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Abstract	commercial marine fish spec farmed individuals escape fro because of the difficulty to d differences evidence that the farm or wild origin at a diffe been shown to be a valuable to of escapees to local habitats of	<i>urata</i> L.) and European seabass (<i>Dicentrarchus labrax</i> L.) are important ies both for aquaculture and fisheries in the Mediterranean. It is known that m farm facilities, but the extent of escape events is not easy to report and estimate istinguish between wild and farmed individuals. In this study, significant cranial and body regions of seabream and seabass are different regarding their rent scales are provided through morphometry. Morphological variations have bool for describing changes in shape features. Therefore, the biomass contribution could be determined by identifying escaped individuals from fisheries landings otential negative effects of fish farm escapees on the environment, and their local fisheries.	
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Morphological differences between wild and farmed Mediterranean fish

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9 Abstract Gilthead seabream (Sparus aurata L.) and 10 European seabass (Dicentrarchus labrax L.) are important commercial marine fish species both for 11 aquaculture and fisheries in the Mediterranean. It is 12 13 known that farmed individuals escape from farm 14 facilities, but the extent of escape events is not easy to 15 report and estimate because of the difficulty to 16 distinguish between wild and farmed individuals. In this study, significant differences evidence that the 17 18 cranial and body regions of seabream and seabass are 19 different regarding their farm or wild origin at a 20 different scales are provided through morphometry. 21 Morphological variations have been shown to be a 22 valuable tool for describing changes in shape features. 23 Therefore, the biomass contribution of escapees to

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local habitats could be determined by identifying24escaped individuals from fisheries landings as a first25step to assess the potential negative effects of fish farm26escapees on the environment, and their influence on27wild stocks and local fisheries.28

KeywordsSeabream · Seabass · Morphometry ·39Escapees · Aquaculture · Fisheries landings30

Introduction

Gilthead seabream (Sparus aurata L., Fam. Sparidae) 33 and European seabass (Dicentrarchus labrax L., Fam. 34 Moronidae) are the important commercial marine fish 35 species along the Mediterranean and Eastern Atlantic 36 coastline both for aquaculture and fisheries. In 2008, 37 the total aquaculture production of seabream and 38 seabass in Europe were 89,354 and 58,467 t, respec-39 tively, and total landings reached 7,812 and 8,528 t, 40 respectively (FAO, 2011). It is well known that reared 41 individuals escape from farm facilities due to technical 42 and operational failures (Dempster et al., 2007), but 43 the knowledge concerning ecological and genetic 44 impacts of these escapees on the Mediterranean 45 ecosystem is still sparse. Escaped fish could be present 46 on spawning areas and could interbreed with native 47 populations as was found for salmonids (Naylor et al., 48 2005) and for cod (Uglem et al., 2008; Meager et al., 49 2009). Furthermore, it has been reported that escaped 50 seabream and seabass were able to swim away from 51

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52 farm facilities to nearby farms, local fishing grounds 53 and coastal habitats (González-Lorenzo et al., 2005; Toledo-Guedes et al., 2009; Arechavala-Lopez et al., 54 55 2011a, b). Thus, the potential for negative ecological consequences to occur through predation, competition 56 or transmitting pathogens to closely reared and wild 57 58 populations is significant (Dempster et al., 2007). For 59 a better understanding of these potential negative 60 effects, it is important to quantify the number of individuals that escape from sea-cages, and to analyse 61 62 their mobility, spatial distribution and survival. 63 Because of the difficulty in surveying directly the 64 escapes events, it is imperative to distinguish escapees 65 from native individuals in the natural habitats as a first step to assess their contribution to fisheries landings, 66 for instance examining captured individuals from 67 68 local fisheries after an escape event.

69 In hatcheries, fish grow faster and frequently with 70 different patterns and environment than in the wild and 71 this phenomenon has been mainly utilized to distinguish 72 between wild and reared salmonids with a relatively 73 high degree of certainty (Swaine et al., 1991; Fleming 74 et al., 1994; Hard et al., 2000; Fiske et al., 2005). 75 Differential relative growth of body parts conditioned 76 by environmental factors is a common feature of fish 77 development (Osse, 1990; Osse & van den Boogaart, 78 1995, 1999; Gisbert, 1999; Loy et al., 2001). In several 79 species, developmental modifications may be closely 80 linked also to ontogenetic changes in resource use (Webb & Weihs, 1986; Hernandez & Motta, 1997; 81 82 Sagnes et al., 1997; Ward-Campbell & Beamish, 2005). 83 Such different developmental modifications may exist 84 between wild and farmed fish given that they experience 85 large differences in feeding regimen and environment. 86 Moreover, in reared seabream and seabass, the presence

99

100

of malformations or morphoanatomical anomalies has 87 been widely documented (Paperna, 1978; Francescon 88 et al., 1988; Balebona et al., 1993; Boglione et al., 1993, 89 2001; Marino et al., 1993; Chatain, 1994; Koumoun-90 dourous et al., 1997; Loy et al., 1999, 2000; Afonso 91 et al., 2000; Sfakianakis et al., 2006). The objective of 92 this study is to assess the body measures which can 93 discriminate between farmed or wild origin of seabream 94 and seabass in the Mediterranean Sea, and therefore, if 95 the existence of some specific measurements could be 96 applied to study the contribution on wild populations 97 and fisheries landings. 98

Materials and 1	methods
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Sampling and morphometric measurements

A total of 200 wild seabream and 200 farmed seabream 101 individuals, as well as 200 wild seabass and 200 farmed 102 seabass individuals, from Spain and Greece, were used 103 in this study (Table 1). Wild and farmed fish from 104 Spain were obtained during the period of July 2009-105 June 2010, from two different localities and farms, 106 respectively (Fig. 1). Fish from Greece were obtained 107 in October 2009, from a single locality and a single 108 farm (Fig. 1). Each seabream or seabass was photo-109 graphed with a digital camera (Canon[®] Powershot-110 G10) mounted on tripod with a light source. A ruler was 111 used on each photograph to ensure correct calibration 112 in the following image processing. Morphological 113 landmarks were selected to give a precise definition 114 of the fish morphology (Humphries et al., 1981; Strauss 115 & Bookstein, 1982). Altogether 16 morphological 116 landmarks on seabream (Fig. 2; Table 2) and 17 117

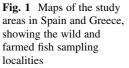
Table 1 Characteristics of seabream and seabass specimens used in this study

Species	Locality	Origin	n	Ls (cm)	Ls (cm)		Wt (g)
				Range	Mean \pm SD	Range	Mean \pm SD
Sparus aurata	Spain	Wild	100	25.3-47.9	34.6 ± 4.8	393–2628	1077 ± 445
		Farmed	100	28.6-39.4	30.7 ± 1.2	796–1105	906 ± 53
	Greece	Wild	100	13.1-17.5	15.3 ± 1.1	47-103	71 ± 1
		Farmed	100	13.0-18.7	15.6 ± 1.1	40-132	79 ± 1
Dicentrarchus labrax	Spain	Wild	100	17.3-54.7	31.1 ± 10.1	84-2920	671 ± 676
		Farmed	100	32.7-38.6	35.6 ± 1.1	821-1075	918 ± 48
	Greece	Wild	100	18.1-27.8	23.6 ± 1.9	80-280	152 ± 37
		Farmed	100	19.0-25.0	21.4 ± 1.2	91–197	128 ± 22

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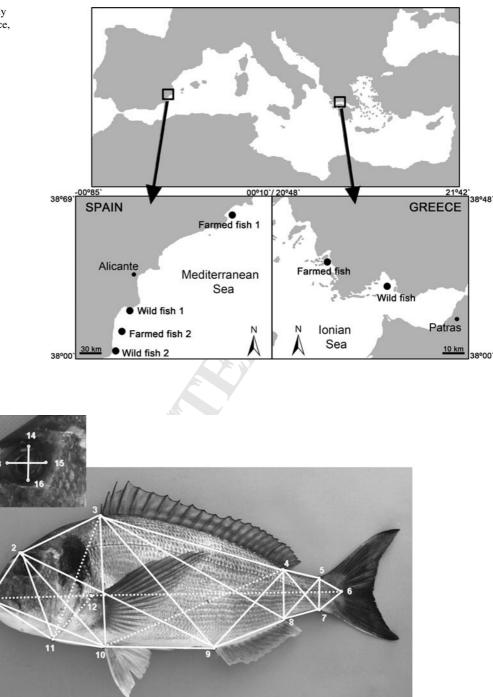


Fig. 2 The 16 landmarks and the distances measured which were used for the morphological analysis on seabream. The morphometric traits described from the landmarks are shown in Table 2. Solid lines TNS; dotted line additional measurements. 1 tip of the premaxillary; 2 point of maximum curvature in the head profile curve; 3 anterior insertion of dorsal fin; 4 posterior insertion of dorsal fin; 5 dorsal point at least depth of caudal peduncle; 6 posterior extremity of the lateral line; 7 ventral point at least depth of caudal peduncle; 8 posterior insertion of anal fin; 9 anterior insertion of anal fin; 10 anterior insertion of pelvic fin; 11 insertion of the operculum on the profile; 12 dorsal insertion of pectoral fin; 13 most anterior point of the eye; 14 most dorsal point of the eye; 15 most posterior point of the eye; 16 most ventral point of the eye

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118	morphological landmarks on seabass were used
119	(Fig. 3; Table 2), and they were placed using the
120	image processing programme ImageJ (Abramoff et al.,
121	2004), in which the morphological landmarks are given
122	as x and y co-ordinates. This tool is called Truss
123	Network System (TNS) and covers the entire fish in a
124	uniform network which should theoretically increase
125	the likelihood of extracting morphometric differences
126	within and between species. A regionally unbiased
127	network of morphometric measurements over the
128	two-dimensional outline of a fish should give more
129	information about local body differences than a con-
130	ventional set of measurements (Bookstein, 1982;
131	Strauss & Bookstein, 1982). A total of 31 morpholog-
132	ical vectors were selected among the landmarks on
133	seabream and 30 morphological vectors on seabass
134	(Table 2). The distances between the landmarks were
135	determined from their co-ordinates. The repeatability
136	of all measurements was determined by measuring 20
137	seabream and 20 seabass from each group three differ-
138	ent times. The coefficient of variation ranged from
139	0.5 to 2%, which indicates a high accuracy and
140	repeatability of this method. Moreover, morphometric
141	indices such as Fulton's Condition Index [$K = 100 \times \text{total}$]
142	weight/(total length) ³], Cephalic Index $[CI = (head)$
143	length/total length)] and Relative Profile Index [RP =
144	(maximum body height/total length)] were computed

(maximum body height/total length)] were from linear and weight measurements. 145

146 Statistical analysis

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147 In order to avoid the effect of the different specimen's 148 lengths in the study, all morphological traits were size 149 adjusted using the method described by Reist (1985), 150 because heterogeneity in size among samples pro-151 duces heterogeneity in measurements. These transformations were done separately for the different group 152 analysis (Spain, Greece and both together Spain-153 154 Greece) to avoid interference from the other groups. All the size-correlated traits were standardized to a 155 mean of zero and a standard deviation of 1. Multivar-156 iate statistics (SPSS, version 15.0 for Windows) were 157 used to test for intra- and inter-groups variation. 158 Statistical differences for size and all the morphomet-159 160 ric indices among groups was tested by ANOVA at P < 0.05. A principal component analysis (PCA), 161 with varimax rotation was selected because the 162 163 rotation minimizes the number of variables that have

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Table 2 Morphological traits of seabream and seabass measured from the landmarks in Figs. 2 and 3

Sparus aur	Sparus aurata		hus labrax
Code	Landmark	Code	Landmark
A1	1–2	A1	1–2
A2	2-10	A2	2-12
A3	10-11	A3	1–12
A4	1-11	B1	2–3
A5	1–10	B2	3-11
A6	2–11	В3	11-12
B1	2–3	B4	2-11
B2	3–9	B5	3-12
B3	9–10	C1	3–4
B4	2–9	C2	4–10
B5	3–10	C3	10-11
B6	3–11	C4	3–10
C1	3–4	C5	4-11
C2	4–8	D1	4–5
C3	8–9	D2	5–9
C4	3–8	D3	9-10
C5	4–9	D4	4–9
C6	4–10	D5	5-10
D1	4–5	E1	5–6
D2	5–7	E2	6–8
D3	7–8	E3	8–9
D4	4–7	E4	5-8
D5	5-8	E5	6–9
E1	5–6	F1	6–7
E2	6–7	F2	7–8
F1	1–12	F3	1–13
F2	11-12	F4	7–13
F3	6–12	Eye L	14–16
Eye L	13–15	Eye H	15-17
Eye H	14–16	SL	1–7
SL	1–6		

high loadings on a factor. All PCAs with eigen-164 value >1.00 were considered as important (Chatfield 165 & Collins, 1983) and variables were tested by 166 ANOVA at P < 0.05. Discriminant analyses were 167 then used to test for group membership. The different 168 discriminant functions are hereafter described as DC1, 169 DC2, etc. ANOVA was used to test if there were 170 differences in morphological traits between the wild 171 and the farmed seabream and seabass, respectively. 172

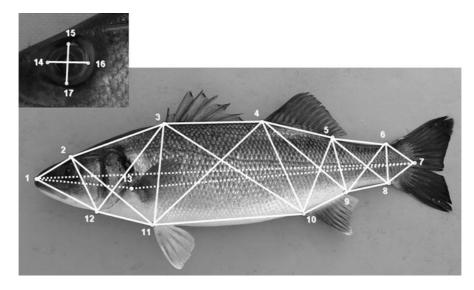


Fig. 3 The 17 landmarks and the distance measured which were used for morphological measurement on seabass. The morphological traits described from the landmarks are shown in Table 2. *Solid lines* TNS; *dotted line* additional length measures. *1* tip of the premaxillary; 2 point of maximum curvature in the head profile curve; *3* anterior insertion of the first dorsal fin; *4* anterior insertion of the second dorsal fin; *5* posterior insertion of the second dorsal fin; *6* dorsal point at least

173 Results

174 Results evidenced clear differences between wild and farmed fish, mainly on the cranial and body regions, 175 176 for both seabass and seabream. It should be noted that 177 seabream from Spain and Greece were of different sizes (ANOVA, P < 0.05), while sizes of seabass 178 179 were similar in the two countries (ANOVA, P > 0.05; 180 Table 1). Fulton's Condition Index (K) revealed sig-181 nificant differences between wild and farmed individ-182 uals of both studied species (ANOVA; $P \le 0.01$) with 183 the farmed fish exhibiting the highest values (Fig. 4a, b). Cephalic Index (CI) values were significantly 184 different in seabass (ANOVA; $P \leq 0.05$), where wild 185 186 fish showed the highest values in both countries 187 (Fig. 4c); but there were no significant differences 188 between wild and farmed seabream specimens (ANOVA; P > 0.05; Fig. 4d). However, values of 189 190 Relative Profile Index (RP) were significantly differ-191 ent among seabream from different origins (ANOVA; 192 $P \leq 0.05$), where farmed fish showed higher values than wild fish (Fig. 4e), while there were no differ-193 194 ences for seabass in both countries (ANOVA; 195 P > 0.05; Fig. 4f).

depth of caudal peduncle; 7 posterior extremity of the lateral line; 8 ventral point at least depth of caudal peduncle; 9 posterior insertion of anal fin; 10 anterior insertion of anal fin; 11 anterior insertion of pelvic fin; 12 insertion of the operculum on the profile; 13 dorsal insertion of pectoral fin; 14 most anterior point of the eye; 15 most dorsal point of the eye; 16 most posterior point of the eye; 17 most ventral point of the eye

A combination of five principal components 196 explained as much as 87.03% of the variation of 197 size-adjusted body morphology variables for Spanish 198 seabream (ANOVA, $P \le 0.01$; Table 3). In case of 199 Greece, eight principal components explained as much 200 as 85.69% of this variation in seabream, but only four 201 with significant differences (ANOVA, $P \le 0.01$; 202 Table 3). In both countries, the most important 203 differences were located in the anterior body portion, 204 principally in head measurements and body height. 205 Discriminant analysis presented four differentiated 206 groups in Spain, belonging to the two fish farms and 207 two control localities (Fig. 5). Two percent of wild 208 fish were not adequately assigned, which may indicate 209 a cultivated origin, while 100% of the farmed fish were 210 correctly classified. Since there were only two groups 211 from Greece, the discriminant analysis gave only one 212 function and it was therefore not possible to plot the 213 relationship between components. However, classifi-214 cation score for the discriminant analysis resulted in 215 98% of wild fish and 99% of farmed fish from Greece 216 being correctly classified. Comparisons between wild 217 and farmed seabream according to their Spanish or 218 Greek origin showed clear differences for almost all of 219



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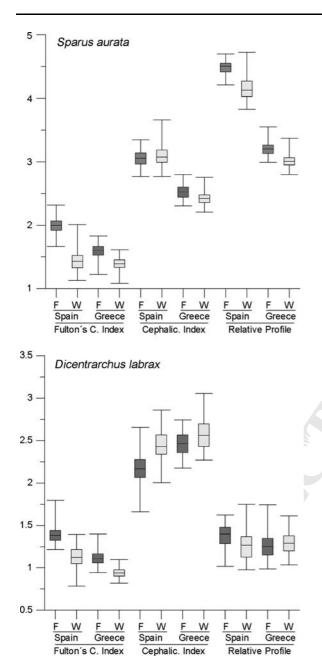


Fig. 4 Morphometric indices of wild and farmed seabream and seabass from Spain and Greece. *Bars* show mean values \pm standard deviation

220 the taken measurements (Fig. 6). Nonetheless, dis-221 criminant analysis exhibited that around 3% of wild 222 individuals, both from Greece and Spain, could be of 223 cultivated origin (Table 4). It is remarkable that these 224 individuals presented high indices values. The differ-225 ences in morphological traits were significant 226 (ANOVA, $P \le 0.05$) for all discriminant functions

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for all groups, and could be explained by the group 227 origin (Wilks' λ , ANOVA, $P \le 0.01$; Table 5). 228

Significant differences in morphological traits 229 between wild and farmed seabass in Spain were 230 described by two components in the PCA analysis 231 which explained 86.47% of the variation (ANOVA, 232 $P \leq 0.01$; Table 6). First component principally cor-233 related with longitudinal and transversal body mea-234 surements, while head and eye measurements were 235 most representative for the second component. Vari-236 ation in morphological traits between farmed and wild 237 seabass from Greece was explained by five principal 238 components (80.12%) but only three of them pre-239 sented significant differences (ANOVA, $P \le 0.05$; 240 Table 6). These differences were mainly due to eye 241 and head measurements (PC1) and some transversal 242 body measurements (PC2). Discriminant analysis plot 243 for Spanish seabass groups illustrated a pronounced 244 variation in the morphological traits between wild 245 and farmed fish, where the two locations of farmed fish 246 were more similar between them, and the two wild 247 groups were considerably more heterogeneous 248 (Fig. 7). However, the 2% of wild fish from Spain 249 were not correctly classified, whereas 100% of the 250 farmed fish were correctly assigned. Since there were 251 only two groups of seabass from Greece, the discrim-252 inant analysis gave only one function and it was 253 therefore not possible to plot the relationship between 254 components. However, discriminant analysis correctly 255 grouped the 100% of individuals within their respec-256 257 tive group.

When comparing morphological traits for seabass 258 from Spain and Greece together, significant differ-259 ences were explained by two principal components 260 (93.52%; ANOVA, $P \le 0.01$). Body measurements 261 were mainly located on the first component (PC1: 262 56.2%), while head and eyes measurements were more 263 important in the second one (PC2: 37.2%). The first 264 two resulting functions from discriminant analysis 265 explained 70.4 and 23.1% of the variation, respec-266 tively (Table 8); and the differences in morphological 267 traits were significant (Wilks' λ , ANOVA, $P \leq 0.01$; 268 Table 8). Plotting these two functions, the first one 269 grouped the seabass according to their geographical 270 origin, while the second function grouped the samples 271 according to their wild or farm origin (Fig. 8). 272 Moreover, 98 and 99% of reared seabass from Spain 273 and Greece, respectively, were correctly grouped 274 (Table 7). Furthermore, 88% of wild seabass from 275

Spain						Greece								
	PC1	PC2	PC3	PC4	PC5		PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Eye H	0.954					A5	0.859							
B2	0.920					A3	0.849							
B5	0.920					A2	0.848							
A6	0.907					В5	0.823							
C4	0.879					B6	0.708							
A5	0.869					D2	0.661							
A4	0.866					F1	0.660							
B6	0.866					F2	0.652							
B4	0.855					B4	0.639							
C6	0.850					A6	0.524							
B3	0.827					B3	0.516							
B1	0.818					C1		0.878						
A2	0.808					C4		0.853						
C5	0.802					B2		0.739						
F1	0.795					B1		-0.557						
C2	0.767					C3			0.897					
D4	0.756					C5			0.830					
E2	0.754					F3	E.		0.614					
D2	0.752					C6			0.574					
D5	0.750					D3				0.868				
C3	0.729					D5				0.844				
D3	0.725					C2				0.525				
D1		-0.661				E2					0.831			
F2		0.477				E1					0.813			
C1			0.628			Eye L						0.850		
A1			0.430			Eye H						0.723		
F3			0.484			A4						0.596		
A3			0.463			D4							0.746	
E1				0.517		D1							0.832	
Eye L					0.594	A1								0.861
% V	30.03	20.52	16.51	14.81	5.17		24.18	11.12	10.93	10.07	8.93	8.56	6.67	5.22
Eigenv.	9.01	6.15	4.95	4.44	1.55		7.25	3.34	3.28	3.02	2.68	2.57	2.01	1.59
ANOVA	< 0.01	< 0.01	< 0.01	< 0.01	< 0.01		< 0.01	< 0.01	< 0.01	0.61	0.16	0.92	< 0.01	0.82

Table 3 Component loadings, percent of variance (% V) and eigenvalues (Eigen.) for the principal components (with varimax rotation) in the Spain and Greece groups analyses for seabream

Components with significant differences (ANOVA; $P \le 0.05$) in morphological traits between farmed and wild seabream are marked in bold (see Table 2 for definition of characters)

Spain were correctly assigned, but 5 and 7% were
assigned to Greek and Spanish farm origin. Only 1%
of wild seabass from Greece were not correctly
grouped (Table 7).

280 Discussion

Body morphology was clearly different between wildand farmed fish for both species. The spatial

consistency of these results indicate the usefulness of 283 these indices in discriminating the origin of the studied 284 species, such as the CI for seabass, the RP for 285 seabream or Fulton's Condition Index for both 286 species. In addition, morphometric analyses suggest 287 that most differences are located primarily in the head 288 and anterior region of the body of the fish. Specifically, 289 these differences on seabream were focused either on 290 the head height (B5) or the distances from the base of 291 the pectoral fin to the edges of the mouth (A5) and to 292



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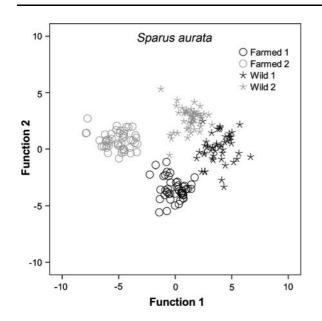


Fig. 5 Scatterplot of functions 1 and 2 for the discriminant analysis at Spain group including the two locations of farmed seabream and the two localities of wild seabream

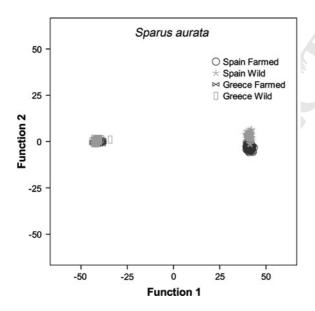


Fig. 6 Scatterplot of functions 1 and 2 for the discriminant analysis including the groups of farmed and wild seabream from Spain and Greece

forehead (A2), (see Table 2; Fig. 2); while for seabass
they were on head and body length (F3 and F4,
respectively), proportions of the eye and the distances
from the base of the operculum to the edge of the
mouth (A2) and to the forehead (A3), (see Table 2;
Fig. 3).

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These morphological differentiations could be due 299 to either the selective breeding programmes applied 300 in aquaculture, genetic drift following founding 301 generations, or the different origin of fish used as 302 broodstocks (Karaiskou et al., 2009). Although the 303 accidental escapes of fish from farms have certainly 304 contributed to a mix of all gilthead seabream genetic 305 stocks (Sola et al., 2006), a high genetic differentia-306 tion between cultivated and wild populations from the 307 same area has been reported, which might indicate no 308 evidence for significant genetic flow between them 309 (Alarcón et al., 2004). The first genetics studies 310 carried out on gilthead seabream populations reported 311 conflicting data concerning the existence of panmictic 312 (Cervelli et al., 1985) or subdivided populations 313 (Funkenstein et al., 1990). More recent studies have 314 depicted a picture of species subdivision that still 315 needs to be clarified. The results of Arabaci et al. 316 (2010) suggest a slight but significant population 317 structure for the Mediterranean Sea and Atlantic 318 Ocean, but not apparently associated with geographic 319 or oceanographic factors (Alarcón et al., 2004; Ben-320 Slimen et al., 2004; De Innocentiis et al., 2004; 321 Karaiskou et al., 2005; Rossi et al., 2006). In addition 322 to fish origin, it should be noted that the mean sizes 323 among Spanish and Greek seabream in this study were 324 significantly different. Mean size (both length and 325 weight) of Spanish seabream proved to be higher than 326 the group from Greece. Thus, some morphological 327 variations between regions may be the result of 328 differences in individual's age, and hence body size. 329 Gilthead seabream are characterized by remarkable 330 anatomical changes throughout their life history 331 (Cataldi et al., 1987), and this species is known to 332 undergo ontogenetic shifts in feeding habits (Mariani 333 et al., 2002; Tancioni et al., 2003). Furthermore, a 334 pattern of allometric growth on different body regions 335 was characterized for each age-stage (Russo et al., 336 2007). Further studies will be necessary to compare 337 different sizes of farmed and wild seabream from 338 339 different geographical regions.

In the case of European seabass, numerous genetic 340 population differentiation studies at different geo-341 graphic scales have led to the identification of three 342 genetically distinct zones: the northeastern Atlantic 343 Ocean, the western Mediterranean and the eastern 344 Mediterranean (Patarnello et al., 1993; Allegrucci 345 et al., 1997; García de León et al., 1997; Castilho & 346 McAndrew, 1998; Sola et al., 1998; Bahri-Sfar et al., 347

Sparus aurata	Group	Spain		Greece		Total
		Farmed	Wild	Farmed	Wild	
Origin group (%)	Spain farmed	100	0	0	0	100
	Spain wild	3	97	0	0	100
	Greece farmed	0	0	98	2	100
	Greece wild	0	0	3	97	100

Table 4 Inter-group classification score result (in %) for the discriminant analysis of the four groups of seabream

Table 5	Data from	the intra-	and inter-groups	discrimination	analyses
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	F	Eigenvalue	Percent variance	Cumulative variance	Canonical correlation	$\begin{array}{c} \text{Wilks'} \\ \lambda \end{array}$	χ^2	df	Р
Spain	1	10.849	65.6	65.6	0.957	0.009	884.059	60	< 0.001
Spain	2	5.132	31.0	96.6	0.915	0.105	421.750	38	< 0.001
Spain	3	0.555	3.4	100.0	0.598	0.643	82.608	18	< 0.001
Greece	1	4.975	100.0	100.0	0.912	0.167	327.129	30	< 0.001
Spain– Greece	1	1695.914	99.5	99.5	1.000	0.000	4073.060	90	< 0.001
Spain– Greece	2	5.206	0.3	99.8	0.916	0.040	1232.292	58	< 0.001
Spain– Greece	3	3.057	0.2	100.0	0.868	0.247	534.946	28	< 0.001

The groups of seabream were classified from these functions (F) in the discriminant analysis

2000; Castilho & Ciftci, 2005; Ergüden & Turan, 348 2005; Katsares et al., 2005; Lemaire et al., 2005). In 349 350 this study, through discriminate analysis, some wild 351 seabass from Spain (7%) were grouped along with 352 farmed fish from Spain, which probably belong to an 353 escapee group; but some others (5%) were grouped with seabass from Greek farms. Cases in which 354 355 individuals do not cluster with other samples belong-356 ing to the same geographical origin are not surprising, 357 since eggs or fingerlings originating from the western basin were most likely used to seed many hatcheries 358 359 around the Mediterranean when seabass aquaculture, and therefore, escapes into the wild, began in the early 360 1980s (Haffray et al., 2006). 361

On the other hand, phenotypic differences are 362 not necessarily indicative of genetic differentiation 363 between populations (Ihssen et al., 1981; Allendorf, 364 1988), and thus the detection of morphological 365 366 differences among populations cannot usually be taken as evidence of genetic differentiation (Turan, 367 1999). Phenotypic plasticity of fish allows them to 368 369 respond adaptively to environmental change by mod-370 ification to their physiology and behaviour which

leads to changes in their morphology, reproduction or 371 survival that mitigate the effects of environmental 372 variation (Stearns, 1983; Meyer, 1987). Unlike wild 373 populations, farmed fish live inside the cages with a 374 periodic feeding rate and easily available food, 375 suggesting that foraging is different from wild fish 376 (Arabaci et al., 2010). Therefore, the morphological 377 differences found in this study between wild and 378 farmed seabream agree with those differences found 379 by Grigorakis et al. (2002) where wild seabream 380 presented lower body height, sharper snout and more 381 spindle-shaped body than cultured seabream. More-382 over, such differences could be partly explained by 383 dietary shifts, which induce changes on the body 384 shape (Keast, 1978), influencing prev selection 385 and catch efficiency (Mérigoux & Ponton, 1998). 386 Furthermore, as they have been widely reported for 387 farmed seabream and seabass, all fish species may 388 develop shape abnormalities under farming conditions 389 (Divanach et al., 1996). Some of such anomalies are 390 observable in the cranial and ventral region (Loy et al., 391 2000; Tulli et al., 2009), fin erosion by erodibility 392 (Arechavala-Lopez et al., unpublished data), otoliths 393

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Spain			Greece					
	PC1	PC2		PC1	PC2	PC3	PC4	PC5
F4	0.945		F3	0.904				
E4	0.905		Eye L	0.805				
D2	0.890		A3	0.801				
C2	0.887		A2	0.729				
C5	0.885		Eye H	0.725				
E3	0.884		B4	0.692				
C4	0.875		D5	0.543				
D4	0.872		B3	0.419				
E5	0.867		F2		0.724			
D5	0.859		F4		0.675			
C3	0.855		F1		0.671			
B2	0.851		C1		0.664			
E1	0.847		A1		-0.655			
E2	0.839		D3		0.583			
C1	0.835		C5		0.554			
B5	0.815		E2		0.491			
D1	0.812		D1			0.780		
B1	0.787		C2			0.748		
B3	0.771		D4			0.712		
D3	0.756		C4			0.627		
B4	0.697		B2			0.597		
F3		0.919	C3			0.581		
A3		0.914	E4				0.907	
A1		0.853	E1				0.885	
Eye L		0.830	E3				0.659	
A2		0.800	D2				0.626	
F2		0.695	E5				0.516	
Eye H		0.685	B1					0.758
F1		0.632	B5					0.687
% V	57.72	33.75		22.64	18.01	16.01	14.98	8.48
Eigenv.	16.74	9.79		6.56	5.22	4.64	4.34	2.46
ANOVA	< 0.01	< 0.01		< 0.01	< 0.01	0.24	0.11	0.03

Table 6Component loadings, percent of variance (% V) and eigenvalues for the principal components (with varimax rotation) in theSpain and Greece groups analyses for seabass

Components with significant differences (ANOVA; $P \le 0.05$) in morphological traits between farmed and wild seabass are marked in bold (see Table 2 for definition of characters)

and scale modifications (Carrillo et al., 2001; Arec-394 395 havala-Lopez et al., 2011c), and also bent body shape by skeletal anomalies, mainly in the haemal and 396 caudal body regions (Paperna, 1978; Francescon et al., 397 398 1988; Balebona et al., 1993; Boglione et al., 1993, 399 2001; Marino et al., 1993; Chatain, 1994; Koumoun-400 dourous et al., 1997; Loy et al., 1999, 2000; Afonso 401 et al., 2000; Sfakianakis et al., 2006). However, wildcaught seabream and seabass present a low number of 402 malformations and are scarcely affected by any severe 403 anomalies (Boglione et al., 2001; Loy et al., 2000). In 404 this study, farmed fish were carefully selected from the 405 captures looking for streamlined wild-like profiles, 406 associated with absence or light anomalies cadres 407 (Loy et al., 2000), to avoid these morphoanatomical 408 differences cited above. Despite this, significant 409



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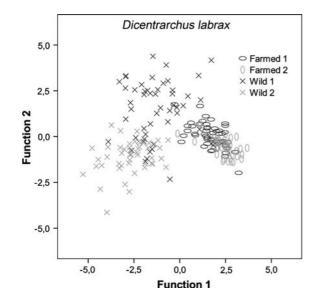


Fig. 7 Scatterplot of functions 1 and 2 for the discriminant analysis at Spain-group including the two locations of farmed seabass and the two localities of wild seabass

410 differences have been detected mainly in the anterior

411 region for both species, resulting from neither mal-

412 formations nor abnormalities.

413 In conclusion, this study provides evidences 414 that body morphology of seabream and seabass are different according to their origin at different scales, 415 which could be attributed to both rearing environment 416 and genetic differentiation. Even more, the use of 417 morphoanatomical indices (K, CI and RP) seems to 418 have wider applicability than image processing (TNS) 419 in the identification of wild and farmed fish. Such 420 indices entail no great scientific expertise and they 421 have been shown to be a valuable tool for describing 422 changes in shape features, and could be used as a 423 useful technique in the field to identify escapees within 424 the wild stocks, and therefore, to monitor their 425 potential negative effects on the environment and 426 their influence on local fisheries landings. However, it 427 must be taken into account that an escapee that 428 survives over time may resemble a wild individual due 429 to the changes on habitat and food. The use of the 430 combined approach, such as morphometry, genetic 431 and other biological indicators (e.g. growth pattern of 432 scales and otoliths, fatty acids and trace elements), 433 should be considered for the more precise quantification 434 of escapes within natural populations, fisheries landing or 435 for evaluation of re-stocking programs. This will not only 436 contribute greatly to biological and ecological clarifica-437 tion of the species but will also help to the development of 438 a strategy for natural stocks conservation and improving 439 the aquaculture sustainability. 440

Table 7 Inter-group classification score result (in %) for the discriminant analysis of the four groups of seabass

Dicentrarchus labrax	Group	Spain		Greece		Total
		Farmed	Wild	Farmed	Wild	
Origin group (%)	Spain farmed	98	2	0	0	100
	Spain wild	7	88	5	0	100
	Greece farmed	0	0	99	1	100
	Greece wild	0	1	0	99	100

Table 8	Data from	the intra-	and	inter-groups	discrimination analyses	

Group	F	Eigenvalue	Percent variance	Cumulative variance	Canonical correlation	Wilks' λ	χ^2	df	Р
Spain	1	4.405	77.5	77.5	0.903	0.071	485.064	81	< 0.001
Spain	2	0.930	16.4	93.9	0.694	0.384	175.457	52	< 0.001
Spain	3	0.348	6.1	100.0	0.508	0.742	54.848	25	< 0.001
Greece	1	7.596	100.0	100.0	0.940	0.116	394.768	29	< 0.001
Spain-Greece	1	9.818	70.4	70.4	0.953	0.011	1709.278	87	< 0.001
Spain-Greece	2	3.227	23.1	93.5	0.874	0.124	798.482	56	< 0.001
Spain-Greece	3	0.908	6.5	100.0	0.690	0.524	247.106	27	< 0.001

The groups of seabass were classified from these functions (F) in the discriminant analysis

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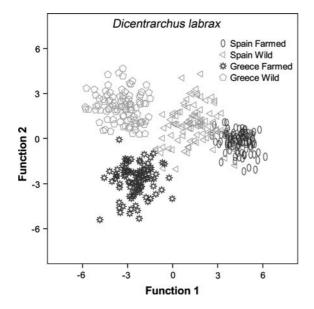


Fig. 8 Scatterplot of functions 1 and 2 for the discriminant analysis including the groups of farmed and wild seabass from Spain and Greece: white circle Spain Farmed; white triangle Spain Wild; black star Greece Farmed; grey pentagon Greece Wild

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