Sexually dimorphic transcription of estrogen receptors in cod gonads throughout a reproductive cycle

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Abstract

The role of sex steroid regulation in gonadal maturation is a very complex process that is far from being fully understood. Hence, we have investigated seasonal changes in gonadal expression of estrogen receptors (ERs) in Atlantic cod (Gadus morhua L.), a batch spawner, throughout the annual reproductive cycle. Three nuclear ER partial cDNA sequences (esr1, esr2a, and esr2b) were cloned and all esr transcripts were detected mainly in liver and gonads of fish of both sexes. In situ hybridization of esrs along with germ cell (vasa) and gonadal somatic cell markers (gonadal soma-derived factor (gsdf), 3β-hydroxysteroid dehydrogenase (3βhisd), and anti-Müllerian hormone (amh) for testicular, or gsdf for ovarian somatic cells) showed that all three esrs were preferentially localized within interstitial fibroblasts composed of immature and mature Leydig cells in testis, whereas they were differentially expressed in both follicular cells and oocytes in ovary. Quantitative real-time PCR analysis revealed a sexually dimorphic expression pattern of the three esr paralogs in testis and ovary. A significant increase in esr2a expression was identified in testis and of esr2b in ovary, whereas esr1 transcripts were elevated in both testis and ovary in February and March before the spawning period. The localization and sexually dimorphic expression of esr genes in gonads indicate a direct function of estrogen via ERs in gonadal somatic cell growth and differentiation for Leydig cell in testis and follicular cells in ovary throughout the annual reproductive cycle in Atlantic cod.

Key Words
- androgen receptor (ar)
- Atlantic cod
- cytochrome P450 aromatase (cyp19a1a)
- estrogen receptor (esr)
- sexual maturation

Introduction

Estrogens, mainly 17β-estradiol (E2), act directly to promote sex differentiation and gonadal maturation (Korach 1994). Estrogen action has been classically shown to act in liver via specific nuclear estrogen receptors (ERs), which act as ligand-dependent DNA-binding transcription factors (Dahlman-Wright et al. 2006) in order to stimulate vitellogenin and choriogenin production during oocyte growth in vitellogenic stages for all vertebrates studied (Kazeto et al. 2011). Two distinct subtypes of nuclear ERs (ERα and ERβ) have been cloned in a number of organisms from humans (Keaveney et al. 1991) to nematodes (Mimoto et al. 2007). The role of ERs in gonadal
development has been elucidated from the phenotypic alterations of knockout (KO) mice. KO mice lacking Esr1 showed complete infertility in both males and females (Lubahn et al. 1993), whereas both male and female Esr2-KO animals developed normally, albeit with reduced ovulation efficiency (Krege et al. 1998).

Interestingly, there have been a considerable number of reports that show predominant ER transcripts in gonads rather than other organs, indicating the possible direct action of estrogen in gonadal cells in vertebrates. It is known that the concentration of estrogen in testis and rete testis fluid far exceeds that in male serum in various species (Hess 2000), indicating a central role for estrogen may function in testicular and epididymal cells (O’Donnell et al. 2001). To obtain an overview of the localization of ER subtypes within gonads, O’Donnell et al. (2001) surmised the likely localization of ERs in adult rodent testis from numerous items of conflicting data: Leydig cells express both ERα and ERβ, whereas Sertoli cells and testicular germ cells (e.g. spermatogonia, pachytene spermatocytes, and round spermatids) predominately expressed ERβ. The direct effects of estrogen on gonad development have been observed following administration of diethylstilbestrol (DES) to rats. DES exposure revealed that estrogen plays an inhibitory role in Leydig cell proliferation (Abney & Myers 1991) and Sertoli cell maturation (Sharpe et al. 1998). In addition, there are several lines of evidence showing that estrogen has a stimulatory effect on germ cells. In particular, a report in which neonatal rats were treated with estrogen displayed increased numbers of undifferentiated and differentiating type A spermatogonia (Kula 1988). Within rodent ovaries, both ERα and ERβ are expressed in granulosa cells in follicles (Drummond et al. 1999). Administration of estrogen to hypophysectomized rats resulted in a stimulatory effect on granulosa cell growth and differentiation (Drummond & Findlay 1999). In addition, androgen receptor (Ar) KO mice that lack functional aromatase (Britt et al. 2001) – an alternative model of ER depletion – exhibit abnormal folliculogenesis with seminiferous tube-like structures due to apoptotic mechanisms underlying the direct effects of E2 signaling on gonadal maturation and batch spawning have been poorly investigated, even if the final maturation process by maturation-inducing steroids has been studied ex vivo (Tveiten et al. 2010). To deepen our understanding of the role played by estrogen regulation in gonadal maturation, we kept 2-year-old Atlantic cod in land-based tanks and examined their annual reproductive cycle. However, molecular mechanisms underlying the direct effects of E2 signaling on gonadal maturation and batch spawning have been poorly investigated, even if the final maturation process by maturation-inducing steroids has been studied ex vivo (Tveiten et al. 2010). To deepen our understanding of the role played by estrogen regulation in gonadal maturation, we kept 2-year-old Atlantic cod in land-based tanks and examined their annual reproductive cycle throughout 1 year. In this report, we focus on the ERs in gonads: ERα (esr1) and two paralogs of ERβ (esr2a and esr2b). We also analyzed the relative mRNA levels of ar, which mainly acts in spermatogenesis (Shi et al. 2012), and cytochrome P450 aromatase (cyp19a1a) catalyzing the biosynthesis of estrogens (Johnsen et al. 2013) to determine their association with esr expression in gonads.
**Materials and methods**

**Fish husbandry and sample collection**

Atlantic cod were hatched and reared at Mørkvedbukta Research Station (University of Nordland, Norway). In 2009, when the fish were 2-year-old adults (initial weight of 1.1±0.2 kg, mean±s.d., n=18), they were transferred to three land-based flow-through tanks (40 m³) at a density of ~100 individuals/tank from August 2009 to May 2010. Seawater (7.4±0.4 °C) was pumped from 200 m depth. A commercial diet (Amber Neptun, Skretting AS, Stavanger, Norway) was provided daily at 5% (w/w) body weight.

Eight fish were sampled from each tank (n=24), killed by exposure to 0.5 g/l tricaine methanesulfonate (Sigma–Aldrich), total length, total body weight (TW), and gonad weight (GW) were measured, and the gonadosomatic index (GSI, 100×GW/TW (%)) was calculated at each sampling time point (August, November in 2009, and February, March, and May in 2010; Table 1). Differences in all numerical data for each sampling point within fish of the same sex were determined using a Tukey’s multiple comparison test using the GraphPad Prism Software, when the one-way ANOVA was significant. Normality and equal variance conditions were met, and the significance level was set at P<0.05. In order to minimize blood contamination, the fish were exsanguinated after terminal anesthesia by cutting their gill arches before sampling of other tissues. Excised tissues were then rinsed three times with PBS. For semi-quantitative RT-PCR, brain, gill, heart, head kidney, kidney, liver, spleen, stomach, midgut, testis (GSI=4.7%), ovary (GSI=1.5%), skeletal muscle, skin, and blood were collected, snap-frozen in liquid nitrogen, and stored at −80 °C for subsequent RNA extraction. For histological observations and quantitative real-time PCR (qPCR) analysis, testes (n=5) and ovaries (n=5) were sampled from individual fish at each sampling time point, fixed with 4% paraformaldehyde (PFA)/PBS at 4 °C for 24 h, or snap-frozen and stored at −80 °C respectively. PFA-fixed gonads were then washed, embedded in paraffin, sectioned at 4.5-μm thickness, and stained with hematoxylin–eosin.

All procedures used in this study were in accordance with the guidelines set by the National Animal Research Authority (Forsøksdyrutvalget, Norway) and approved by the Faculty of Biosciences and Aquaculture (University of Nordland, Norway) Ethics Committee.

**RNA extraction and cDNA synthesis**

Total RNA was extracted from various tissues using QIAzol lysis reagent (Qiagen) as detailed elsewhere (Campos et al. 2010) and quantified by spectrophotometry with a NanoDrop ND-1000 instrument (Thermo Scientific, Saven & Werner AS, Kristiansand, Norway). RNA integrity was assessed by electrophoresis on a 1% (w/v) agarose gel. Total RNA (1 μg) was transcribed to cDNA using a Quantitect reverse transcriptase kit (Qiagen) as reported previously (Campos et al. 2010).

**cDNA cloning of ER (esr) genes in Atlantic cod**

In order to identify genomic sequences that contain putative coding regions for esr genes in Atlantic cod, TBLASTN searches were performed in Ensembl (http://www.ensembl.org/) against the cod genome assembly (release 69, October 2012; Flicek et al. 2013). The following protein sequences were used as queries: i) gilt-head sea bream ERα (AAD31032.2), ERβ1 (AAD31033.1), and ERβ2 (CAE30470.1) and ii) rainbow trout ERα1 (NP_001117821.1), ERα2 (NP_001118030.1), ERβ1 (NP_001118225.1), and ERβ2 (NP_001118042.1). After extracting the corresponding genomic sequences.

**Table 1** Total length (TL), total body weight (TW), gonad weight (GW), and gonadosomatic index (GSI, 100×GW/TW) of Atlantic cod sampled throughout a sexual maturation cycle

<table>
<thead>
<tr>
<th>Sex</th>
<th>Sampling point</th>
<th>TL (cm)</th>
<th>TW (g)</th>
<th>GW (g)</th>
<th>GSI (%)</th>
<th>n</th>
</tr>
</thead>
<tbody>
<tr>
<td>Male</td>
<td>August 2009</td>
<td>44.3±0.7a</td>
<td>1050.0±75.8a</td>
<td>0.1±0.5a</td>
<td>0.1±0.0a</td>
<td>9</td>
</tr>
<tr>
<td></td>
<td>November 2009</td>
<td>50.7±1.0b</td>
<td>1566.7±92.5b</td>
<td>37.9±6.9a</td>
<td>2.5±0.2a</td>
<td>9</td>
</tr>
<tr>
<td></td>
<td>February 2010</td>
<td>50.9±1.4b</td>
<td>1746.2±158.0b</td>
<td>218.1±27.9b</td>
<td>12.4±1.0b</td>
<td>8</td>
</tr>
<tr>
<td></td>
<td>March 2010</td>
<td>53.6±1.7b</td>
<td>2346.0±211.6c</td>
<td>198.0±25.9b</td>
<td>11.2±1.2b</td>
<td>9</td>
</tr>
<tr>
<td>Female</td>
<td>August 2009</td>
<td>45.2±1.0a</td>
<td>1452.3±121.2b</td>
<td>12.1±1.4a</td>
<td>0.9±0.1a</td>
<td>7</td>
</tr>
<tr>
<td></td>
<td>November 2009</td>
<td>51.4±1.3b</td>
<td>1143.3±65.7a</td>
<td>15.9±1.8a</td>
<td>1.4±0.1a</td>
<td>9</td>
</tr>
<tr>
<td></td>
<td>February 2010</td>
<td>52.6±1.0b</td>
<td>1563.6±72.5a</td>
<td>38.9±3.2a</td>
<td>2.5±0.2a</td>
<td>14</td>
</tr>
<tr>
<td></td>
<td>March 2010</td>
<td>53.8±1.0b</td>
<td>2098.2±134.1b</td>
<td>231.4±21.1b</td>
<td>11.2±1.0b</td>
<td>14</td>
</tr>
<tr>
<td></td>
<td>May 2010</td>
<td>53.6±0.9b</td>
<td>1855.0±119.9b</td>
<td>400.1±51.7b</td>
<td>18.3±1.7b</td>
<td>16</td>
</tr>
</tbody>
</table>

Values with different lower-case letters display significant differences within the same sex (P<0.05).
Table 2. Primers used for cDNA cloning, semi-quantitative RT-PCR, quantitative real-time PCR (qPCR), and in situ hybridization (ISH). Gene names, GenBank accession numbers, PCR efficiencies (E, %), coefficient of determination values (R²), and amplicon sizes (bp) are indicated.

<table>
<thead>
<tr>
<th>Gene</th>
<th>GenBank</th>
<th>Forward primer (5’ → 3’)</th>
<th>Reverse primer (5’ → 3’)</th>
<th>Purpose</th>
<th>E</th>
<th>R²</th>
<th>Size (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>esr1</td>
<td>JX178935</td>
<td>TGCAGTCCCTGAGG-CAGTGGGTCCACCA</td>
<td>TGAACCTCGGTG-TAGGGCCGGTTGTCATCT</td>
<td>Cloning/ISH</td>
<td>–</td>
<td>–</td>
<td>822</td>
</tr>
<tr>
<td></td>
<td>–</td>
<td>AGGCAACCTGGAAGACGACGACGATG</td>
<td>TGGGCTCACAGCATCCTCCAG-CAGCAGGT</td>
<td>Cloning/ISH</td>
<td>–</td>
<td>–</td>
<td>643</td>
</tr>
<tr>
<td></td>
<td>–</td>
<td>AAGGAGCTATGCGCAAGG</td>
<td>TGAACCTCGGTG-TAGGGCCGGTTGTCATCT</td>
<td>RT-PCR/qPCR</td>
<td>83.0</td>
<td>0.999</td>
<td>307</td>
</tr>
<tr>
<td>esr2a</td>
<td>JX178936</td>
<td>GGACACTGACATGGACT-AGAGGAGTTA</td>
<td>TGCACTGACATGGACT-AGAGGAGTTA</td>
<td>Cloning</td>
<td>–</td>
<td>–</td>
<td>655</td>
</tr>
<tr>
<td></td>
<td>–</td>
<td>CTTTACACCGACCTGGCCCATGCT</td>
<td>TGCACTGACATGGACT-AGAGGAGTTA</td>
<td>Cloning/ISH (5’RACE)/ISH</td>
<td>–</td>
<td>–</td>
<td>1438</td>
</tr>
<tr>
<td></td>
<td>–</td>
<td>CTTTACACCGACCTGGCCCATGCT</td>
<td>Cloning</td>
<td>Cloning</td>
<td>–</td>
<td>–</td>
<td>213</td>
</tr>
<tr>
<td>esr2b</td>
<td>JK993476</td>
<td>TGCAGTCCCTGAGG-CAGTGGGTCCACCA</td>
<td>CAGACCAACA-CACCTCTCTGCGCTGTCCT</td>
<td>RT-PCR/qPCR</td>
<td>85.4</td>
<td>0.999</td>
<td>304</td>
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<tr>
<td>ar</td>
<td>FJ288742</td>
<td>CGATATGTTCCCAGGAATGAG</td>
<td>GTGGTTCTTTTAACTCTGCTGTAGGGAGGCTTCT</td>
<td>QPCR</td>
<td>92.3</td>
<td>0.977</td>
<td>183</td>
</tr>
<tr>
<td>actb</td>
<td>DQ402370</td>
<td>ATGTCTCTGAGTGGG-GACGTGTGTCT</td>
<td>GTGGTTCTTTTAACTCTGCTGTAGGGAGGCTTCT</td>
<td>QPCR</td>
<td>80.4</td>
<td>0.982</td>
<td>152</td>
</tr>
<tr>
<td>arf</td>
<td>EX721840</td>
<td>CAAGTTAAGGAGTTAAGAGAGTAGT</td>
<td>GTGGTTCTTTTAACTCTGCTGTAGGGAGGCTTCT</td>
<td>QPCR</td>
<td>86.0</td>
<td>0.991</td>
<td>76</td>
</tr>
<tr>
<td>eef1a</td>
<td>HM451456</td>
<td>AGGCTGACATGGACT-AGAGGAGTTA</td>
<td>CAGACCAACA-CACCTCTCTGCGCTGTCCT</td>
<td>RT-PCR/qPCR</td>
<td>88.9</td>
<td>0.955</td>
<td>142</td>
</tr>
<tr>
<td>vasa</td>
<td></td>
<td>CAGACCAACA-CACCTCTCTGCGCTGTCCT</td>
<td>Cloning</td>
<td>Cloning</td>
<td>–</td>
<td>–</td>
<td>920</td>
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<tr>
<td>gsd</td>
<td>KC204828</td>
<td>ATGA-CAGTTACTGGTGGGCTGCCTTCC-CA</td>
<td>ACAGCCACACTGGCAGCCGCCACG</td>
<td>ISH</td>
<td>–</td>
<td>–</td>
<td>600</td>
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<tr>
<td>3hsd</td>
<td>KC204829</td>
<td>ATGCTTCTGAGTGGG-GACGTGTGTCT</td>
<td>TGGCTTCTGGTACCGGAAGCT-GAAGC</td>
<td>ISH</td>
<td>–</td>
<td>–</td>
<td>786</td>
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<tr>
<td>amh</td>
<td>JN802292</td>
<td>TCCACACCACCATCCGGTCTT-CCAGG</td>
<td>TCCAGGCGCGGACCA-CACTCTTCTGCGGCA</td>
<td>ISH</td>
<td>–</td>
<td>–</td>
<td>849</td>
</tr>
</tbody>
</table>

Bioinformatic analysis

Identity of cod esr cDNA sequences was confirmed by TBLASTN searches against the non-redundant database at NCBI BLAST (www.ncbi.nlm.nih.gov). For phylogenetic analysis, Atlantic cod cDNA sequences were extended by in silico cloning using the Ensembl genome browser and their deduced amino acid (AA) sequences were aligned with corresponding orthologs in various species (Supplementary Table 1, see section on supplementary data given at the end of this article) using MUSCLE (www.drive5.com). Poorly aligned or divergent regions were trimmed using Gblocks 0.91b (molevol.cmi.mai.csic.es). The resulting multiple sequence alignment was used for Bayesian (MrBayes v3.1.2, mrbayes.csit.fsu.edu) phylogenetic reconstruction as detailed elsewhere (Fernandes et al. 2010). A graphical representation of the phylogenetic tree was obtained using the PhyloWidget (www.phylowidget.org).

Semi-quantitative RT-PCR

Semi-quantitative RT-PCR was performed with cDNAs from the various tissues mentioned above (male, GSI = 4.7% and female, GSI = 1.5%) using gene-specific primer sets (Table 2). Thermocycling parameters were 94 °C for 3 min, followed by 35 cycles (25 cycles for acidic ribosomal protein (arp)) of 30 s at 94 °C, 30 s at 60 °C, and 30 s at 72 °C, with a final elongation step of 72 °C for 3 min.
PCR products were separated by electrophoresis on a 1% (w/v) agarose gel and visualized with the Kodak gel documentation system v.4.0.5. Expression patterns were confirmed using two biological replicates of each sex.

**In situ hybridization**

Spatial expression patterns of *esr* paralogs were determined by *in situ* hybridization (ISH), along with those of known germ cell and gonadal somatic cell markers reported in other teleosts. The gene *vasa* was used for detection of spermatagonia/spermatocytes in testes or oogonia/oocytes in ovaries because of its well-conserved spatio-temporal expression pattern among teleosts, including Atlantic cod (Presslauer et al. 2012). The gonadal somatodermal factor (*gsdf*) was used to identify Sertoli cells in testes or follicular cells in ovaries, as it is a proven marker of these cells in rainbow trout (Sawatari et al. 2007), medaka (Shibata et al. 2010), and zebrafish (Gautier et al. 2011). In addition to *gsdf*, anti-Müllerian hormone (*amh*) has been used as a Sertoli cell marker in zebrafish (Rodriguez-Mari et al. 2005). Leydig cells were detected using 3β-hydroxysteroid dehydrogenase (3β*hsd*) as a marker, as reported for rainbow trout (Kobayashi et al. 1998), swamp eel (Lo Nostro et al. 2004), and Nile tilapia (Ruksana et al. 2010). The *gsdf* and *3βhsd* genes were cloned from Atlantic cod in this study. Digoxigenin-labeled sense and anti-sense RNA probes for all genes (*esr1*, *esr2a*, *esr2b*, *vasa*, *gsdf*, *amh*, and *3βhsd*) were individually *in vitro* transcribed using T3 or T7 RNA polymerase (Roche) from corresponding DNA fragments amplified using the primers listed in Table 2. Tissue samples were obtained from 2-year-old Atlantic cod reared at Mørkvedbukta Research Station. Testes (GSI=0.4%) and ovaries (GSI=1.3%) were fixed with Bouin’s solution (Sigma–Aldrich) and 4% PFA/PBS respectively at 4°C for 12–24 h, washed out with nuclease-free water, dehydrated with an ascending ethanol series, and then embedded in paraffin. Cross sections of testes and ovaries samples were prepared at 4-µm thickness, attached onto polysilane-coated glass slides (Polysine, VWR international, Leuven, Belgium), and used for ISH analysis as reported by Fernandes et al. (2006) with slight modifications. Sense and anti-sense probes for all genes (*esr1*, *esr2a*, *esr2b*, *vasa*, *gsdf*, *amh*, and *3βhsd*) were individually hybridized at 70°C for 24 h and then washed out with RNase A treatment (Sigma–Aldrich) as reported previously (Nagasawa et al. 2009). Sections were mounted on gelatin embedding medium (Sigma–Aldrich) and observed under a BX-51 microscope (Olympus).

**Quantitative real-time PCR**

Twenty-fold diluted samples of cDNA synthesized as described above were used in duplicate, as were negative (minus reverse transcriptase) and no template (water) controls. Gene-specific qPCR primers for the three *esr* paralogs were designed using the GenScript Real-time PCR Software (www.genscript.com) to span at least one intron/exon border whenever possible (Fernandes et al. 2008). The qPCR was run at 95°C for 15 min, followed by 45 cycles of 15 s at 94°C, 20 s at 60°C, and 20 s at 72°C using LightCycler 480 SYBR Green I Master chemistry (Roche) on a LightCycler 480 (Roche), as described previously (Campos et al. 2010). Specificity of the reactions was evaluated by melting curve analysis and further by Sanger sequencing of amplicons. Amplification efficiencies were calculated by standard curves from a fivefold dilution series (1:1, 1:5, 1:25, 1:125, and 1:625) of pooled cDNA as detailed by Fernandes et al. (2008). Cycle threshold (*Ct*) values were determined using the LightCycler 480 Software with a level of fluorescence intensity arbitrarily set at 1. Three endogenous reference genes, β-actin (*actb*), *arp*, and eukaryotic elongation factor 1α (*eef1a*) were validated as reported by Fernandes et al. (2008) and Nagasawa et al. (2012). Their geNorm stability values (*M*) were 0.812, 0.779, and 0.618 for *actb*, *arp*, and *eef1a* respectively. The most stable gene combination was found to be *arp+eef1a* with an average pairwise variation *V*2/3 = 0.258. Therefore, raw qPCR data of target genes were corrected using the geometric average of *arp* and *eef1a* quantities as normalization factors. Differences in relative expression levels of three genes *esr*, *ar*, and *cyp19a1a* among different sampling time points or between sexes were examined by Mann–Whitney *U* tests using the GraphPad Prism Software (San Diego, CA, USA), as the data were not normally distributed. The significance level was set at *P* < 0.05.

**Results**

**Gonadal maturation status throughout an annual reproductive cycle in 2-year-old Atlantic cod**

Atlantic cod kept in land-based tanks throughout a year showed a clear reproductive cycle with a significant increase in GW (Table 1) and differentiation of germ cells in both testes and ovaries (Fig. 1). Throughout a reproductive cycle, testis and ovary weights reached a peak in February (GSI = 12.4 ± 1.0%, *n* = 8) and March (GSI = 18.3 ± 1.7%, *n* = 16) respectively (Table 1). Spermiation was seen in some male individuals in February and March,
Figure 1
Histology of representative testes and ovaries at different maturation status using hematoxylin–eosin staining in 2-year-old Atlantic cod throughout an annual reproductive cycle. (A) Spermatogonia and cysts of primary spermatocytes. (B) Cysts of spermatocytes. (C and D) Cysts of spermatocytes and lobules containing spermatzoa. (E) Gonadal myoid cells with remaining spermatzoa. (F) Perinuclear stage oocytes with a large circular nucleus and peripheral nucleoli. (G) Oocyte with cortical alveoli, chorion, and nucleus with detached nucleoli. (H) Vitellogenic oocytes with yolk granules filling most of the cytoplasm and a large central nucleus. (I) Vitellogenic oocyte with enlarged yolk granules, eccentric nucleus, and chorion. (J) Hydrated egg in follicle sac with post-ovulatory follicle. Arrowheads, spermatogonia; arrows, primary spermatocytes; ca, cortical alveoli; ch, chorion; ct, connective tissue; f, follicle layer; gmc, gonadal myoid cells; he, hydrated egg; n, nucleus; nu, nucleolus; SC, spermatocytes; SZ, spermatozoa; and yg, yolk granule. The scale bars represent 100 μm. A full colour version of this figure is available at http://dx.doi.org/10.1530/JME-13-0187.
Three esr paralogs in Atlantic cod

Partial cDNA sequences of three esr genes in Atlantic cod were obtained using a combination of in silico and experimental cloning: esr1 (JX178935), esr2a (JX178936), and esr2b (JK993476). Partial ERα AA sequences (479 AA) overlapped on 83% of the region of full-length orange-spotted grouper ERα with 81% similarity and 75% identity, and five conserved essential domains of ERs were identified: A/B (98 AA (partial)), C (84 AA), D (62 AA), E (240 AA), and F (64 AA). For ERβ1, the 532 AA partial sequence covered 94% of the region of the full-length Japanese flounder ERβ with 83% similarity and 74% identity and contained the essential domains A/B (157 AA), C (82 AA), D (47 AA), and E (246 AA (partial)). In addition, the 61 AA ERβ2 partial sequence corresponded to 9% of full-length gilt-head sea bream ERβ and comprised A/B (24 AA in (partial)) and C (37 AA in (partial)) domains. Bayesian analysis using in silico-extended cod sequences containing the E-domain produced a consensus phylogenetic tree that displayed a clear separation of ERα, ERβ1, and ERβ2 subtypes into three main clades, whereas all the homologs of estrogen-related receptor α (ESRRA) were grouped outside of all ER clades (Fig. 2). In the teleost ERα clade, an isolated subcluster containing ERα1 and ERα2 from a few teleost species (e.g. Carassius auratus, O. mykiss, and Spinibarbus denticulatus) was observed. G. morhua ERα was grouped in the ERα clade. The two clades of teleost ERβ1 and ERβ2 displayed similar topologies. In both the teleost ERβ1 and ERβ2 clades, G. morhua ERβ1 and ERβ2 were most closely related to O. mykiss ERβ1 and ERβ2 respectively. Unexpectedly, some Cyprinididae species (e.g. S. denticulatus, Varicorhinus barbatulus, C. auratus, and Danio rerio) showed an isolated subcluster distinct from teleost ERβ1 and ERβ2.

Figure 2
Phylogenetic inference of ER subtypes found in vertebrates. The numbers at the nodes indicate posterior probability obtained from Bayesian analysis. GenBank accession numbers of all ERs are given in Supplementary Table 1.

Tissue distribution of esr transcripts

The genes esr1, esr2a, and esr2b were differentially expressed across various tissues in both adult male and female Atlantic cod (Fig. 3). The esr1 transcripts were mainly found in liver and gonads in both sexes, but prominent in testes and in livers of females. The esr2a
transcripts were widely distributed in several tissues with varied expression levels. Nevertheless, the esr2a transcripts exhibited a sex-dependent distribution in liver and gonads, similar to esr1. Expression of esr2a was found in skin of males and blood of females, whereas the esr2a transcripts were seen in the pronephros and excretory kidney in males but not much in females. The esr2b transcripts had a broad distribution in female tissues, while their expression was found in fewer male tissues, including testis and liver. Notably, expression of esr genes in liver was more prominent in females than in males and all esr transcripts were consistently present at higher levels in testis than in ovary, except for esr2b. In brain, low transcript levels of esr1 in females and esr2a in males were observed but expression of esr2b was not detected.

Localization of esr transcripts in testis

The central region of the testes was sampled for histological analyses (Fig. 4A) and sequential cross sections of the testicular lobe were prepared (Fig. 4B). Hematoxylin staining showed the presence of spermatogonia and spermatocytes (Fig. 4C). ISH with a vasa probe specifically stained germ cells (Fig. 4D), while staining with gsdf or amh probes affected Sertoli cells surrounding germ cell cysts (Fig. 4E and F). A 3βhsl probe detected Leydig cells in the interstitial tissue between lobule segments (Fig. 4G). There was no visible difference in localization between esr1 and esr2a in testis, even though the staining intensity of esr2a was higher than that of esr1 (Fig. 4H and I). These two esrs were preferentially observed in the testicular interstitial fibroblasts, whereas weak signals for esr2b were detected in some interstitial fibroblasts (Fig. 4J). No hybridization signals were observed with sense probes (Supplementary Figure 1, see section on supplementary data given at the end of this article).

Localization of esr transcripts in ovary

Sequential cross sections of ovary were prepared and used for histological analyses (Fig. 5A and B). Several developmental stages of oocytes could be visualized by hematoxylin staining (Fig. 5C). ISH with a vasa probe strongly stained pre- and early-vitellogenic oocytes rather than mid-vitellogenic oocytes (Fig. 5D), while a gsdf probe stained the follicular cell layer surrounding oocytes at all developmental stages (Fig. 5E). Signals for esr1 were predominantly observed in follicular cells, (Fig. 5F), whereas, esr2a signals were mainly detected in the follicular cell layer and the cytoplasm of pre- and early-vitellogenic oocytes (Fig. 5G). In both follicular cells and the cytoplasm of all oocytes, esr2b signals were detected (Fig. 5H). No hybridization signals were observed in any of the cells with negative control probes (Supplementary Figure 2, see section on supplementary data given at the end of this article).

Sexually dimorphic expression of ar, cyp19a1a, and esr genes during a reproductive cycle

The levels of esr1 mRNA were upregulated by 12.6- and 7.0-fold from August to March in both testes and ovaries respectively (Fig. 6A). In March, esr1 mRNA levels in testes were 5.0-fold higher than those in ovaries (Fig. 6A). A significant increase in esr2a mRNA level in testes was particularly evident in February and March (P<0.05; Fig. 6B), but no significant alterations in esr2a in ovaries were observed throughout the reproductive cycle. The level of esr2a mRNA in testes was 13.3- and 12.0-fold higher than that in ovaries in February and March respectively (Fig. 6B). The level of esr2b mRNA in ovaries was elevated up to 24.9-fold from August to March and then rapidly decreased by May, showing a temporal pattern similar to esr1 in testis (Fig. 6C). In addition, ar mRNA levels in testes were elevated up to 6.5-fold from August to March and then decreased in May, while ar expression in ovaries had a modest peak in November (Fig. 6D). Remarkably, cyp19a1a transcript levels in ovaries increased by 37.5-fold from August to March, whereas cyp19a1a was barely detected in testes throughout the reproductive cycle (Fig. 6E).
Discussion

Knowledge about the direct functions of estrogen in gonadal cells, and particularly the role of ER subtypes, is still limited to a few mammal species. In this study, we characterized three esr paralogs in Atlantic cod that were hitherto unknown in the teleost superorder Paracanthopterygii. The sexually dimorphic expression of esr transcripts in gonads with peaks before the spawning period throughout a reproductive cycle represents the first observation, to our knowledge, in a batch spawner.

Figure 4
Localization of transcripts of three esr, vasa, gsdf, 3βhsd, and amh in Atlantic cod testes. (A) Excised testis from 2-year-old Atlantic cod (GSI = 0.4%). The dashed line indicates the region sampled for ISH analysis. a, anterior and p, posterior. (B) Schematic representations of a testicular lobe connected to efferent duct (left panel in (B)) and its cross-sectional image (right panel in (B)). The dashed line indicates the section location. The area enclosed by the black box in (B) indicates the position of low-magnification fields (insets in (C, D, E, F, G, H, I and J)). (C, D, E, F, G, H, I and J) Hematoxylin staining (C) and ISH staining with sense or anti-sense probes for vasa (D), gsdf (E), amh (F), 3βhsd (G), esr1 (H), esr2a (I), and esr2b (J). (C, D, E, F, G, H, I and J) High-magnification fields taken from the areas adjacent to insets. White arrowheads indicate spermatogonia. SC, spermatocytes. Arrows indicate the position of weak signals that were detected in interstitial fibroblasts. The bars represent 5 cm (A), 100 μm (C, D, E, F, G, H, I and J), and 200 μm (insets in (C, D, E, F, G, H, I and J)). A full colour version of this figure is available at http://dx.doi.org/10.1530/JME-13-0187
In teleost fish, two subtypes of ERβ (ERβ1 and ERβ2 – also named ERγ) have been identified in distant taxa. In contrast, most fish species have only ERα, but two ERα isoforms (ERα1 and ERα2) have recently been reported in salmonids (rainbow trout; Nagler et al. (2007)) and cyprinids (goldfish C. auratus and phoenix barb S. denticulatus; Zhu et al. (2008)). Atlantic cod has a single ERα subtype, supporting the hypothesis that the two ERα subtypes (ERα1 and ERα2) reported in goldfish, rainbow trout, and phoenix barb are derived from the recent tetraploidization event that is thought to have occurred in the salmonid and cyprinid lineages.

Within the ERβ subtype, esr2a and esr2b were in silico mapped on different scaffolds in the Atlantic cod genome. The chromosomal localization of esr2a and esr2b indicates that these paralogs arose from the 3R teleost-specific whole-genome duplication event that occurred 350 million years ago (Meyer & Van de Peer 2005).

Teleost esrs exhibit a wide variety of tissue distribution patterns but with common E2 target tissues associated with reproduction such as liver and gonads (Filby & Tyler 2005, Chen et al. 2011). In Atlantic cod, all three esr transcripts were present in liver and gonads with a sexual dimorphic expression pattern. Prominent expression of esrs in livers of females compared with livers of males could be caused by the higher endogenous E2 level in female serum (Norberg et al. 2004). In gonads, esr1 and esr2a were predominantly expressed in testes compared with ovaries indicating an

Figure 5
Localization of transcripts of three esrs, vasa, and gsdf in Atlantic cod ovary. (A) Excised ovary from 2-year-old Atlantic cod (GSI = 1.3%). The region sampled for ISH analysis is indicated by the dashed line. a, anterior and p, posterior. (B) Schematic representation of cross section of ovary. The area enclosed by the black box in (B) indicates the position of low-magnification fields (insets in (C, D, E, F, G and H)). (C, D, E, F, G and H) Hematoxylin staining (C) and ISH staining with anti-sense probes for vasa (D), gsdf (E), esr1 (F), esr2a (G), and esr2b (H). (C, D, E, F, G and H) High-magnification fields taken from the areas adjacent to insets. The bars represent 5 cm (A), 100 μm (C, D, E, F, G and H), and 200 μm (insets in (C, D, E, F, G and H)). A full colour version of this figure is available at http://dx.doi.org/10.1530/JME-13-0187
important role of both ERs in spermatogenesis, as proposed for other teleost species (Pinto et al. 2006, Zhu et al. 2008).

In rodents, several studies have demonstrated that the spatial distribution of ER subtypes in testis varies significantly among species, as reviewed by O’Donnell et al. (2001), but there is a consensus that both ERα and ERβ in rodent ovary are expressed in granulosa cells of follicles (Drummond & Findlay 1999). In testolets, there is very limited knowledge about the localization of ER mRNA or protein in adult gonads and their expression pattern is controversial (Bouma & Nagler 2001, Wu et al. 2001, Andreassen et al. 2003, Chakraborty et al. 2011b). This study delivers significant insights into this matter by identifying the cells expressing esr paralogs in fish gonads for both sexes. In cod testis, all three esr transcripts were preferentially found in testicular interstitial fibroblasts, similar to the localization of rainbow trout ERα protein in testis (Bouma & Nagler 2001) but not in the Sertoli cells surrounding spermatogonia. It has been reported that rainbow trout ERα protein is expressed in interstitial fibroblasts containing Leydig cell precursors and is involved in differentiation of precursors into mature Leydig cells (Bouma & Nagler 2001). In Atlantic cod testis, the number of the esr1/esr2a-expressing interstitial fibroblasts was larger than that of the 3βhsd-expressing interstitial fibroblasts (Fig. 3G, H and I), indicating that esr1/esr2a-expressing cells in testicular interstitial fibroblasts could be both precursor and mature Leydig cells. Therefore, the main target cells of E2 via ERs in Atlantic cod testicular cells could be Leydig cells, and ERs (particularly in esr1 and esr2a) may be involved in growth and maturation of Leydig cells to maintain their steroidogenesis. Nevertheless, there are reports of results conflicting with our observations, which show predominant localization of esr in fish mitotic or meiotic germ cells in eelpout (Andreassen et al. 2003) and channel catfish (Wu et al. 2001), indicating a diversity of E2 signaling requirements of spermatogenic cells among teleosts. There are only two other reports describing the localization of esr in teleost ovarian cells so far: esr1 in eelpout (Andreassen et al. 2003) and esr1, esr2a, and esr2b in medaka (Chakraborty et al. 2011b). In Atlantic cod, transcripts of the three esr genes were differentially localized in ovaries even though they were all observed in follicular cells surrounding mid-vitellogenic oocytes. Some degree of conservation in esr expression patterns may be noted between cod and the above two species. First, esr1 is preferentially weakly expressed in follicular cells of pre-to mid-vitellogenic oocytes. In contrast, esr2a is predominantly expressed in the cytoplasm of pre- and early-vitellogenic oocytes rather than their follicular cells. Furthermore, esr2b is mainly expressed in both the follicular layer and cytoplasm of oocytes. These observations of ovarian cells highlight the potential importance of all three esr in follicular cell growth and differentiation during cod folliculogenesis, as suggested for rodents (Drummond & Findlay 1999, Drummond et al. 1999). Further studies are required to specify the function of ER in fish oocytes.

It is noteworthy that Atlantic cod testes have a unique structure in each individual testicular lobe: undifferentiated spermatogonia and the most advanced germ cells are distributed in the periphery of the lobe and in the vicinity of the collecting duct respectively (Almeida et al. 2008). Interestingly, this gradient distribution of different germ cell types was also visualized in our study using the ISH detection system with a gsf probe (upper right panel in Fig. 4E). Similar to rainbow trout (Sawatari et al. 2007), Atlantic cod gsf was highly expressed in the Sertoli cells surrounding undifferentiated and/or early spermatogonia rather than the Sertoli cells surrounding cysts of advanced germ cells such as spermatocytes and spermatozoa. In contrast, amh transcripts

Figure 6
Quantification of three esrs (A, B and C), ar (D), and cyp19a1a (E) in gonads of Atlantic cod throughout the reproductive cycle. Black and white bars show the relative mRNA expression in testes and ovaries respectively. Transcript levels were quantified by real-time PCR. Error bars show S.E.M. at each sampling time point. Different superscript letters indicate significant differences within the same sex throughout the reproductive cycle (capital letters, testes and lower-case letters, ovaries; n = 25). Asterisks (*) indicate significant differences between testes and ovaries at a particular sampling point at P < 0.05 (n = 5).
were distributed in Sertoli cells with similar signal intensities regardless of germ cell developmental progression. To the best of our knowledge, this is the first paper examining seasonal changes in all three esr transcripts in both testes and ovaries of a batch spawner throughout an annual reproductive cycle. At several time points, the three esr paralogs were differentially expressed in male vs female gonads. The results of GSI changes and histological observations of gonads enabled us to assume that their main spawning period may be April and revealed a clear annual reproductive cycle in 2-year-old Atlantic cod under the experimental conditions used, with a similar sexual maturation process to that reported by Karlsen et al. (2006).

Gonadal esr1 mRNA expression increased significantly in both testes and ovaries as gonadal maturation progressed and decreased after the spawning period, resembling the results of esr1 expression in orange-spotted grouper ovaries at different developmental stages (Chen et al. 2011). A similar increase in mRNA level was also found for esr2a in testes and for esr2b in ovaries. These sexually dimorphic expression patterns of esr paralogs along with the observed significant increase in their relative mRNA levels indicate that E2 signaling via ERs may be essential for Leydig cells in testes and follicular cells in ovaries during gonadal maturation period. As esr1/esr2a genes are preferentially expressed in Leydig cells in cod testes and esr1 is specifically expressed in the follicular layer in cod ovaries, it is plausible that this increase in their mRNA levels may be associated with Leydig cell proliferation before the spawning period and proliferation of follicular cells during oocyte growth and maturation respectively. Recently, an in vitro study uncovered the novel pathway of the direct function of estrogen in the marsupial mammal gonad: the function of estrogen mediated by ER blocks the nuclear entry of SOX9 transcription pathway by activated ER in gonadal somatic cells in fish.

AR plays a key role in androgen action and it is essential for the maintenance of spermatogenesis in testis (Ikeuchi et al. 2001). Almeida et al. (2009) reported that Atlantic cod plasma 11-ketotestosterone levels increased in February and March along with the advancement of spermiogenesis and spermiogenesis, in agreement with an increase in GSI. Moreover, they showed that ar mRNA was prominently localized in Sertoli cells regardless of growing spermatogonial clones. In our study, we observed a gradual increase in ar expression in testis toward the spawning season and significantly higher transcript levels in February and March along with the increase in GSI in testis, indicating that the number of Sertoli cells is increasing at this point. Taken together with the concomitant increase in plasma androgen levels (Almeida et al. 2009), our data indicate the potential importance of androgen signaling in Sertoli cells for maintaining spermatogenesis and spermiogenesis in cod. In contrast, we found only a modest peak of ar expression in ovaries in November, implying proliferation of the follicle cells and the epithelial cells of the ovigerous lamellae, as reported in ovary of Japanese eel Anguilla japonica (Tosaka et al. 2010). It should be noted that the molecular function of AR in teleost ovaries still remains to be investigated.

Aromatase is a key enzyme for converting androgens to estrogens during sexual development. It is encoded by a single gene in mammals, with exception of the domestic pig and other suiformes, which have multiple cyp19 genes (Corbin et al. 2009). In contrast, teleosts have two cyp19 genes: cyp19a1a is preferentially expressed in ovaries, whereas cyp19a1b is found predominantly in brain (Tchoudakova & Callard 1998). Our current knowledge of seasonal changes of cyp19a1a expression in fish ovaries throughout a reproductive cycle is still very limited (Sampath Kumar et al. 2000, Rocha et al. 2009, Johnsen et al. 2013). In Atlantic cod, cyp19a1a transcripts are constantly present at higher levels in ovaries than in testes, with a significant increase in expression in ovaries but not in testes towards the spawning season. Importantly, these data indicate that cyp19a1a has potential as a molecular indicator of ovarian maturation status in batch-spawning teleosts. It should be noted that the upregulation pattern of mRNA levels for cyp19a1a and esr1/esr2b in ovaries coincided with the increase in plasma E2 levels in female cod reported by Norberg et al. (2004), indicating that estrogen biosynthesis and its signaling via ERs are particularly important during the period before spawning. In conclusion, we identified three ER subtypes in Atlantic cod, representing the superorder Paracanthopterygii, and found that esr1, esr2a, and esr2b transcripts were detected mainly in liver and gonads of fish of both sexes. All three esr paralogs were predominantly localized within interstitial fibroblasts in testes, whereas they were differentially expressed in both follicular cells and oocytes in ovaries. Throughout an annual reproductive cycle, the mRNA level of three esr genes, as well as ar and cyp19a1a, displayed sex-dependent upregulation in gonads with a peak during the period before spawning, indicating their importance in
preparation for this event, perhaps through activation of ER-responsive genes and proliferation of Leydig/Sertoli and follicular cells. These findings provide new insights into the role of ERs in gonadal development during the reproductive cycle of batch-spawning teleosts.

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**Supplementary data**

This is linked to the online version of the paper at http://dx.doi.org/10.1530/JME-13-0187.

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**Declaration of interest**

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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**Author contribution statement**

I B and J M O F conceived and designed the experiments. K N, C P, and L K performed the experiments. K N and C P analyzed the data. I B and J M O F contributed reagents/materials/analysis tools. K N, C P, L K, I B, and J M O F wrote the paper.

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