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Characterization of the peripheral thyroid system of gilthead seabream acclimated to different ambient salinities

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ABSTRACT
Thyroid hormones are involved in many developmental and physiological processes, including osmoregulation. The regulation of the thyroid system by environmental salinity in the euryhaline gilthead seabream (Sparus aurata) is still poorly characterized. To this end seabreams were exposed to four different environmental salinities (5, 15, 40 and 55 ppt) for 14 days, and plasma free thyroid hormones (fT3, fT4), outer ring deiodination and Na+/K+-ATPase activities in gills and kidney, as well as other osmoregulatory and metabolic parameters were measured. Low salinity conditions (5 ppt) elicited a significant increase in fT3 (29%) and fT4 (184%) plasma concentrations compared to control animals (acclimated to 40 ppt, natural salinity conditions in the Bay of Cádiz, Spain), while the amount of pituitary thyroid stimulating hormone subunit β (tshb) transcript abundance remained unchanged. In addition, plasma fT4 levels were positively correlated to renal and branchial deiodinase type 2 (dio2) mRNA expression. Gill and kidney T4-outer ring deiodination activities correlated positively with dio2 mRNA expression and the highest values were observed in fish acclimated to low salinities (5 and 15 ppt). The high salinity (55 ppt) exposure caused a significant increase in tshb expression (65%), but deiodinase gene expression (dio1 and dio2) and activity did not change and were similar to controls (40 ppt). In conclusion, acclimation to different salinities led to changes in the peripheral regulation of thyroid hormone metabolism in seabream. Therefore, thyroid hormones are involved in the regulation of ion transport and osmoregulatory physiology in this species. The conclusions derived from this study may also allow aquaculturists to modulate thyroid metabolism in seabream by adjusting culture salinity.

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1. Introduction

Thyroid hormones (THs) are truly pleiotropic in fish, affecting metabolism, reproduction, growth and osmoregulation, relevant physiological processes for aquaculture (Blantón and Specker, 2007). Thus, understanding how this system is regulated by the environment in cultured species, is key for the optimization of their culture. In the aquaculture ponds of the South of Spain, where culture of gilthead seabream (Sparus aurata) is carried out, salinity is highly variable and may well influence the thyroid system. In general, the fish thyroid system responds to stimuli by regulating the release of thyroid stimulating hormone (Tsh) that in turn stimulates the thyroid follicle to secrete thyroxine (T4) into the blood stream (Eales and Brown, 1993). Within the plethora of stimuli regulating the release of Tsh in fish, different salinity concentrations are postulated (Leatherland and Farbridge, 1992). Pituitary thyroid stimulating hormone subunit β (tshb) gene expression is under negative feedback control by plasma (free) thyroid hormones (Cohn et al., 2010; Manchado et al., 2008). The pro-hormone T4 is deiodinated into bioactive triiodothyronine (T3) in the peripheral tissues (Bernier et al., 2009; Klaren et al., 2008). The regulation of deiodination in peripheral tissues is therefore a determining factor for the physiological effects of thyroid hormones.

Two iodothyronine deiodinases (Dio1 and Dio2) have outer ring deiodination (ORD) activities and in peripheral organs such as the gills and the kidney produce T3 from T4 that are directly involved in ion...
transport and osmoregulation (Arjona et al., 2008). The inactivation pathways of THs are catalysed also by Dio1 and by a third iodothyronine deiodinase, Dio3. Both Dio1 and Dio2 ORD activities have distinct substrate and co-substrate preferences (Klaren et al., 2012; Orozco et al., 2000). Reverse T3 (rT3) is usually the preferred substrate for Dio1 in mammals (Orozco et al., 1997) while T4 is the preferred substrate of Dio2 (García-G et al., 2004).

One consequence of increased TH activity is the stimulation of the basal metabolic rate, which seems to result, at least in part, in increased oxygen consumption and ATP hydrolysis. Several studies have reported species-specific changes in plasma TH levels, ORD activity (Arjona et al., 2008) or deiodinase gene expression (Lorgen et al., 2015) when fish are submitted to an osmotic challenge. Osmotic acclimation in fish is also associated with variations in plasma THs and in gillhead seabream plasma free T4 and gill ORD activity respond to a change in environmental salinity from 35 ppt to 1 ppt (Klaren et al., 2007).

Other authors have studied the thyroid system in S. aurata in hypo-saline conditions (Klaren et al., 2007; Power et al., 2001). To our knowledge, there are no previous studies characterizing the effects of acclimation to iso- or hypersaline conditions on the thyroid system in this species. We therefore set out to compare the effects of environmental hypo- and hyper-salinity on the thyroid system of the euryhaline gillhead seabream, an important aquaculture species.

2. Materials and methods

2.1. Animal maintenance prior to experimentation

Immature juvenile gillhead seabream juveniles (N = 32; 200 ± 44 g body mass, mean ± SD) were provided by Servicios Centrales de Investigación en Cultivos Marinos (SCI-CM, CASEM, University of Cádiz, Spain; Operational Code REGA ES11028000312), and maintained in the fish husbandry facility of the Faculty of Marine and Environmental Sciences (Puerto Real, Cadiz, Spain). Fish were acclimated for 35 days in 400-L tanks to seawater (40 ppt, natural salinity condition in the Bay of Cadiz, Spain) in a flow-through system under natural photoperiod (month of May in Cadiz, 14 h light:10 h dark) and temperature (environmental temperature of approximately 19.5 °C). Fish were fed commercial pellets (1% body mass) once a day (9:00) (Dibaq-Diproteg, Madrid, Spain). Each tank had a water recirculation system, the mass and length of the animals were recorded. Experimental salinities were achieved by mixing full-strength seawater with seawater with natural marine salt (Salina La Tapa, Puerto de Santa María, Cádiz, Spain). Clustal Omega (SeaView v4 software, Gouy et al., 2010) with default parameters was used to generate a multiple sequence alignment of tshb sequences from representatives of the main vertebrate taxa.

2.2. Acclimation to different environmental salinities

Fish were lightly anaesthetized in 0.05% (v/v) 2-phenoxyethanol, netted and randomly allocated to 400-L cubic tanks with different salinities (5, 15, 40 and 55 ppt with 140, 364, 1090 and 1546 mOsm kg\(^{-1}\) osmolality, respectively) (N = 8 per group). During transfer to the experimental tanks, the mass and length of the animals were recorded. Experimental salinities were achieved by mixing full-strength seawater with dechlorinated tap water (Puerto Real, Spain) or by mixing seawater with natural marine salt (Salina La Tapa, Puerto de Santa María, Cádiz, Spain). Each tank had a water recirculation system, which consisted of an external filter (Hydro Prime 30, Sacramento, CA, USA) to ensure optimal water conditions. Water conditions during experimentation were: temperature, ranging between 19.1 and 19.8 °C; 5, 15, 40 and 55 ppt salinity (variations < 1 ppt for each tank); pH, ranging between 7.82 and 7.88; dissolved oxygen, >5 mg O\(_2\) L\(^{-1}\); nitrates, between 0.05 and 1.69 mg L\(^{-1}\); nitrates, between 4.13 and 36.41 mg L\(^{-1}\); and ammonium, 0.0–0.2 mg L\(^{-1}\). These parameters were checked daily and did not vary significantly for the duration of the experiment. 20% of the water in circuits was replaced every other day. Fish were maintained in these conditions for 14 days and were fasted for 24 h before sampling. No mortality was observed during the acclimation period.

2.3. Sampling

Fish were netted, anaesthetized in 0.1% (v/v) 2-phenoxyethanol, weighed and sampled. Blood was collected with ammonium-heparinized syringes from the caudal vessels and placed into heparinized tubes. Plasma was separated from cells by centrifugation of whole blood (3 min, 10,000 × g, 4 °C). Fish were then euthanized by spinal transection and the pituitary gland was collected from each fish. The first gill arch on the left side of fish was excised. Adherent blood was removed by blotting with absorbent paper and a smaller subsample consisting of a few branchial filaments was collected using fine-point scissors. A small portion of the caudal part of the kidney was also collected. Gill filaments and kidney were placed in 100 μL of ice-cold sucrose-EDTA-imidazole (SEI) buffer (150 mM sucrose, 10 mM EDTA, 50 mM imidazole, pH 7.3) for the analysis of Na\(^+\)/K\(^+\)-ATPase activity. The remaining gill tissue and kidney were snap frozen in liquid nitrogen and stored at −80 °C until measurement of outer ring deiodination activities or mRNA extraction. Liver was also collected and weighed to determine the hepatosomatic index (HSI).

2.4. Water chemistry

Water samples were filtered (0.22 μm pore size) prior to analysis. Na\(^+\), K\(^+\) and Mg\(^2+\) levels were measured using a flame atomic absorption spectrophotometer (UNICAM 939, Servicios Centrales, University of Cadiz). Cl\(^−\) and Ca\(^{2+}\) levels were measured with commercially available kits following the manufacturers protocol (Spinreact S.A, Sant Esteve d’en Bas, Girona, Spain). Osmolality was measured using a vapour pressure osmometer (Fiske One-Ten osmometer, Fiske, Massachusetts, USA) and expressed as mOsm kg\(^{-1}\) H\(_2\)O. Water chemistry data are shown in Supplementary File 1.

2.5. Cloning of tshb

The sequence of the beta subunit of tshb was originated using a cDNA cloned from a seabream pituitary cDNA library (Louro et al., 2005). Plasmid DNA was extracted using the alkaline lysis procedure (Birnboim and Doly, 1979) and sequenced using the Sanger sequencing method. Sequence identity was determined using the tblastx and blastn algorithms (Altschul et al., 1994) against the non-redundant nucleotide (nr db) and GenBank EST databases. Homologues were defined as those with an E-value < 1e-5 and a score of >40. Several CDNA clones corresponding to tshb were identified; one cDNA clone (281 EP10C7 5a) was selected as reference and fully sequenced in order to obtain 3-fold coverage.

2.6. Phylogenetic analyses

Clustal Omega (SeaView v4 software, Gouy et al., 2010) with default parameters was used to test which substitution model best fitted the amino acid (aa) sequence alignment data. The Maximum Likelihood (ML) method, based on the selected optimal matrix-based model (JTT) (Jones et al., 1992), was used for the evolutionary analyses conducted in MEGA6 (Tamura et al., 2013). The bootstrap consensus tree was inferred from 1000 replicates (Felsenstein, 1985), and only branches corresponding to partitions reproduced in >50% bootstrap replicates were presented. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with a superior log likelihood value. A discrete gamma distribution was used to model evolutionary rate differences among sites [5 categories (+G, parameter = 1.7029)]. All positions containing gaps and missing data were eliminated.
2.7. Real-time quantitative PCR (qPCR)

Total RNA was extracted from the pituitary, gills and kidney using Mini or Midi RNeasy kits (Qiagen, Hilden, Germany) following the manufacturer’s protocol. The concentration of RNA was determined at 260 nm using BioPhotometer Plus Spectrophotometer (Eppendorf, Hamburg, Germany) and its quality was determined in a 2100 Bioanalyzer using the RNA 6000 Nano Kit (Agilent Technologies, Santa Clara, CA, USA). Only samples with an RNA Integrity Number (RIN) higher than 9.0 were used for qPCR. Synthesis of cDNA was carried out in a final reaction volume of 20 μL using qScript cDNA synthesis kit (Quanta BioSciences, Gaithersburg, MD, USA). Primers used for the analysis were designed using Primer3 software (http://frodo.wi.mit.edu/primer3) and searced cDNA sequences available in GenBank: deiodinase type 1 (dio1, DQ888894); deiodinase type 2 (dio2, DQ888895); tshb (KM014688); and β-actin (actb, X98920). qPCR assay linearity and amplification efficiencies (Supplementary File 2) were checked using dilution curves (six serial 1/4 dilutions, in triplicate, starting from 10 ng of cDNA, calculated from total input of 2) were checked using dilution curves (six serial 1/4 dilutions, in triplicate, starting from 10 ng of cDNA, calculated from total input of 2). All optimized qPCR assay were linear through 6 serial dilutions (dio1: r² = 0.982, efficiency (E) = 0.90; dio2: r² = 0.982, E = 0.90; tshb: r² = 0.988, E = 0.90; β-actin: r² = 0.999, E = 1.01). To confirm the correct amplification of these primer pairs, the obtained PCR amplicons were cloned and sequenced (CloneJET PCR Cloning Kit, ThermoFisher Scientific, Waltham, MA, USA). qPCR was carried out with a Fluorescent Quantitative Detection System (Mastercycler ep realplex2, S. Eppendorf, Hamburg, Germany). Each reaction was carried out in triplicate and contained 10 ng cDNA/total input of RNA, 0.5 μL of each specific forward and reverse primer, and 5 μL of PerfeCTa SYBR® Green FastMix™ (Quanta BioSciences) in a final reaction volume of 10 μL. The thermal cycle utilized was 10 min at 95 °C; 40 cycles of 20 s at 95 °C, 40 cycles of 20 s at 95 °C; 30 s at 60 °C; melting curve (60 °C to 95 °C, 20 min); 95 °C, 15 s. A final melt curve showed single product/dissociation curves in all reactions. The results for each gene were normalized to actb, which was stable between all samples analysed (< 0.35 Ct variation). Relative gene quantification was performed using the ΔΔCt method (Livak and Schmittgen, 2001).

2.8. Outer ring deiodination (ORD) activities

Tracers used for measurements of deiodinase activity were prepared using the chloramine-T method to produce [125I]3,3′,5′-T3, [125I]3,5′-T3 and [125I]T4 from the 3,3′-T2, 3,5′-T2 and 3,5,3′-T3, respectively (Visser et al., 1977). All those molecules have been reported as substrates for ORD activity in teleost fish (Klaren et al., 2005). Protein concentrations in the homogenates were measured with a Coomassie Brilliant Blue reagent kit (Bio-Rad, München, Germany) using bovine serum albumin (BSA) as the standard. Deiodination rates were normalized using the total homogenate protein in the reaction and were corrected for non-enzymatic deiodination.

2.9. Plasma parameters

Plasma osmolality was measured with a vapour pressure osmometer and expressed as mOsM kg⁻¹ H₂O. Plasma glucose, lactate and triglyceride levels were measured using commercial kits from Spinreact adapted to 96-well microplates. The total plasma protein concentration was determined in diluted plasma samples using a bicinchoninic acid BCA Protein Assay Kit (Pierce, IL, USA) using BSA as a standard. All assays were performed with a Bio Kinetic EL-340 Automated Microplate Reader (BioTek Instruments, Winooski, VT, USA) using Deltasoft 3 software for Macintosh (BioMetallcs Inc., Princeton Junction, NJ, USA). Plasma cortisol was measured by radioimmunoassay (RIA) (Arends et al., 1999). Plasma free thyroxine (fT4) concentrations were determined using a commercially available kit (DELFIA® fT4, PerkinElmer Life and Analytical Sciences, Turku, Finland), which consists of a solid phase time-resolved fluorimmunoassay reaction and measurements were performed using a Wallac Victor® 1420 multilabel counter. Serially diluted S. aurata charcoal-stripped plasma produced binding curves that were parallel to the standard curve (results not shown).

Plasma free triiodothyronine (fT3) levels were measured with a solid phase competitive ELISA (Human Diagnostics, Wiesbaden, Germany) according to the manufacturer’s instructions as previously described for this species (Vargas-Chacoff et al., 2016). Absorbance was measured in a Bio-Rad Model-680 microplate reader (Bio-Rad, Veenendaal, The Netherlands). Samples were diluted with S. aurata charcoal-stripped plasma when the measured concentrations of fT3 were above the maximum standard concentration.

2.10. Na⁺/K⁺-ATPase activity

Na⁺/K⁺-ATPase activities in gill and kidney homogenates were determined in microplates using McCartney’s method (McCormick, 1993) with modifications (Mancera et al., 2002).

2.11. Statistics

Differences between groups were tested using a one-way ANOVA with environmental salinity as the factor of variance. When necessary, data were logarithmically transformed to fulfill the requirements for parametric ANOVA. Normality was analysed using the Kolmogorov-Smirnov’s test. The homogeneity of variances was analysed using Levene’s test. When ANOVA yielded significant differences, Tukey’s post-hoc test was used to identify significantly different groups. When data did not comply with the premises of the parametric ANOVA, data were analysed using a Kruskal–Wallis ANOVA by ranks. Correlations between free THs, relative to mRNA parameters measured in the experimental groups, as previously described (Speers-Roesch et al., 2015). Statistical significance was accepted at p < 0.05. All the results are given as mean ± standard error of the mean (SEM).

3. Results

3.1. Biometrics

None of the groups differed in length or body mass at the start of the 14-days acclimation period (data not shown). No mortality was recorded during the experimental period. At the end of the acclimation period HSI decreased significantly in animals exposed to 55 ppt (HSI 0.67 ± 0.05%) compared to animals acclimated to 15 ppt (HSI 0.94 ± 0.06%) or 40 ppt (HSI 0.96 ± 0.06%).
3.2. Tshb amino acid sequence

The full-length sequence of *S. aurata* tshb consisted of 870 bp (accession number KM014688) and had an open reading frame (ORF) of 438 nucleotides that encoded a 146 aa protein (Supplementary File 3). Multiple sequence alignment of Tshb (Supplementary File 4) from seabream and a wide selection of vertebrates revealed they shared from 39% aa sequence conservation with mammals and reptiles (anole lizard) up to 92% aa sequence conservation with Perciformes (European sea bass) (Supplementary File 5). In common with other jawed vertebrates *S. aurata*, Tshb possessed a signal peptide of 20 aa and contained 12 conserved cysteine residues and a putative site for asparagine-linked glycosylation (Supplementary File 5).

Evolutionary analysis of *S. aurata* Tshb using the maximum likelihood method confirmed its identity and revealed that the branching of the consensus phylogenetic tree was consistent with established evolutionary relationships (Fig. 1). The exception was the chondrostean Siberian sturgeon that grouped with the tetrapods. Perciforms grouped into one clade, with tetraodontidae (82–84% aa sequence conservation), cichlids (84% aa sequence conservation) and ovalentaria (medaka and platy fish, 71–78% aa sequence conservation) in subclades. The Perciforms grouped into a consistent clade with the exception of the ovalentaria, a newly established fish clade (Wainwright et al., 2012). Seabream Tshb shared 70% aa sequence identity with Salmoniformes and 60% with Cypriniformes. The aa sequence identity between seabream Tshb and tetrapod TSHB was approximately 40%.

3.3. Pituitary tshb mRNA expression

Pituitary tshb gene expression was significantly (*p* < 0.05) higher (65%) in animals acclimated to 55 ppt salinity compared to groups acclimated to 5 or 40 ppt salinity (Fig. 2). No significant differences were detected between animals acclimated to 15 ppt and any of the other groups.

3.4. Plasma fTH levels

Free T4 (T4) concentrations in plasma were significantly (*p* = 0.0002, one-way ANOVA followed by a Tukey post hoc test; salinity effect *p* = 0.014; *N* = 4 per group) in animals acclimated to 5 and 15 ppt compared to fish acclimated to 40 and 55 ppt salinities. Plasma free T3 was also significantly higher (*p* between 0.019 and 0.010, one-way ANOVA followed by a Tukey post hoc test; salinity effect

![Fig. 1. Phylogenetic analysis of vertebrate Tshb amino acid sequences using the maximum likelihood method based and a JTT matrix-based model. A bootstrap test of phylogeny was performed with 1000 replications. Branches with >50% bootstrap support are collapsed into a single clade. The consensus tree is drawn to represent the evolutionary history of the taxa analysed. Partial proteins were not used for phylogenetic analysis. Species included in the analysis were gilthead seabream (*S. aurata*), European seabass (*Dicentrarchus labrax*), fugu (*Takifugu rubripes*), green spotted pufferfish (*Tetraodon nigroviridis*), zebra mbuna (*Maylandia zebra*), princess of Burundi (*Neolamprologus brichardi*), Nile tilapia (*Oreochromis niloticus*), three-spined stickleback (*Gasterosteus aculeatus*), platty (*Xiphophorus maculatus*), medaka (*Oryzias latipes*), Atlantic cod (*Gadus morhua*), rainbow trout (*Oncorhynchus mykiss*), Atlantic salmon (*Salmo salar*), blind cave fish (*Astyanax mexicanus*), zebra fish (*Danio rerio*), common carp (*Cyprinus carpio*), Japanese eel (*Anguilla japonica*), spotted gar (*Lepisosteus oculatus*), Siberian sturgeon (*Acipenser baerii*), anole lizard (*Anolis carolinensis*), chicken (*Gallus gallus*), Chinese softshell turtle (*Pelodiscus sinensis*), human (*Homo sapiens*), and mouse (*Mus musculus*).]
3.5. Deiodinases type 1 and 2 mRNA expression in gills and kidney

Branchial dio1 transcript abundance was significantly lower in seabream acclimated to 5 ppt salinity, with 37% lower mRNA expression in the 5 ppt-acclimated fish relative to those maintained at 40 ppt (control) and 55 ppt salinity (salinity effect $p = 0.025$; $N = 5$ per group). Conversely, deiodinase type 2 (dio2) gene expression was significantly higher (salinity effect $p = 0.007$; $N = 5$ per group) in fish acclimated to 15 ppt compared to fish at 40 and 55 ppt salinity (Fig. 4A). In contrast, transcript abundance of deiodinase type 1 (dio1) in kidney did not vary between groups. However, dio2 expression was significantly higher in the 5 ppt group (210% higher than the control group) compared to the 55 ppt salinity group (25% less expression than the control group (Fig. 4B)).

3.6. ORD activity in gills and kidney

Branchial and renal T4-ORD activities were higher in animals acclimated to salinities of 5 and 15 ppt compared to animals acclimated to 40 and 55 ppt salinity (Fig. 5). However, when incubated with rT3, gill and renal ORD activities were not significantly different between groups. Kidney T3-ORD activity increased with increased salinity with T3-ORD rates measured at 40 and 55 ppt twice as high as those measured at 5 ppt.

3.7. Plasma osmolality, metabolites and cortisol levels

Plasma parameters significantly differed between the experimental groups (Table 1). Plasma osmolality increased with increasing salinity. In general, all plasma metabolite concentrations were significantly higher in fish at 55 ppt and lower in fish at 5 ppt compared with fish at 15 ppt and 40 ppt salinities. Plasma cortisol concentrations were similar between all the experimental groups.

3.8. Correlations between components of the thyroid system

Correlations between elements of the thyroid system in fish exposed to different salinities are indicated in Supplementary File 6. Correlation
3.9. Na\(^+/K^+\)-ATPase activity in gills and kidney

Branchial Na\(^+/K^+\)-ATPase activity as a function of ambient salinity is regulated by changes in salinity in gilthead seabream. In this sense, a range covering 5 to 55 ppt salinity modified tshb gene expression, fTHs concentrations in plasma, ORD activities and relative mRNA levels of deiodinases in osmoregulatory organs (gills and kidney). The change in the thyroid system in response to a salinity challenge suggests it is involved and/or affected during the acclimation of seabream to changing osmolality conditions. Physiological processes regulated by the thyroid system such as growth or reproduction (Nugegoda and Kibrìa, 2016), of paramount relevance for the aquaculture, will consequently be modified when seabream culture occurs at different salinities.

Although pituitary tshb is differentially expressed in response to environmental salinity, only 67.2\% of its variance is explained by changes in plasma fT3, and less by plasma fT4 (23.6\%) (Supplementary File 6). Our findings reveal that although fT3 levels partially modulate pituitary expression of tshb, its fine regulation is dependent on the total amount of T3 and/or T4 in plasma. Thus, the classical feedback mechanism in which plasma T3 regulates TSH secretion was evident only in the extreme-salinity groups (5 and 55 ppt). On the other hand, the absence of a clear correlation between plasma fT3s and pituitary expression of tshb may suggest that the thyroid system is not fully controlled by the pituitary, but may be fine-tuned at the peripheral tissue level.

Our findings indicate that gilthead seabream maintains thyroidal homeostasis (viz. stable fT3 concentrations in plasma) in a wide range of environmental salinities (from 15 to 55 ppt) by changing plasma fT4 levels (higher levels at hypo- and isosmotic environments), in common with what occurs in Solea senegalensis (Arjona et al., 2008) and Acipenser stellatus (Krayushkina et al., 2015). The differences in plasma fT4 levels in our study are probably due to changes in T4 production/secretion by the thyroid gland, and/or changes in peripheral thyroid hormone metabolism.

Deiodination of T4 towards the formation of active T3 is carried out by Dio1 and Dio2 enzymes (Klaren et al., 2008). The substrate specificity of gilthead seabream Dio1 and Dio2 is not well established. In the present study, incubations with different substrates for the Dio1 and Dio2 deiodinases (T3, rT3 and T4), reveal that T4-ORD activity in gills and kidney decreases with environmental salinity while no changes in T3 activity between the gills and the kidney may be explained by differing ratios of Dio1 and Dio2 enzymes in these tissues. Thus, the apparent substrate preference of mammalian and fish Dio1 for T3 rather than T4 (Klaren et al., 2005; Kohrle, 1999) could indicate that the main deiodinase in gilthead seabream gills is Dio1. Herein, the expression of dio2 in both tissues positively correlates with T4-ORD activity (Supplementary File 6), pointing to T4 as the preferential substrate for gilthead seabream Dio2. Thus, the high T4-ORD activity revealed for the seabream kidney in the present study may indicate that the predominant deiodinase in this tissue is Dio2 rather than Dio1, even though Dio1 is also expressed.
The presence of Dio2 in gills seems to depend on the fish species studied (Loren et al., 2015; Orozo et al., 2000), although recent studies in S. aurata have illustrated that the thyroid metabolism canonical pathway is clearly regulated by salinity changes in this osmoregulatory tissue (Martos-Sitcha et al., 2016). In S. aurata dio2 mRNA expression occurs not only in gills, but also in kidney indicating that Dio2 is relevant in osmoregulatory organs. We provide some correlations between plasma fT4 concentrations and expression of dio2 in both gills and kidney, indicating an enhancement in peripheral ORD activity when circulating T4 levels increase. The results of the present study in seabream coincide with those of previous studies in fish, as the expression of Dio2 is described to increase in hyposmotic salinities (López-Bojórquez et al., 2007) due to the presence of osmotic response elements in the dio2 promoter region (Loren et al., 2015). Moreover, gill dio1 expression increases with environmental salinity in S. aurata (Fig. 4A), and this may suggest that TH inactivation pathways (as this enzyme also presents inner ring deiodinase activity) are involved in acclimation to hyperosmotic conditions. The results obtained ex vivo when T3 was used as the substrate for kidney were negatively correlated with renal dio2 expression (Supplementary File 6), and this may indicate that high levels of T3 inhibit dio2 expression in this tissue. ORD and IRD (inner ring deiodination) processes could then be modulated jointly, as renal dio1 expression was upregulated by plasma fT3 concentrations (Supplementary File 6), sustaining an increased IRD activity in the kidney when T3 levels were high. However, the enhanced T3-ORD activity in kidney at higher salinities (40 and 55 ppt) was not accompanied by differences in dio1 transcript abundance suggesting that regulation of deiodinase transcription and translation diverge. Overall, our results of ORD activity and mRNA expression support the idea of Dio2 as the main “osmoregulatory deiodinase” in seabream with Dio1 taking a secondary role.

The elevated fT3 levels measured in hyposmotic conditions (5 ppt) can be interpreted as an acclimation response that may increase the activity of ion transporters in osmoregulatory organs (Laiz-Carrion et al., 2005a). In this sense it was postulated that THs interact with other hormones such as cortisol and GH/IGF-I in order to increase the osmoregulatory capacity of fish (McCormick, 2011). As the highest fT3 levels shown in this study (fish acclimated to 5 ppt) are related to reduced growth rates (Laiz-Carrion et al., 2005b), it could be suggested that T3 reallocates metabolic energy from growth processes to ion transport and osmoregulation so that seabream can cope with the ionoregulatory demands dictated by low salinity (5 ppt) environments (higher ion transport and water retention). In agreement with this, gill Na⁺/K⁺-ATPase activity was maximal at 5 ppt. The metabolic actions of THs have been associated with increased plasma levels of energy metabolites (Vargas-Chacoff et al., 2016). However, the results of the present study are not in total concordance with this idea as seabream acclimated to 55 ppt had low levels of fTHs but a high concentration in S. aurata studied (Lorgen et al., 2015; Orozco et al., 2000), although recent studies “

Changes than Dio1, and we propose Dio2 should be considered as the main “osmoregulatory deiodinase” in the seabream. Our results indicate that the peripheral tissue plays an important role in TH regulation during osmoregulation in seabream.

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