.m., standard error of means. ³420, 450, and 490 g kg⁻¹ of dietary crude protein.
 566 ⁴150 and 180 g kg⁻¹ of dietary lipid.

567

568 TABLE 3 Regression analysis of dietary macronutrient concentrations or analytical residue on
569 DP:DE ratio
570

Component, x	Regression, DP:DE=	R ²
Crude protein (CP)	22.4 + 18.7x	0.895
Lipid	32.4 - 0.056x	0.37
Ash	62.7 + 1.19x	0.48
Residue ¹	31.7 - 0.036x	0.48

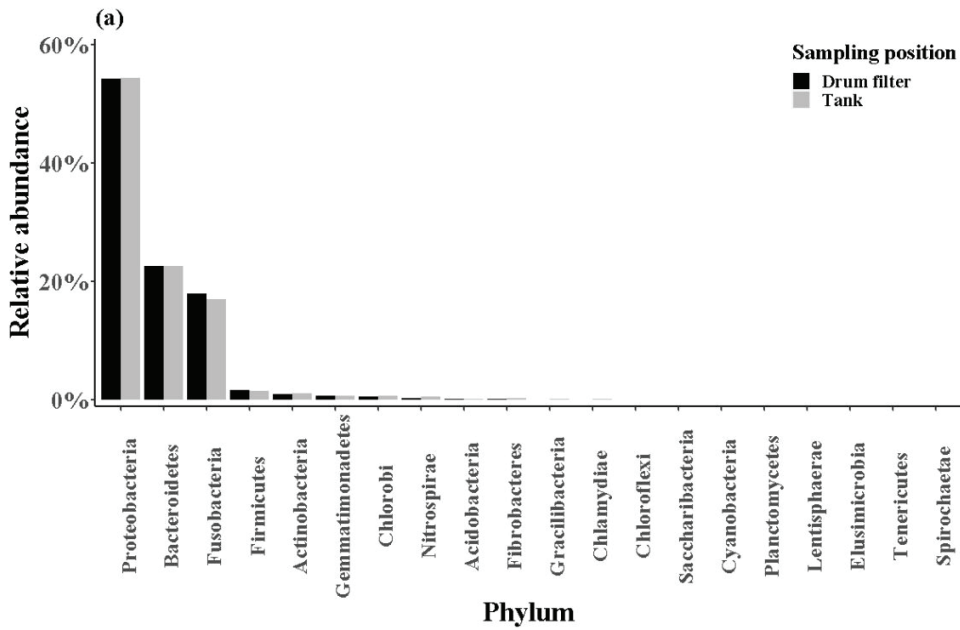
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572 ¹ Dry matter – (CP + lipid + ash)

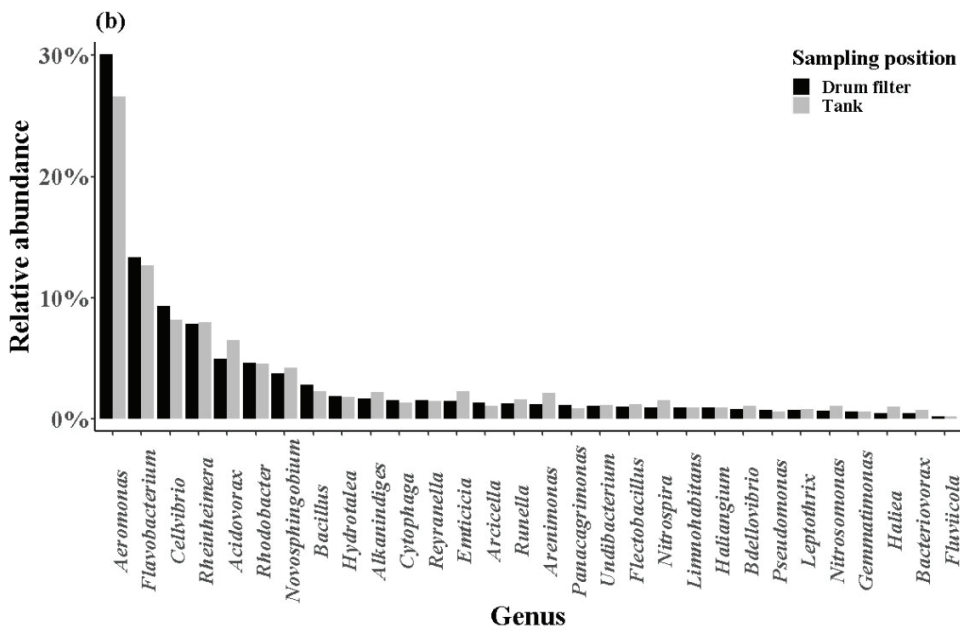
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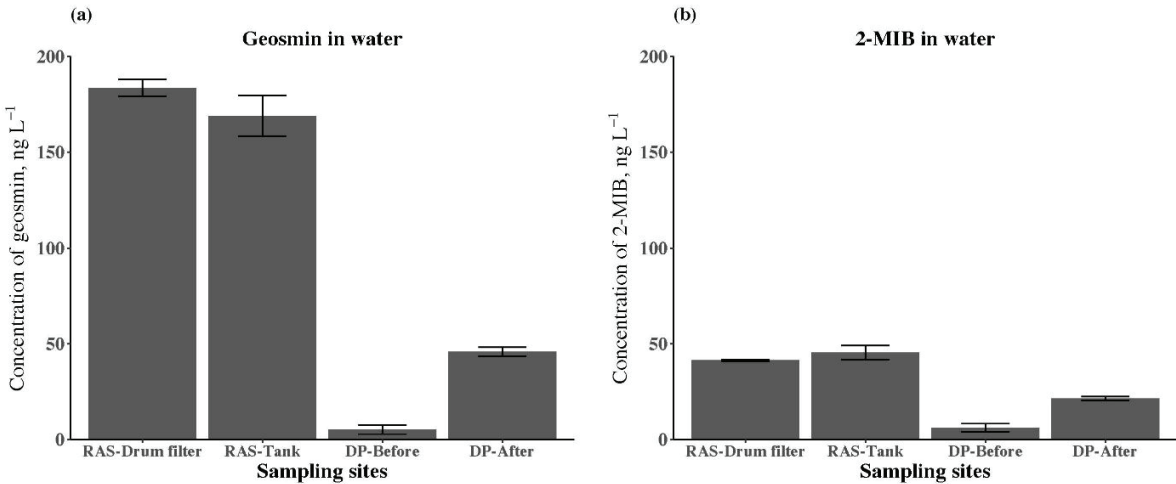
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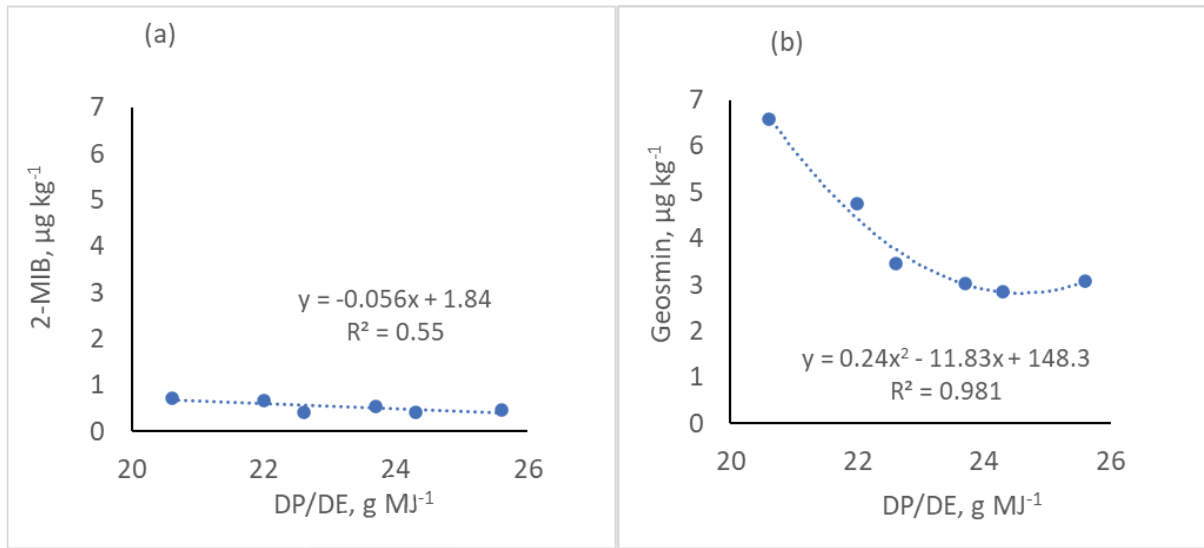
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FIGURE 1 Relative abundance of bacteria community structures of phylum (a) and genus (b) in water sampled from the drum filter (black bars) and in the raising tanks (grey bars) with fed fish.



581
582 FIGURE 2 Concentrations of geosmin and 2-MIB in the water. DP-Before and DP-After show
583 water from depuration tank before onset of the depuration period and after the depuration period,
584 respectively. Data presented as mean ± SD
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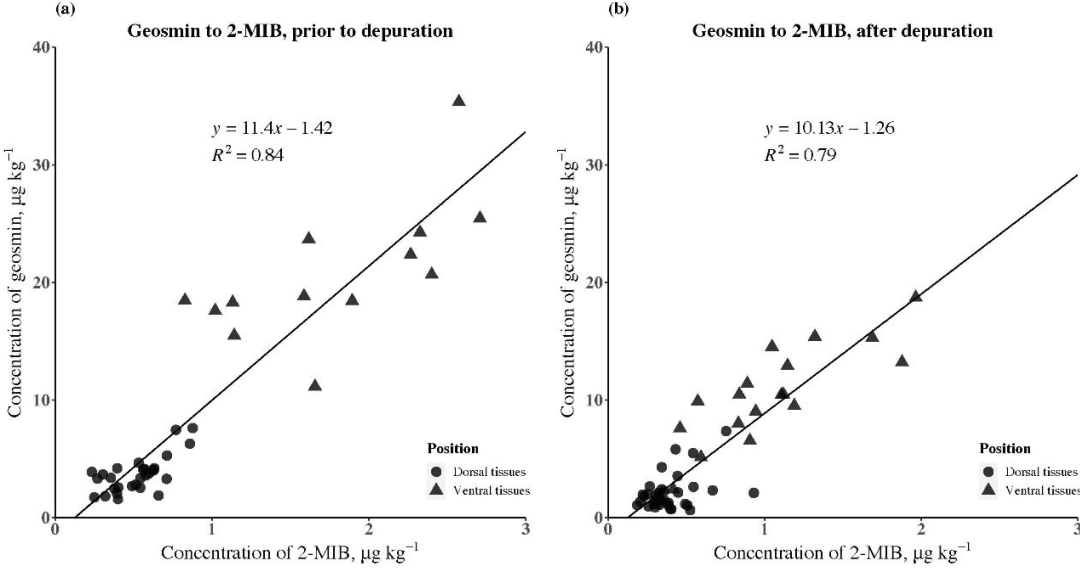


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FIGURE 3 Regression analysis of the ratio between digestible protein and digestible energy (DP/DE) on the concentration of 2-MIB (a) and geosmin (b) in dorsal tissues of Japanese seabass.

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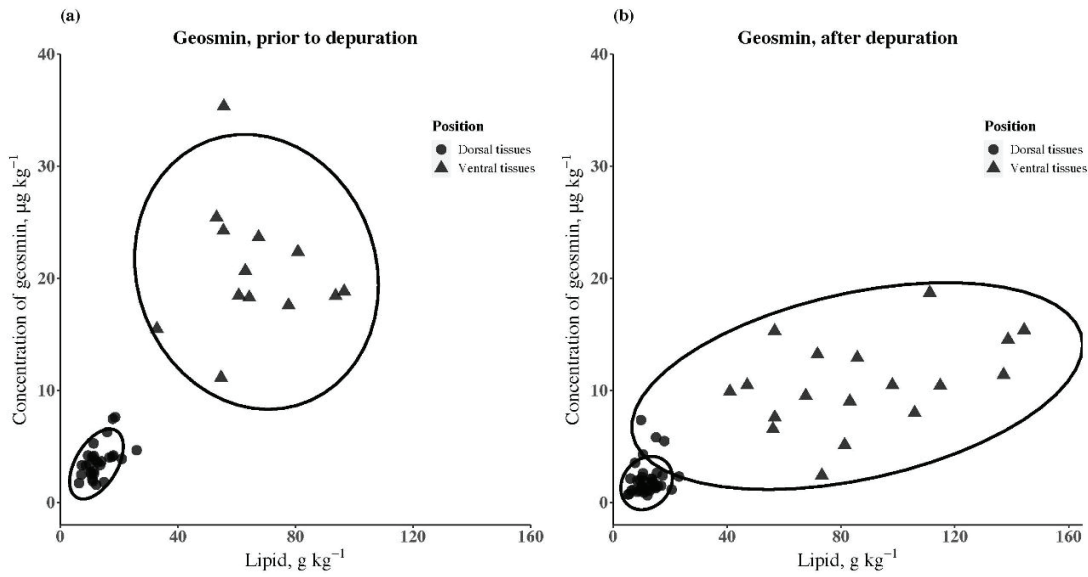
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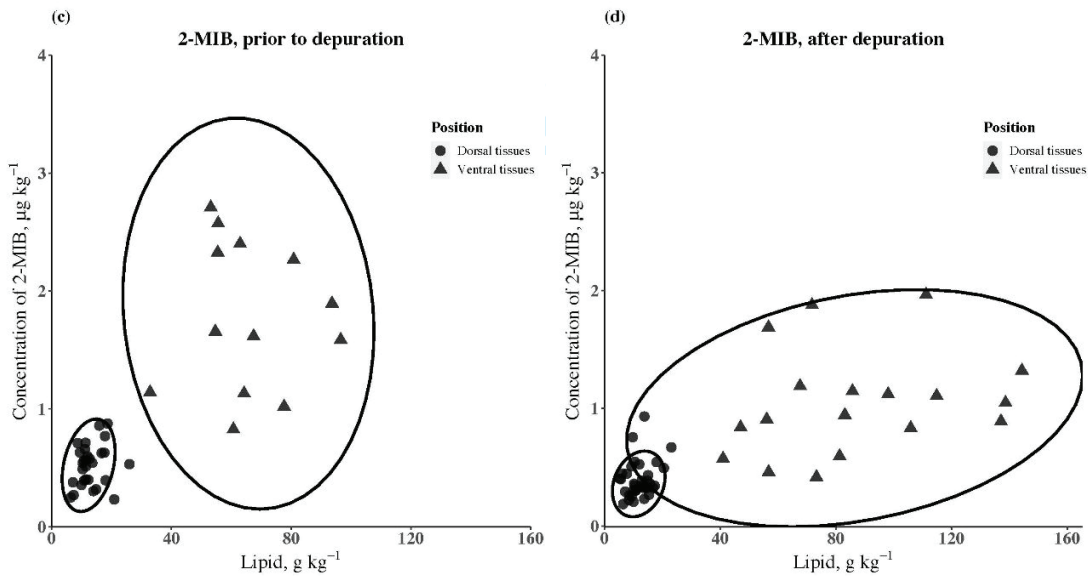
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FIGURE 4 Scatter plots of geosmin related to 2-MIB in Japanese seabass, before (a) and after (b) depuration.

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601 FIGURE 5 Scatter plots of geosmin and 2-MIB related to lipids in fish

602