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### ► **To cite this version:**

Emilie Le Luherne, Françoise Daverat, Mathieu Woillez, Christophe Pécheyran, Hélène de Pontual. Coupling natural and electronic tags to explore spawning site fidelity and natal homing in northeast Atlantic European seabass. *Estuarine, Coastal and Shelf Science*, 2022, 278, pp.108118. <10.1016/j.ecss.2022.108118>. <hal-03855407>

**HAL Id: hal-03855407**

**<https://hal.inrae.fr/hal-03855407v1>**

Submitted on 17 Aug 2025

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## Coupling natural and electronic tags to explore spawning site fidelity and natal homing in northeast Atlantic European seabass

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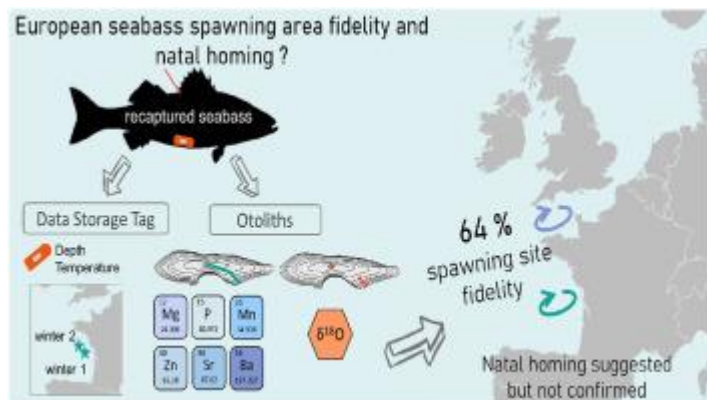
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### Abstract :

The structure and connectivity of European seabass (*Dicentrarchus labrax*) populations remain poorly known and ecological evidence is missing to support the current delineation between the northern (southern North Sea, English Channel and Celtic Sea) and southern French stocks (Bay of Biscay). Adult spawning site fidelity and natal homing were analysed by coupling Data Storage Tag (DST) information and otolith microchemistry of recaptured fish to investigate, within the study area, the population structure and connectivity in European seabass. Trajectory reconstructions inferred from DST data were used to assign a spawning area (English Channel or Bay of Biscay) to each spawning winter record. In addition, otolith composition (Mg, P, Mn, Zn, Sr, Ba and  $\delta^{18}\text{O}$ ) was measured in both larvae and adults otolith increments corresponding to a winter spawning event. We built a training dataset using coupled spawning area assignments and otolith elemental signatures (Mg, P, Mn, Zn, Sr and Ba) for winters with DST data. The training dataset was used to calibrate a Random Forest model and assign spawning areas based on otolith winter signatures outside the DST recording period. Results revealed that 64% of the seabass expressed spawning site fidelity. We also found a geographical gradient of site fidelity, with the highest proportions of spawning site fidelity found in seabass tagged at the northern and southern limits of the studied area. Significant ontogenetic effects were observed for trace elements and  $\delta^{18}\text{O}$  with ratios significantly lower in the larval stage than in the adult stage. These biases and the variability across cohorts prevented us to use the assignment model fitted on adults to study natal homing. At the larval stage, the analysis of spatio-temporal effects on otolith trace elements did not reveal any significant difference between spawning areas. However, the patterns of difference were similar for larval and adult Zn, Sr and Ba between the two spawning areas, suggesting a homing behaviour.

## Graphical abstract



## Highlights

► Investigation of seabass spawning site fidelity and natal homing. ► Data Storage Tag information was coupled to otolith microchemistry to infer spawning areas. ► Spawning site fidelity was found for 64% seabass individuals. ► Otolith tracers (elements and  $\delta^{18}\text{O}$ ) were significantly biased by ontogenetic effects. ► Homing behaviour analysis provided inconclusive results.

**Keywords** : Spawning site fidelity, metapopulation, otolith microchemistry, Data Storage Tags, European seabass *Dicentrarchus labrax*

## 55 1. Introduction

56 The structure and connectivity of exploited fish species populations is a knowledge of major importance  
57 and the correspondence between stock management units and biological populations is a key issue for  
58 sustainable fishery management (Artetxe-Arrate et al., 2019). Yet, fisheries science has a long history of  
59 mismatches between stock management and the ecology of the target species, with potential threats  
60 to the sustainability of the resource (Kerr et al., 2017).

61 Population structure and connectivity are influenced by several environmental and biological factors  
62 throughout the life cycle of the fish (Kerr et al., 2017). At the adult stage, movements and survival are  
63 primarily driven by the essential habitat requirements of the fish. Among them, spawning site fidelity  
64 and natal homing are key processes affecting population differentiation and connectivity (Petitgas et  
65 al., 2013). Investigating the reproductive behaviour of fish is challenging and requires knowledge of the  
66 location of fish in the larval and adult stages to explore natal homing and spawning site fidelity  
67 processes. Under such constraints, the combination of direct and indirect estimates of fish location from  
68 electronic and natural tags appears to be a relevant and innovative choice (Fromentin et al., 2009). Data  
69 Storage Tags (DSTs) with pressure and temperature sensors are useful tools to explore fish movements  
70 as they provide data on individual fish behaviour over several years with high temporal accuracy (de  
71 Pontual et al., 2019). Individual trajectories are reconstructed based on the correlation between the

72 environmental parameters experienced by the fish and spatio-temporal reference fields derived from  
73 satellite observations and/or operational hydrodynamic models (Woillez et al., 2016). The record time  
74 of DSTs is now long enough to study spawning site fidelity, but this technology cannot provide useful  
75 data to explore natal homing. The analysis of otolith composition is the only alternative to study the  
76 movements of individuals throughout their entire life. Otoliths are calcified structures that incorporate  
77 environmental chemical signatures throughout the life of the fish. They have a great potential to provide  
78 indirect tracers of fish movements (Campana and Thorrold, 2001). Otolith elemental composition has  
79 been extensively used to discriminate fish stocks (Tanner et al., 2016). Among the elements used for  
80 these discriminations, Sr and Ba have been successfully linked to the mixing dynamics of fresh and  
81 marine waters and have proven to be robust spatial tracers for fish habitat occupancy across a wide  
82 range of ecosystems (Elsdon et al., 2008). The oxygen isotopic ratio ( $\delta^{18}\text{O}$ ) of the otolith is also a relevant  
83 tool for fish geolocation as it differs between water masses with contrasting hydrology (LeGrande and  
84 Schmidt, 2006) and reflects temperature and salinity gradients (Trueman et al., 2012). Otolith  $\delta^{18}\text{O}$  has  
85 been frequently used to identify the marine origin of fish and differentiate fish stocks (Darnaude and  
86 Hunter, 2017). Coupling electronic tag data with otolith composition appears well suited to study  
87 population structure and connectivity and has been successfully used to infer life traits such as growth,  
88 migration, and reproductive behaviour (Darnaude and Hunter, 2017).

89 European seabass (*Dicentrarchus labrax*) is a partially migratory species that inhabits the demersal  
90 waters of the northeast Atlantic. Its life cycle consists of an offshore phase in winter during which adults  
91 reproduce, followed by larval transport to coastal and estuarine areas, and a coastal phase in summer  
92 during which the juveniles establish for a few years and adults feed (Jennings and Pawson, 1992; Beraud  
93 et al., 2018). It is a key species for both recreational and commercial fisheries, assessed in the northeast  
94 Atlantic by the International Council for the Exploration of the Sea (ICES), which has defined four stocks  
95 (Fig. 1). The present study focussed on the two stocks separated by the 48<sup>th</sup> parallel north. The northern  
96 stock includes the English Channel, the Celtic Sea and the southern part of the North Sea. The southern  
97 stock corresponds to the Bay of Biscay, excluding the northern coast of Spain. The northern stock

98 declined to the point where the European Commission agreed on emergency conservation measures in  
99 2015 (ICES, 2020a, 2020b). A better understanding of the spatio-temporal population structure and  
100 dynamics is needed to improve management, as evidence is missing to support the current delineation  
101 of these stocks (de Pontual et al., 2019). Genetic analyses revealed two lineages, one Mediterranean  
102 and one Atlantic, with a weak genetic structure for the Atlantic population (Souche et al., 2015).  
103 However, using the percentage of Mediterranean introgressive hybridisation in the genome of Atlantic  
104 seabass populations, Robinet et al. (2020) showed that the tip of Galicia and the Cotentin peninsula act  
105 as barriers to gene flow. The authors also suggested a subtle structure of the Bay of Biscay and the  
106 western English Channel populations compared to those of the eastern English Channel. Further  
107 evidence of a spatio-temporal population structure was provided by DST data in Western Brittany (i.e.,  
108 around the 48<sup>th</sup> parallel north (de Pontual et al., 2019). Western Brittany was found to be a feeding area  
109 where populations mix in summer when adult fish migrate between winter spawning areas and summer  
110 feeding grounds, showing fidelity to both essential habitats (de Pontual et al., 2019). Few western  
111 Brittany seabass have resident behaviour (de Pontual et al., 2019), suggesting that they have alternative  
112 spawning strategies.

113 The aim of the present study was to analyse the spawning site fidelity and natal homing of the northeast  
114 Atlantic seabass population. This was performed by coupling fish location inferred from DST data and  
115 otolith microchemistry from recaptured fish. The hypothesis was that otolith composition matching with  
116 DST derived locations during spawning events was different between English Channel and Bay of Biscay.  
117 We assumed that coupled DST location-otolith composition during spawning events was a reference  
118 (set up into a model of assignation), that could be used to retrieve fish spawning area inferred from  
119 otolith composition outside the DST period. Otolith trace elements were therefore used as proxies of  
120 fish location. Natal homing was explored using otolith microchemistry at the larval and adult stages on  
121 individuals that had expressed spawning site fidelity.

122

## 123 2. Material and methods

### 124 2.1. Sample collection

125 The samples were taken from wild seabass recaptured after tagging during a large-scale DST tagging  
126 program carried out by Ifremer in the English Channel (EC) and the Bay of Biscay (BoB) in 2014-2016  
127 (Fig. 1). Recaptured seabass came from either the commercial or the recreational fisheries. Among the  
128 470 (38.5%) tags recovered by August 2021 out of the 1220 tagged seabass (de Pontual et al.,  
129 submitted), 42 recaptured fish were selected based on a minimum of two winters of freedom after  
130 tagging (Supp. Mat. 2). Scales were collected on each individual seabass at tagging and recapture, with  
131 otoliths collected at recapture. Analyses were conducted in the first quarter of each year (winter) as the  
132 seabass spawning season extends from January to March in the Bay of Biscay and from February to April  
133 in the English Channel (e.g., Dambrine et al., 2021). Spawning areas were designated as the English  
134 Channel (EC) for the northern seabass stock and the Bay of Biscay (BoB) for the southern seabass stock.

### 135 2.2. Calcified structures selection and analysis

136 Right otoliths were used for  $\delta^{18}\text{O}$  analysis and, left otoliths were used for trace element analysis. Otoliths  
137 were embedded in epoxy resin for both analyses. The transverse sections were ground with ultra-pure  
138 water and silicium carbide paper to reach the nucleus and ensure high flatness of the otolith sections.

#### 139 2.2.1. Age estimation

140 No standard protocol for seabass age estimation based on otolith increment counting was available,  
141 and an indirect validation of seabass age was obtained by comparing scales collected during tagging and  
142 otolith and scales collected at recapture. Age was estimated by three readers. Each circulus for scale  
143 and annulus for otolith was counted as one year (Supp. Mat. 3). Finally, the otolith chronology was  
144 obtained by identifying otolith annuli corresponding to the winter periods recorded by the DST.

145

#### 146 2.2.2. Trace element ratio – LA ICP-MS analysis

147 The elemental analyses were performed using a high-resolution inductively coupled plasma mass  
148 spectrometer (ICP-MS), Thermo Element XR, coupled to a high repetition rate UV femtosecond laser  
149 ablation system, Lambda 3 (Amplitude system, France), at the IPREM PAMAL platform in Pau (France).  
150 Calibration, sampling design and instrumental bias correction of LA ICP-MS analysis are available in  
151 Supp. Mat. 4. Otolith material was ablated on transects from the nucleus to the dorsal edge,  
152 perpendicular to the growth increments. Transects consisted of a 20  $\mu\text{m}$  wide central line, a scanner  
153 speed of 1  $\text{mm}\cdot\text{s}^{-1}$  and a deck speed of 5  $\mu\text{m}\cdot\text{s}^{-1}$ . The following elements were quantified:  $^{25}\text{Mg}$ ,  $^{31}\text{P}$ ,  $^{43}\text{Ca}$ ,  
154  $^{55}\text{Mn}$ ,  $^{66}\text{Zn}$ ,  $^{88}\text{Sr}$  and  $^{138}\text{Ba}$ . The average detection limits ( $\mu\text{g}\cdot\text{g}^{-1}$ ) LOD achieved in this study were as  
155 follows:  $^{25}\text{Mg}$  0.51,  $^{31}\text{P}$  3.49,  $^{43}\text{Ca}$  250,  $^{55}\text{Mn}$  0.12,  $^{66}\text{Zn}$  1.07,  $^{88}\text{Sr}$  0.39,  $^{138}\text{Ba}$  0.14. The P concentrations  
156 along the otolith transects showed seasonal patterns (Heimbrand et al., 2020) synchronised with the  
157 otolith structure, allowing the delimitation of winter sequences. The larval stage was delineated using  
158 otolith structure and maximum P concentration within the nucleus region (Thomas and Swearer, 2019).  
159 For each larval stage and each winter sequence, the mean of the seven elements was calculated.

### 160 2.2.3. Oxygen isotope ratio – SIMS analysis

161 The  $\delta^{18}\text{O}$  analyses of the otolith were performed on a CAMECA IMS 1270 ion microprobe at the  
162 Edinburgh Ion Microprobe Facility (UK). Triplicate  $\delta^{18}\text{O}$  point measurements were performed in the  
163 nucleus area (larval phase) and in the DST recorded winter bands. A transect of 61 points from the core  
164 to the edge was also performed to validate the position of winters according to  $\delta^{18}\text{O}$  values. We provide  
165 the calibration, the sampling design and the instrumental bias correction of the SIMS analysis in Supp.  
166 Mat. 5. All the  $\delta^{18}\text{O}$  values were reported in per mil ‰ relative to SMOW. We used the following  
167 equation to convert  $\delta^{18}\text{O}$  values from SMOW to PDB (Coplen et al., 1983):

$$168 \quad \delta^{18}\text{O}_{\text{PDB}} = 0.97002 \delta^{18}\text{O}_{\text{SMOW}} - 29.98 \text{ (eq. 1)}$$

169 When several measure points were available per life stage, the mean of the  $\delta^{18}\text{O}$  values was used.

### 170 2.2.4. Oxygen isotope ratio – Prediction of otolith $\delta^{18}\text{O}$

171 Predicted otolith  $\delta^{18}\text{O}$  values were estimated at the EC and BoB spawning areas (Fig. 1) during the  
 172 spawning events from 2003 to 2018 for larval and adult stages. Estimates were based on daily  
 173 temperature and salinity predicted by the Atlantic Margin Model FOAM with a 49 km<sup>2</sup> resolution grid  
 174 (UK Met Office Operational Suite, <https://marine.copernicus.eu/>) for northern Cotentin (-1.95 to -1.64  
 175 °W and 49.97 to 50.21 °N) and the Rochebonne Plateau (-2.60 to -2.29 °W and 46.04 to 46.28 °N), within  
 176 the main spawning hotspots of the EC and BoB stocks (Dambrine et al., 2021; Fig. 1), respectively. Daily  
 177 winter (from January to March) temperature and salinity from the surface to 30 m deep were extracted  
 178 to study the larval stage (Jennings and Pawson, 1992) and those from the surface to 150 m to study the  
 179 adult stage (Woillez et al., 2016).

180 Oxygen isotope ratios of ambient seawater ( $\delta^{18}\text{O}_{\text{sw}}$ ) were estimated from salinity (S) using the following  
 181 equation applied to the North Sea (Harwood et al., 2008):

$$182 \quad \delta^{18}\text{O}_{\text{sw SMOW}} = 0.274 \times S - 9.3 \quad (\text{eq. 2})$$

183  $\delta^{18}\text{O}_{\text{sw SMOW}}$  were then converted into  $\delta^{18}\text{O}_{\text{sw PDB}}$  using equation eq. 1. Finally, we used the theoretical  
 184 equation for inorganic aragonite deposition to predict  $\delta^{18}\text{O}_{\text{otolith PDB}}$  (Kim et al., 2007):

$$185 \quad 1000 \ln \alpha = \left( 17.88 \times \frac{1000}{T} \right) - 31.14 \quad (\text{eq. 3})$$

186 with  $\alpha = \frac{1000 + \delta^{18}\text{O}_{\text{otolith}}}{1000 + \delta^{18}\text{O}_{\text{sw}}}$  and T, the temperature in Kelvin.

187

### 188 2.3. Reproductive event validation and spawning area attribution

189 Data were treated as specified in Fig. 2. Spawning events were defined as winter months in the otolith  
 190 calendar following age at maturity (> 5 yo for males and > 6 yo for females; Pickett and Pawson, 1994).  
 191 DST data were used as validation as follows: spawning events covered by DST records were identified  
 192 when depth was greater than 30 m during the first quarter of the year (Pickett and Pawson, 1994;  
 193 Pawson et al., 2007; Supp. Mat. 2). Spawning area (i.e. EC or BOB stock areas) was assigned to an otolith  
 194 spawning event, based on the corresponding DST derived position using the average location of the

195 individual reconstructed trajectory computed over the spawning month showing the highest vertical  
196 movements (Woiillez et al., 2016; de Pontual et al., submitted). Skip spawning outside the period  
197 recorded by DST, could not be considered as otoliths and scales of seabass do not record past spawning  
198 events. We used the hypothesis that seabass reproduced each year after the DST recorded period  
199 provided it matched with age at maturity.

200

## 201 2.4. Data analysis

### 202 2.4.1. Comparison of predicted and measured otolith $\delta^{18}\text{O}$

203 An ANOVA was performed to test the effects of life stage, year and spawning area on predicted otolith  
204  $\delta^{18}\text{O}$  values. Another ANOVA was used to test the effect of life stage on otolith  $\delta^{18}\text{O}$  measurements.

### 205 2.4.2. Adults' fidelity to spawning areas

206 Normal distribution was not reached for any of the tracers, hence, a non-parametric PERMANOVA was  
207 used to test if the microchemical elements varied spatially and annually (Anderson, 2017). This  
208 investigation was first performed on the training dataset, i.e., the coupled DST-otolith elemental  
209 signatures. We then used the Random Forest (RF) algorithm to explore seabass spawning site fidelity  
210 (Mercier et al., 2011). The calibration of the RF model (number of trees = 500, mtry = 2) was performed  
211 on coupled DST-otolith elemental signatures (Mg, P, Mn, Zn, Sr and Ba) (Fig. 2). To deal with the  
212 imbalanced training dataset, cut-off parameter was tuned by the proportion of the rare class (EC  
213 spawning area). The assignment of a spawning area by the RF model was limited to a maximum of two  
214 years before and after DST records. The calibrated RF model was used to predict spawning areas for  
215 winters outside the DST recording period (Fig. 2). Spawning site fidelity was identified when the  
216 sequences of the spawning area assigned to each year by the RF model had similar spawning areas for  
217 all consecutive winters. The contribution of the tracers to the discrimination of EC and BoB spawning  
218 areas was studied with a PCA applied to individuals expressing spawning site fidelity.

219

### 220 2.4.3. Natal homing

221 The effect of life stages on elemental composition was tested with a PERMANOVA. We hypothesised  
222 that these fish were born in the same area where they had spawned repeatedly (Fig. 2) by comparing  
223 otolith larval signatures between adult spawning origins (either EC or BoB).

224

## 225 3. Results

226 Of the 42 seabass in this study, 25 were tagged along the BoB coast and 17 along the EC coast (Supp.  
227 Mat. 2). The age of the seabass ranged between 6 and 18 years old at the time of recapture (Supp. Mat.  
228 2). There were 27 females, 13 males and 2 undetermined sex (Supp. Mat. 2). The study encompassed  
229 143 effective spawning events, including 74 coupled DST-otolith elemental signatures. Effective  
230 spawning events were recorded between 2003 and 2018 with a majority of events between 2014 and  
231 2017, and mainly for seabass between 6 and 8 years old (Supp. Mat. 2). Larval signatures were available  
232 from 1998 to 2011, with a majority of larval signatures between 2007 and 2009 (Supp. Mat. 2).

233 The reconstructed trajectories inferred from the DST data assigned 19 spawning events to the EC and  
234 55 offshore spawning events to the BoB (Supp. Mat. 6). Two individuals (DK\_A10572 and DK\_A10591)  
235 tagged and recaptured in the EC had been allocated to the BoB spawning area using trajectory  
236 reconstruction, but this was found to be highly unlikely (de Pontual et al., submitted). We thus  
237 performed the analysis by assigning them first to the EC spawning area (Supp. Mat. 6) and then to BoB  
238 spawning area (Supp. Mat. 7 Table 7.2).

239

### 240 3.1. Oxygen isotope ratios

241 The predicted  $\delta^{18}\text{O}$  values were very close in both larvae and adult (Supp. Mat. 8.a). The ANOVA revealed  
242 significant differences between years and spawning areas for larval (year:  $F_{1,2881} = 38.38$ ;  $p = <0.001$ ;  
243 spawning site:  $F_{1,2881} = 3907.34$ ;  $p = <0.001$ ) and adult stages (year:  $F_{1,2881} = 38.70$ ;  $p = <0.001$ ; spawning

244 site:  $F_{1,2881} = 3873.85$ ;  $p = <0.001$ ) (Supp. Mat. 8.a). The predicted  $\delta^{18}\text{O}$  were consistently higher in the  
245 EC than in the BoB over time, with a mean difference of 0.4 PDB. The difference varied between years,  
246 with overlapping values between areas in 2006 and 2007. The minimum difference was observed in  
247 2005 and the maximum difference in 2011 (Supp. Mat. 8.a).

248 The ANOVA revealed a significant difference between stages, with the adult signatures being higher  
249 ( $F_{1,112} = 290.13$ ;  $p = <0.001$  ; Supp. Mat. 8.b). This  $\delta^{18}\text{O}$  difference between stages was also evident on  
250 otolith transects between the nucleus to the edge throughout the life of the seabass (Supp. Mat. 9).  
251 Along this  $\delta^{18}\text{O}$  “life transect”,  $\delta^{18}\text{O}$  variations were found to show seasonal patterns that matched the  
252 structure of the otoliths (Supp. Mat. 9). The difference in measured  $\delta^{18}\text{O}$  was not obvious between  
253 spawning areas, and the  $\delta^{18}\text{O}$  differences observed between spawning areas for adult otoliths varied  
254 between years (Supp. Mat. 8.b).

255 The inter-annual variation in  $\delta^{18}\text{O}$  measured at the adult stage between spawning areas and the  
256 significant effect of the stage precluded the use of  $\delta^{18}\text{O}$  as a location tracer in this study. Therefore, the  
257 study of spawning site fidelity and natal homing was based on elemental signatures only.

258

### 259 3.2. Spawning site fidelity

260 Within the training dataset, adult otolith signatures were significantly different between the EC and the  
261 BoB spawning areas for Zn, Sr and Ba (Fig. 3). Although P, Zn and Sr varied significantly between years,  
262 the effect of spawning area on Zn and Sr overweighed this temporal effect (Fig. 3 and Table 1). We  
263 detected a significant interaction between spatial and temporal factors for Zn (Table 1). Sr increased in  
264 the BoB between 2015 and 2018 (Fig. 3). Zn and P decreased between 2015 and 2018 in both spawning  
265 areas with consistently higher Zn concentrations in the EC than in the BoB (Fig. 3). A RF model was fitted  
266 using the 74 otolith trace element signatures of the training data set (Fig. 3 and Supp. Mat. 5 and 6).  
267 The RF model was then used to assign spawning areas to the 69 spawning events of unknown location.  
268 The resulting RF model had an average OOB error rate of 25.68 %. The assignment error was consistent

269 for both spawning areas (EC: 21 % and BoB: 27 %). The Gini index indicated that Ba, Zn and Sr (6.72, 6.7  
270 and 4.9, respectively) were the main elements used for the classification followed by Mn, P and Mg (3.9,  
271 2.9 and 2.7, respectively). We assessed the sensitivity of the expert-corrected RF model by comparing  
272 its spawning area assignment results for DK\_A10572 and DK\_A10591 with DST data (expert and DST)  
273 (Supp. Mat. 7). Assigned spawning areas remained virtually unchanged, except for the two individuals  
274 tagged at DK and one tagged at LT (Supp. Mat. 7).

275 Individuals with only a single winter of otolith signature were excluded from the analysis (CB\_A11114,  
276 LT\_A11243 and IO\_A12484; Supp. Mat. 2). The analysis of seabass spawning site fidelity was based on  
277 140 spawning events (71 DST and 69 RF spawning area assignments), and a total of 36 seabass over a  
278 period of 2 to 6 years (Supp. Mat. 6). Our results revealed that 64 % of the seabass expressed spawning  
279 site fidelity (23 seabass; Supp. Mat. 6).

280 Our results showed geographical patterns in site fidelity, with spawning site fidelity most often  
281 expressed by seabass tagged at locations near either the northern limit of the EC stock or the southern  
282 limit of the BoB stock (Fig. 1 and Supp. Mat. 6). Most of the seabass tagged in the western part of the  
283 EC (with the corresponding tagging sites SM, SQ and SV, Fig. 1) have moved between the EC and the  
284 BoB (Supp. Mat. 6). Hence, the group of seabass tagged in the western part of the EC had the highest  
285 proportion of individuals alternating spawning migrations between the EC and the BoB over the years.  
286 None of the seabass with a predicted spawning area in the previous two years and tagged at NO site  
287 expressed fidelity to their spawning site (Supp. Mat. 6). The RF model assignment of NO site spawning  
288 signatures to the EC can be attributed to the lower values of Sr and Ba used in the prediction dataset  
289 compared to the training dataset (Supp. Mat. 10 and 11). Spawning site fidelity was more frequently  
290 found for the 27 female seabass (70% fidelity) compared to the 13 male seabass (46 % fidelity).

291 The results of the RF model were mainly driven by the high Sr and Ba concentrations, as shown in the  
292 first axis (37 % of the variance) of the PCA plot (Fig. 4). The contribution of Zn and Mn was lower. Most  
293 of the BoB signatures had higher Sr and Ba concentrations than the EC signatures (Fig. 4). The second

294 axis of the PCA explained 26 % of the variance and divided the data according to high Zn and high Mn  
295 concentrations (Fig. 4). Most of the EC signatures lied along this second axis, from high Zn  
296 concentrations to high Mn concentrations.

### 297 3.3. Natal homing

298 For the 23 seabass that had expressed fidelity to a spawning area, difference between larval and adult  
299 element signatures was significant for all the tracers (PERMANOVA,  $R^2 = 0.576$ ;  $F_{1,224} = 293.66$ ;  $p =$   
300  $0.001$ ) and the bias was not constant over individuals. This precluded the use of the RF model adjusted  
301 on adult signatures to assign birth locations based on larval signatures.

302 No significant difference in trace element concentrations of the larval otolith between the two spawning  
303 areas (PERMANOVA,  $R^2 = 0.074$ ;  $F_{1,21} = 1.697$ ;  $p = 0.227$ ). However, the differences in spawning areas  
304 between larval signatures for Zn, Sr and Ba followed the same patterns of differences as for the adult  
305 stage (Fig. 5). Although the difference was not significant, the plot of log-transformed otolith trace  
306 elements for the larval and adult stages suggested that both Sr and Ba were lower in the EC than in the  
307 BoB (Fig. 5). This pattern suggests that the seabass spent their larval stages in the same area where they  
308 returned to spawn as adult fish.

309

## 310 4. Discussion

311 To the best of our knowledge, the present work is one of the few studies coupling DST reconstructed  
312 trajectories with otolith structure or chemistry (Hüssy et al., 2009; Bardarson et al., 2017; Darnaude et  
313 al., 2014; Jónsson et al., 2021). Only Darnaude et al., (2014) used a similar method to infer *a posteriori*  
314 adult fish geolocation, using only one otolith tracer. The number of samples (42) was small but provided  
315 important insights into seabass spatial segregation and spawning site fidelity. Our approach provides a  
316 unique insight into the life histories of individual seabass, supporting spawning site fidelity and  
317 suggesting natal homing.

## 318 4.1. Evidence of spawning site fidelity in a temperate marine fish

319 Assessing the structure and connectivity of fish populations is essential for achieving sustainable  
320 fisheries management (Artetxe-Arrate et al., 2019). Studying spawning site fidelity, one of the key  
321 processes affecting the structure of fish populations, is therefore fundamental (Petitgas et al., 2013).  
322 Our results revealed that 64 % of the seabass express spawning site fidelity either to the English Channel  
323 or the Bay of Biscay spawning areas. These results tend to confirm the delineation of the population  
324 revealed by tag-recapture (Fritsch et al., 2007) and trajectory reconstruction studies (de Pontual et al.,  
325 2019). A delineation of the seabass population was not found in previous genetic studies due to the high  
326 level of gene flow (Fritsch et al., 2007; Souche et al., 2015).

327 The results are relevant because of the low uncertainties in the reconstruction of the DST trajectories  
328 and the discrimination of spawning areas from otolith microchemistry data. The spatial resolution  
329 (several hundred kilometres) was relevant for correctly assigning locations based on temperature and  
330 depth (trajectories from DSTs) and locations based on elemental ratios. Current geolocation models  
331 have average errors of about 30–50 and 120 km for demersal and large pelagic fish, respectively, which  
332 is acceptable for studies at the scale of fisheries management units (Gatti et al., 2021). We used  
333 trajectory reconstructions based on an improved version of a published geolocation model developed  
334 for seabass in the Iroise Sea (Woillez et al., 2016). This version was improved to address a larger  
335 geographical scale and a wider range of migration strategies as well as newly encountered behaviours  
336 (de Pontual et al., submitted). The sensitivity analyses and simulation-estimation experiments  
337 demonstrated that the original geolocation model was reliable (Woillez et al., 2016). Here, two  
338 individual trajectories of seabass tagged at DK were considered uncertain as they differ from the  
339 migration strategy of most individuals tagged at the same site (de Pontual et al., submitted). Following  
340 the expert opinion, the DST data recorded for these specific individuals and years were assigned to the  
341 EC. However, the alternative spawning area given by the model did not change significantly the overall  
342 results of the RF model (Supp. Mat. 7).

343 We delineated spawning periods base on otolith structure and high P concentrations that clearly identify  
344 winters (Hüssy et al., 2020; Heimbrand et al., 2020). This temporal proxy of adult spawning events  
345 corresponds to seabass spawning periods of three to four months in the EC and BoB (Dambrine et al.,  
346 2021). Seabass remain in the winter spawning areas for at least one month before moving to their  
347 summer feeding areas (Fritsch et al., 2007). However, seabass have the ability to move rapidly across  
348 large distances and display large vertical movements (de Pontual et al., 2019). The resulting otolith  
349 signatures of fast moving fish would be difficult to interpret, due to the incorporation dynamics of  
350 elements into the otolith making it difficult to identify an accurate reference signature of the spawning  
351 events. Another uncertainty came from the impossibility to consider skip spawning outside the DST  
352 recorded period, despite the fact it might be as common for seabass as for other species (Rideout and  
353 Tomkiewicz, 2011). As skip spawning was only observed in 4 seabass and not for two consecutive years  
354 (Supp. Mat. 2), skip spawning did not seem very frequent.

355 The potential of otolith microchemical tracers to discriminate marine water masses has been  
356 demonstrated previously (e.g., Thorrold et al., 2001; Darnaude et al., 2014). The Sr, Ba and Zn signatures  
357 of adult otoliths were found to discriminate the EC from the BoB. Our results revealed higher Sr and Ba  
358 concentrations in the BoB than in the EC. Although the Sr difference between the spawning areas may  
359 be attributed to the positive correlation between Sr and salinity (Elsdon et al., 2008), as salinity is higher  
360 in the Atlantic and the Bay of Biscay than in the English Channel (Ayata et al., 2010), the salinity  
361 difference is small between the BoB and the EC and overall Sr in seawater is quite uniform (de Villiers,  
362 1999). The difference in seabass otolith Sr would rather be an indirect indication of a difference of  
363 temperature between BoB and EC, and driven by a difference of growth. The Ba difference could be  
364 mainly due to the high concentration of Ba in seabass tagged at CB, NO and IO, possibly correlated with  
365 time spent either in the estuarine plume (Elsdon and Gillanders, 2005) or in deep water (Wolgemuth  
366 and Broecker, 1970), which corresponds to the location of IO near the mouth of the Gironde Estuary  
367 and CB near the submarine canyon in the gulf of Capbreton. Sr and Ba are known to be robust tracers  
368 for juvenile seabass trajectories (Reis-Santos et al., 2013) and have been shown to discriminate marine

369 areas (Soeth et al., 2019). While predicted  $\delta^{18}\text{O}$  significantly discriminated the EC and the BoB, oxygen  
370 isotopes measured in seabass otoliths failed to discriminate the BoB from the EC spawning areas. In  
371 other marine contexts, the  $\delta^{18}\text{O}$  measured in otoliths was successfully linked to the  $\delta^{18}\text{O}$  of ambient  
372 water (Artetxe-Arrate et al., 2021), making it an efficient and predictable tracer of seawater mass  
373 occupancy (von Leesen et al., 2021). Moreover, using entire dissolved otoliths, Neves et al. (2019) found  
374 a significant difference for black seabreams between the EC and the BoB with higher  $\delta^{18}\text{O}$  in the EC than  
375 in the BoB. The IRMS method used by Neves et al. (2019) is more accurate than SIMS but requires a  
376 larger amount of sample, which is incompatible with the amount of otolith material that can be collected  
377 during a spawning event (Pinto et al., 2021).

378 Our study also revealed a geographical feature in spawning site fidelity with seabass tagged at the  
379 northern (DK) or the southern (CB) limits of the study area expressing more frequent spawning site  
380 fidelity than seabass tagged in Brittany near the limit of the two stocks studied (e.g., SQ and AD). These  
381 results are consistent with those of de Pontual et al. (2019). Iroise Sea appears as a major  
382 biogeographical frontier between temperate and cold temperate marine assemblages (Ayata et al.,  
383 2010). Movements outside spawning areas appear to be fairly common for this species (Pickett et al.,  
384 2004; Fritsch et al., 2007; de Pontual et al., 2019). This behaviour has been associated with the use of  
385 alternative summer feeding habitats along Brittany coast (de Pontual et al., 2019). Indeed,  
386 reconstructions of the trajectories of seabass tagged in Western Brittany have revealed individuals  
387 spawning either in the EC or in the BoB, as well as individuals residing permanently in the Iroise Sea (de  
388 Pontual et al., 2019). Despite the imbalanced sex ratio of the sample, spawning site fidelity of female  
389 seabass was greater than the spawning site fidelity of male seabass. A female-biased homing behaviour  
390 was already observed for swordfish (Muths et al., 2009) and bluefish (Miralles et al., 2014). Male-biased  
391 site fidelity was found in a species expressing a strong territoriality (Cresci et al., 2022). For species with  
392 a female-biased sexual size dimorphism such as observed for seabass (Saillant et al., 2001), the male-  
393 male competition is decreased (Horne et al., 2020), which may explain their lower homing behaviour  
394 compared to females.

395 Resident behaviour and fidelity may have been underestimated in the present study. First, investigating  
396 spawning site fidelity at a greater temporal scale than previous studies implied a more conservative  
397 definition of site fidelity. Other studies have focussed their analysis on periods of two to four years  
398 (Skjærraasen et al., 2011; de Pontual et al., 2019). We chose to limit the study period to six years to  
399 overcome potential changes in the signatures of the water masses and the ontogenetic integration of  
400 the elements studied. Second, the behaviour of residents and their site fidelity to very specific spawning  
401 areas along the BoB coast may have led to errors in spawning area assignment. For all the seabass  
402 tagged at NO, a different spawning area was assigned depending on the data used (DST analysis for the  
403 BoB and RF model for the EC). This result tends to indicate a more coastal residency behaviour than  
404 their BoB counterparts, as the elemental signature of coastal areas could be similar to that of the EC.  
405 Residency behaviour was also observed using acoustic telemetry in the EC area for sub-adults (Stamp  
406 et al., 2021).

407 Why seabass express fidelity and why other do not is an open research question, but evidences from  
408 diadromous fish species shows that alternative reproductive strategies (fidelity or straying) is a bet  
409 edging strategy improving the overall fitness of species (Hendry et al., 2004). Fidelity can enhance fitness  
410 by allowing a fish to reproduce where reproduction has already been successful and straying can  
411 enhance fitness by mixing otherwise isolated population, or colonise new spawning areas. Investigating  
412 the ability to navigate and to recognize spawning areas requires innovative methods that were not  
413 considered in this study, as it implies proximal (imprinting, navigation ability, compass) and distal cues  
414 (odours, magnetic field, currents etc.).

#### 415 4.2 Lack of robust evidence for natal homing

416 Our results suggest natal homing in seabass but the low number of larval signatures did not provide  
417 robust evidence for this behaviour. Natal homing in temperate marine fish species is rarely investigated  
418 due to the logistical problems of assigning spawning areas based on natal signatures or tracking  
419 individuals from fertilization to spawning on large spatial scales (Bradbury et al., 2008). Nevertheless,

420 some studies have demonstrated the existence of natal homing on a regional scale for weakfish, a  
421 marine fish spawning in estuaries, and on a trans-Atlantic scale for Atlantic Bluefin tuna populations  
422 (Thorrold et al., 2001; Rooker et al., 2008). This behaviour deeply structures the populations and high  
423 levels of natal homing make the populations more vulnerable to fishing activities (Thorrold et al., 2001).  
424 The lack of discrimination of natal signatures between the BoB and the EC was also due to a strong  
425 physiological effect on tracer incorporation into otoliths for all the measured trace elements and oxygen  
426 isotope ratios. The effects of ontogeny on otolith trace elements have been reported previously in  
427 seabass (Reis-Santos et al., 2018) and other temperate fish species (de Pontual et al., 2003; Daverat et  
428 al., 2005). Our results confirmed the influence of physiology on the integration of elements in otoliths,  
429 with ontogenetic effects being particularly important for physiologically regulated elements such as Mg,  
430 Mn and Sr (Thomas and Swearer, 2019; Thomas et al., 2020; Hüsey et al., 2020). Otolith  $\delta^{18}\text{O}$  was also  
431 strongly influenced by ontogenetic changes, with significantly lower ratios in the larval than in the adult  
432 stage. Increases in  $\delta^{18}\text{O}$  concentrations between stages have been reported for other fish species (Shiao  
433 et al., 2010; Tanner et al., 2012; Matta et al., 2013) and interpreted as a rapid growth bias in bivalve  
434 juveniles (Huyghe et al., 2020). Although these ontogenetic changes are known for most of the elements  
435 studied, in this study the large variations in inter individual stage differences could not be corrected.  
436 Hence, the RF model fitted on adult data could not be used to assign natal areas and subsequently  
437 investigate natal homing.

#### 438 4.5. Conclusions

439 We based our study on two types of indirect location information, otolith signatures and DST data, with  
440 various spatio-temporal scales of integration. Although DSTs have a higher spatio-temporal resolution  
441 than otolith signatures, studying spawning behaviour at the spatial scale of the stock and the temporal  
442 scale of the winter (integrating about three months) matches the resolution of the proxies. Seabass is a  
443 highly mobile species, capable of migrating over long distances and showing individual histories with  
444 high site fidelity to spawning areas. Although we could not prove natal homing, it is suggested in our  
445 results. Even if it remains a challenge, further otoliths microchemistry studies would certainly gain

446 benefit from the analysis of seabass larvae otoliths captured on the spawning sites to obtain references  
447 for specific spawning areas. Our results also suggest that seabass stocks are structured, which calls for  
448 cautious management in the English Channel, Brittany and the Bay of Biscay as local stock depletion  
449 may not be fully compensated by stocks from other spawning areas.

450

#### 451 **Acknowledgements**

452 We are grateful to the IFREMER colleagues who participated in the tagging surveys and particularly to  
453 Stephane Martin who coordinated the recoveries of tagged fish scales and otoliths. Our special thanks  
454 go to J. Craven and M. Hall for their help with sample preparation and the SIMS analysis at the NERC,  
455 Edinburgh University. We also thank T. Deweulf for his participation in the reading of scales and otoliths  
456 to estimate seabass ages.

#### 457 **Competing interests**

458 The authors declare there are no competing interests.

#### 459 **Contributors' statement**

460 ELL: Data curation, Formal analysis, Investigation, Methodology, Resources, Software, Validation,  
461 Visualization, Writing - review & editing

462 FD: Conceptualization, Investigation, Methodology, Resources, Supervision, Roles/Writing - original  
463 draft

464 MW: Formal analysis, Funding acquisition, Methodology, Project administration, Supervision, Writing -  
465 review & editing

466 CP: Methodology, Writing - review & editing

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468 Supervision, Writing - review & editing

469 **Funding statement**

470 This study is part of the BARFRAY project funded by the European Maritime and Fisheries Funded (EMFF-  
 471 OSIRIS N°: PFEA 400017DM0720006)), the French Ministry of Agriculture and Food (MAF), France Filière  
 472 Pêche (FFP) and IFREMER. The DST data are from the national BarGip project funded by FFP, MAF and  
 473 IFREMER. The findings and conclusions of the present paper are those of the authors.

474

475 **Data availability statement**

476 All relevant data are included in the manuscript and its Supporting information files.

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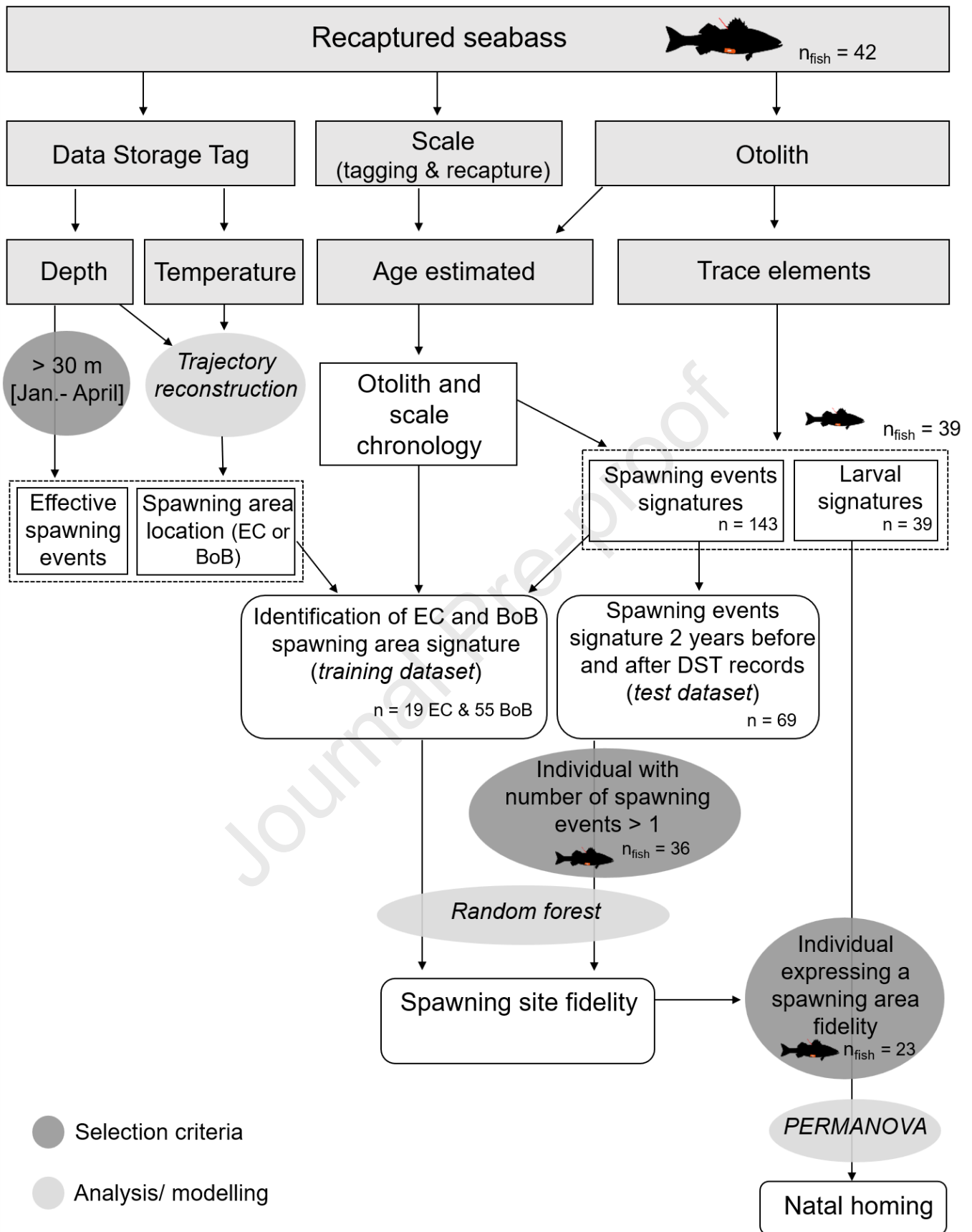
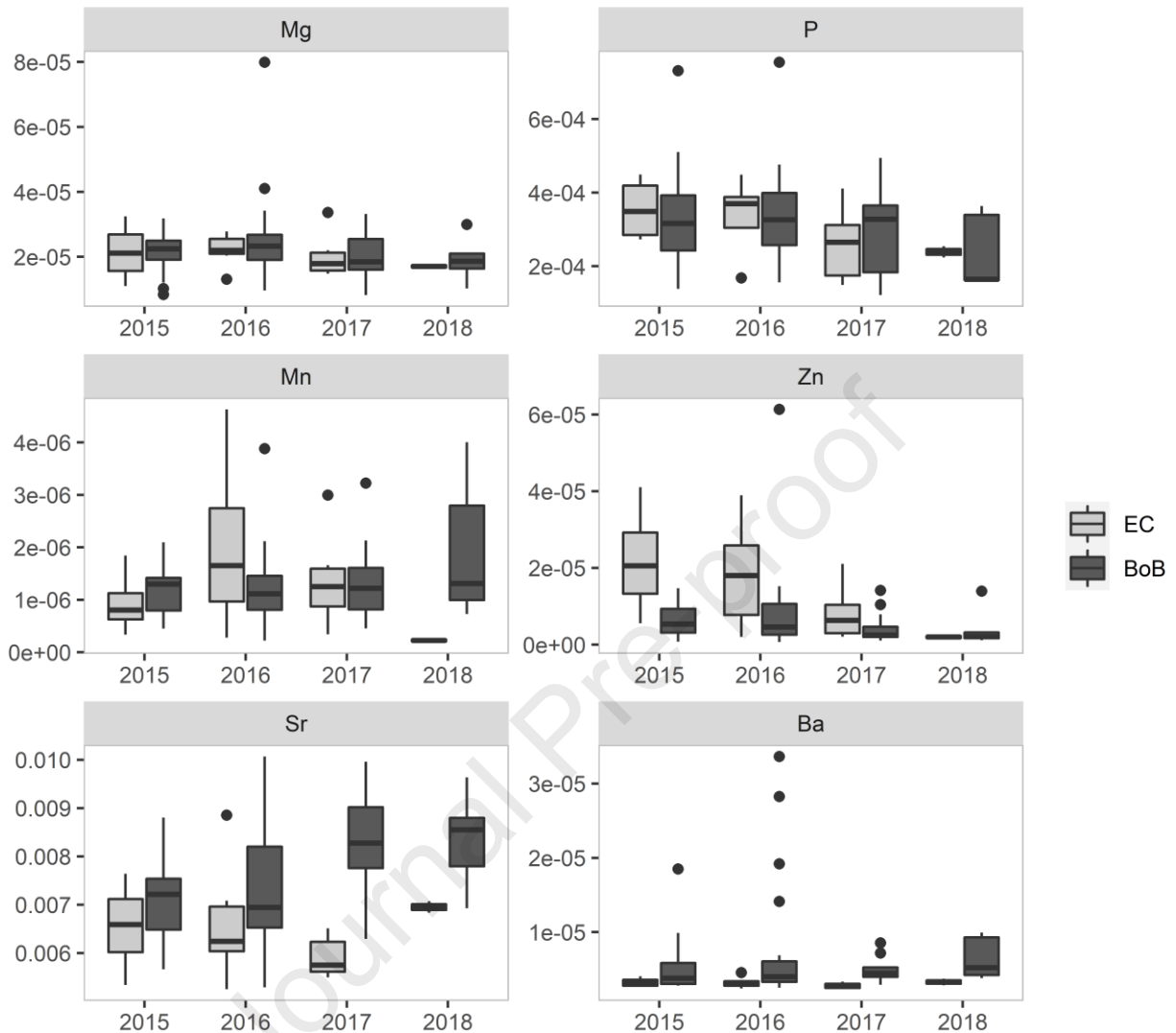
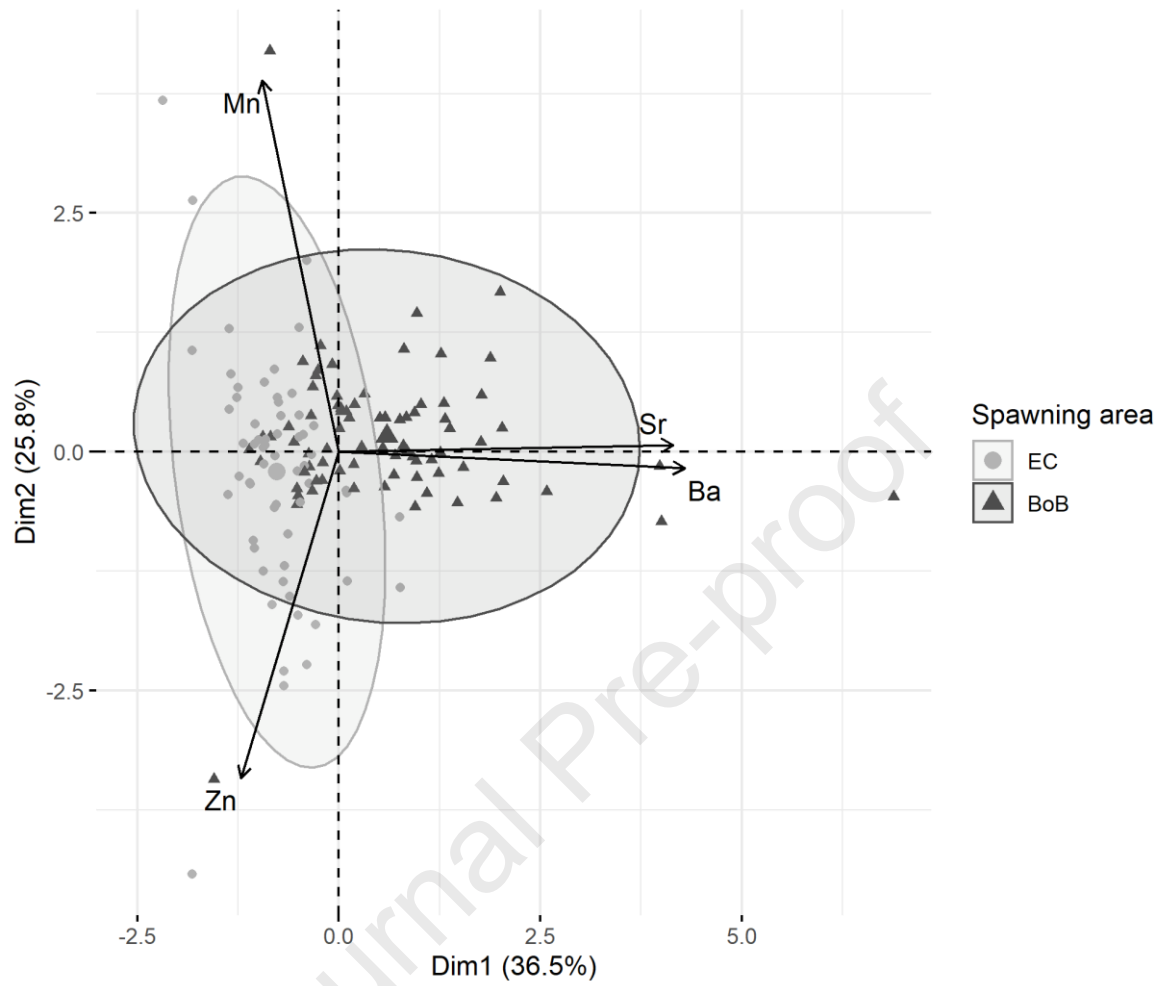


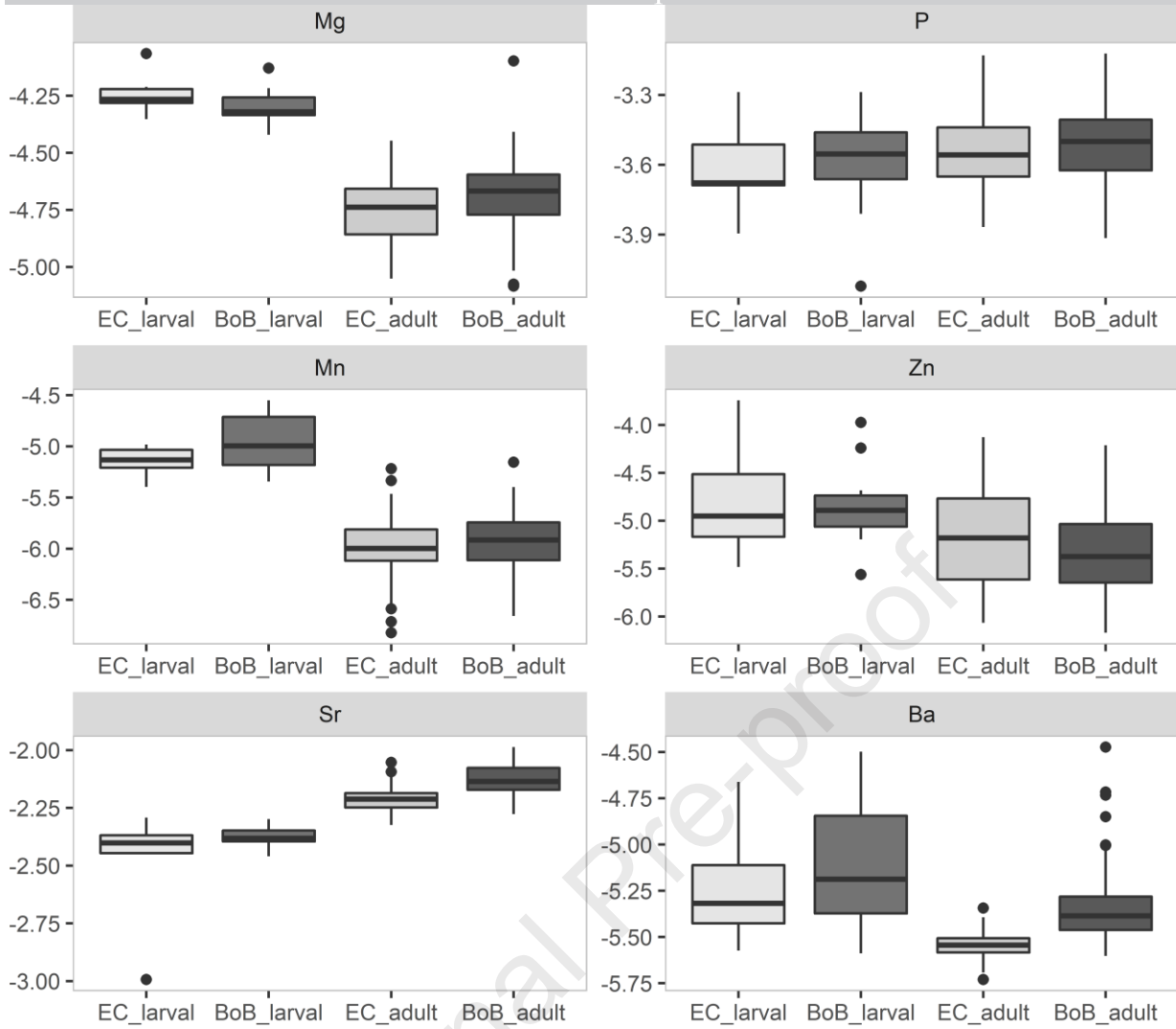
Figure 2. Work flow diagram of the methodology used to explore seabass spawning area fidelity and natal homing.



**Figure 3.** Boxplots of elemental concentrations w.r.t. years. The training dataset consists of adult otoliths (for which otolith winter signatures were coupled to DST assigned spawning area).



**Figure 4.** Principal Component Analysis of winter spawning signatures based on seabass that expressed fidelity to a spawning area (EC or BoB).



**Figure 5.** Boxplots of larval and adult trace elements signatures (log-transformed) for the 23 seabass that expressed fidelity to a spawning area. (EC: English Channel, BoB: Bay of Biscay)

**Table 1.** Results of the PERMANOVA testing the effects of spawning areas, years and the interaction between years and spawning areas on the trace elements for the training dataset (coupled DST/otolith composition). Significant effects are indicated in bold.

Element	Factor	SS	R <sup>2</sup>	F	p
Mg	Spawning area	3.48e-11	0.005	0.363	0.550
	Year	4.37e-11	0.006	0.456	0.500
	Spawning area:Year	5.10e-12	0.0007	0.053	0.804
P	Spawning area	1.78e-09	0.001	0.120	0.744
	Year	6.48e-08	0.058	4.388	<b>0.039</b>
	Spawning area:Year	4.30e-09	0.003	0.290	0.597
Mn	Spawning area	6.10e-14	0.001	0.075	0.801
	Year	5.37e-13	0.009	0.661	0.407
	Spawning area:Year	1.65e-12	0.027	2.035	0.158
Zn	Spawning area	7.93e-10	0.103	9.178	<b>0.005</b>
	Year	3.93e-10	0.051	4.554	<b>0.025</b>
	Spawning area:Year	4.62e-10	0.060	5.346	<b>0.026</b>
Sr	Spawning area	1.84e-05	0.171	16.654	<b>0.001</b>
	Year	7.48e-06	0.069	6.770	<b>0.008</b>
	Spawning area:Year	4.00e-06	0.037	3.622	0.073
Ba	Spawning area	1.47e-10	0.070	5.349	<b>0.020</b>
	Year	2.00e-13	0.0001	0.007	0.934
	Spawning area:Year	3.00e-14	0.00002	0.001	0.973

## Highlights

- Investigation of seabass spawning site fidelity and natal homing.
- Data Storage Tag information was coupled to otolith microchemistry to infer spawning areas.
- Spawning site fidelity was found for most seabass individuals (64 %).
- Otolith tracers (elements and  $\delta^{18}\text{O}$ ) were significantly biased by ontogenetic effects.
- Homing behaviour results were inconclusive.

**Declaration of interests**

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.

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:

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