Cloning and differential expression of estrogen receptor and aromatase genes in the self-fertilizing hermaphrodite and male mangrove rivulus, *Kryptolebias marmoratus*

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Abstract

The mechanisms underlying sex determination and differentiation in fishes are labile in response to environmental parameters. Sex-specific phenotypes are largely regulated by sex steroids, and the inhibition or the stimulation of aromatase can reverse sex as well as alter secondary sexual characteristics in fishes. Among vertebrates, the mangrove rivulus is the only known self-fertilizing hermaphrodite. Throughout most of its range, rivulus appear to exist as clonally reproducing hermaphrodites. However, outcrossing has been documented in Belize, where up to 25% of rivulus collected are males. The direct development of (primary) males occurs when embryos are incubated at 18°C and hermaphrodites develop into secondary males when held at 28°C. Given the importance of sex steroids, their receptors, and aromatase in sex determination and differentiation of fishes, we cloned, sequenced, and quantified the expression of estrogen receptors (*ERα*, *ERβ*) and ovarian (*AroA*) and brain (*AroB*) aromatase genes. Hermaphrodites had increased *ERα*, *ERβ*, *AroA*, and *AroB* gene expression in the liver, gonad, gonad, and brain respectively, compared to males. These data are consistent with the gene expression data reported for other species and are reflective of the presence of ovarian tissue in the hermaphrodites. Interestingly, we show the elevated expression of brain aromatase in the hermaphrodite brain. The role of the dimorphic expression of brain aromatase in the regulation of sex-specific characteristics is intriguing and requires further research. Because of the uniqueness of its reproductive biology, rivulus is an excellent model for elucidating the mechanisms regulating vertebrate sex determination and sexual differentiation.

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Introduction

Sex determination and sexual differentiation

Determination of female or male phenotype in mammals is under strict genetic control, which directs the development of ovaries or testes (Graves 1994). Differentiation of sexually dimorphic characteristics occurs mostly under the control of the sex steroid hormones, androgens and estrogens, which are synthesized primarily in the gonad (Wilson 1994).

Like mammals, most fish species have separate sexes (called gonochorism) and believed to have genetic sex determination. In contrast to mammals, the mechanisms underlying sex determination and differentiation in fishes vary widely and are labile in response to environmental parameters, including temperature and demographic structure of the local population (Devlin & Nagahama 2002). Furthermore, sex can be purposely manipulated via treatment with synthetic chemicals, a common practice in aquaculture (Donaldson 1996). Both sex determination and sexual differentiation are altered in fishes exposed to endocrine disrupting chemicals (Damstra *et al*. 2002, Nagahama *et al*. 2004). A naturally occurring example of lability in sex determination and sexual differentiation is that of hermaphroditic fishes. Hermaphrodites either contain both ovarian and testicular tissues (called simultaneous hermaphroditism) or develop first as one sex and then change to the other (called sequential hermaphroditism) (Shapiro 1994).

Compared to sexual differentiation, little is known about the genetic and the molecular mechanisms that control sex determination in fishes and why genetic sex determination is relatively easier to override by environmental factors compared with mammals. Arguably, the best studied model of sex determination in fishes is the medaka, *Oryzias latipes*, in which the first sex determining gene, *DNA motif on the Y chromosome (DMY)*, in a non-mammalian vertebrate has been identified (Matsuda *et al*. 2002). Analogous to the *SRY* gene in mammals, *DMY* expression has been documented in the Sertoli cells of the XY gonad during the time of sex determination. Two other genes, *DMRT-1b(Y)*...
and the vasa homologs (primary germ cell markers) vas-s and vas, have also been associated with early events during sex determination of medaka and tilapia (*Oreochromis niloticus*). We know that the expression of DMRT-1b(Y) in medaka strictly correlates with the Y chromosome and treatment with exogenous estrogen has no effect on its expression (Scholz et al. 2003), and vas-s is predominantly expressed in oogenesis and vas in spermatogenesis in tilapia (Kobayashi et al. 2002), but the functional connection between these three genes remains unclear at this time.

Other researchers have focused on the primary germ cells as directors of sex determination. In gonochoristic species, ovarian tissue in females develops prior to spermatogenic tissue of males. This is hypothesized to be due to the induction of meiosis, resulting in ovarian tissue, or a block to meiosis in the primary germ cells, resulting in testicular tissue (Koubova et al. 2006). Injection studies of medaka embryos with DMY RNA caused a meiotic block compared to control fish (Kobayashi et al. 2004, Nagahama 2006). Recent research suggests a temporal relationship among DMY, Sox9a, and DMRT-1b(Y) (Kobayashi et al. 2004, Nakumoto et al. 2005, Nagahama 2006). While based on RNA and not on functional proteins, this pattern is strongly suggestive of a rudimentary signaling pathway, with DMY blocking meiosis, Sox9a regulating testicular tubule development, and DMRT-1b(Y) being important to spermatogenesis itself. To date, this information is only available in a single strain of the medaka.

Due to the interest in the aquaculture of ornamental and food fish species, much has been learnt about the differentiation of sex in fishes (Yamamoto 1969, Donaldson 1996, Devlin & Nagahama 2002). Sex-specific phenotypic differences are regulated by androgens, principally testosterone and 11-ketotestosterone, and food fish species, much has been learnt about the maintenance of gametogenesis as well as the differentiation of secondary sex characteristics, including morphology, coloration, and behavior (Yamamoto 1969, Donaldson 1996, Devlin & Nagahama 2002). The importance of the relative concentration of these sex steroids has been documented by the manipulation of aromatase, the enzyme that converts androgens to estrogens. Inhibition or stimulation of aromatase can reverse sex as well as alter secondary sex characteristics.

**Reproductive biology of the mangrove rivulus**

The mangrove rivulus (*Kryptolebias marmoratus*, synonym *Rivulus marmoratus*, referred in this paper as rivulus) is an excellent organism to study the mechanisms of sex determination and sexual differentiation because of the uniformity of its reproductive biology. Among vertebrates, it is the only known self-fertilizing simultaneous hermaphrodite (Harrington 1961). For more information about the life history of the rivulus, see the review paper by Taylor (2000). The cytogenetics of rivulus has been studied, and Sola et al. concluded that the diploid chromosome number is 46 and the chromosomes are homomorphic (Sola et al. 1997). Most rivulus collected from the wild are selfing hermaphrodites, yet in some populations, males are found (only a few males have ever been collected in Florida, yet up to 25% of fish sampled in Carrie Bow Cay, Belize, are males); (Turner et al. 1992a). In addition to selfing, there is evidence of outcrossing, and the degree and prevalence in wild population is presently being investigated by others (Turner et al., 1990 #1820, Lin & Dunson 1995 #1967, Murphy & Collier 1996 #2224, Turner, 1992 #2987, and Mackiewicz et al. 2006).

As a hermaphroditic species, sex determination is plastic and has a strong environmental influence with temperature being known to affect sex determination (Harrington 1967 #3612, Harrington 1968 #3611). In the laboratory, hermaphrodites develop at normal culture temperatures of 25 °C. Primary males (direct development) can be produced when embryos are incubated at 18 °C, although the response is not all or none, i.e. <70% develop as males (Harrington 1967). Some hermaphrodites can be induced to develop into secondary males by holding them at 28 °C (Harrington 1968, 1971), presumably through degeneration of their ovarian tissue, although this transformation has not been studied systematically (Harrington 1975). Since there is evidence of outcrossing in the Belizian population, mating is presumed to occur between hermaphrodites and males (Turner et al. 1992a,b). Further, Belizian males are about the size of hermaphrodites, hence these are hypothesized to be secondary males; high water temperatures in the tropics may induce the herm→secondary male transformation. While hermaphrodites are reported to go through a juvenile female stage prior to ontogeny of testicular tissue (Soto et al. 1992, Cole & Noakes 1997), no one has ever observed or collected functional, adult females in the field or laboratory until recently. In our lab, 100%
juvenile rivulus ≤7 days post-hatching (dph) exposed to ethinyl-estradiol (1 ppb until 28 dph) and raised in untreated water until adulthood (110 dph), developed as females (unpublished data from EFO lab).

Given the importance of sex steroid hormones and their receptors, and the enzyme aromatase in sexual differentiation of fishes, we cloned and sequenced the estrogen receptor (ERα and ERβ), cloned and partially sequenced ovarian and brain aromatase (AroA and AroB respectively) genes. Next, we compared the expression of ERα, ERβ, AroA, and AroB genes between the adult hermaphrodite and male rivulus. We hypothesized that there would be differential expression of these genes between these reproductive morphs and that those differences would reflect the presence of ovarian tissue in the hermaphrodite.

Materials and methods

Fish

Fourteen adult hermaphrodites and 14 primary males (age 11–12 months) were obtained from a breeding colony of rivulus maintained by EFO. Fish were maintained at 24 ± 1 °C, 16 h light:8 h darkness photoperiod, 15 ppt seawater (reverse osmosis water) plus Instant Ocean sea salts (Aquarium Systems, Inc., Mentor, OH, USA) and fed brine shrimp (Artemia salina) nauplii daily ad libitum. Fish were chosen at random, anesthetized with 150 ppm MS-222 buffered with NaH2CO3 (Sigma), and euthanized by severing the spinal cord immediately posterior to the skull. The brain (including pituitary) and liver were excised and immediately snap-frozen in liquid nitrogen and stored at −80 °C for quantitative PCR (QPCR, see below). After a section of the gonad was removed for histology (see below), the remainder was snap-frozen and stored as explained for the brain and liver.

Histological examination of the gonad

A sample of each gonad was fixed in 10% neutral buffered formaldehyde, dehydrated in an ethanol series, cleared in CitriSolv (Fisher Scientific, Hampton, NH, USA), and embedded in paraffin. The tissues were sectioned ventrally at 5 μm on a rotary microtome and stained with hemotoxylin and eosin-Y (Humason 1997). For each fish, three slides were chosen (from approximate third points in the sample) and stained. The gonadal tissue samples were analyzed for the presence of both ovarian and testicular tissues and only for testicular tissue in the hermaphrodites and male fish respectively (Fig. 1). Only reproductively active fish were acceptable for use in this study. Gonadal tissue was acceptable if oocytes, perinuclear follicles, and vitellogenic follicles were observed in the ovarian and spermatocytes, spermatatids, spermatozoa were observed in the testicular tissue (modified from (Grier 1981, Wallace & Selman 1981)).

Cloning and sequencing of ERα and ERβ genes

For the ERα and ERβ, two conserved amino acid regions, YHYGVW and NKGME/DQ of fish ERα and ERβ, were selected and their degenerate oligonucleotides were used as primers for PCR. As a template for PCR, first-strand cDNA was synthesized from 1 μg of poly (A) RNA isolated from the gonad and the brain. After amplification, the amplified DNA fragment was subcloned with TA-cloning plasmid pGEM-T Easy (Promega), sequenced using a BigDye terminator Cycle Sequencing-kit (PE Biosystems, Foster City, CA, USA) with T7 and SP6 primers, and analyzed on the ABI PRISM 377 automated sequencer (PE Biosystems). The 5′- and 3′-ends of the ER cDNA were amplified by rapid amplification of the cDNA end (RACE) using a
SMART RACE cDNA Amplification kit (BD Biosciences Clontech). For 5'-RACE of ERz, two primers were used: 5'-GAGCAGGAGGAGCAGGCCTGGTTCAAGAG-3' for the first round PCR and 5'-TGGTGGCTCGCTCTCCACATGAC-3' for the second round PCR. For 3'-RACE of ERz, two primers were used: 5'-GCCACCGCGCTCCTGCTTCGCCATGCT-3' for the first round PCR and 5'-ACGCGCGCCGCGGTGCAACAATGCTGG-3' for the second round PCR. For 5'-RACE of AroA, two primers were used: 5'-GGTCTGTATATCCGGCCCTTCGAGGAGGAC-3' for the first round PCR and 5'-ACTGCGGCTCACCAGCGGGCTCCGAGATAG-3' for the second round PCR. For 3'-RACE of ERB, two primers were used: 5'-AATATGTTGGCCAGCTCCTCCCGAGGCG-3' for the first round PCR and 5'-GACGGACGCTCTGGGTGAGGCCATCG-3' for the second round PCR.

Cloning and sequencing of AroA and AroB genes

For the AroA and AroB aromatase genes, two conserved amino acid regions, TACNNYN and RYFQPFG of the T7 and SP6 primers, and analyzed on the ABI PRISM pGEM-T Easy (Promega), sequenced using a BigDye DNA fragment was subcloned with TA-cloning plasmid gonad and the brain. After amplification, the amplified synthesized from 1 PCR. As a template for PCR, first-strand cDNA was their degenerate oligonucleotides used as primers for PCR. We quantified gene expression using QPCR performed on the ABI Prism 5700 Sequence Detection System with SYBR Green PCR Master Mix according to the manufacturer's instructions (Applied Biosystems, Foster City, CA, USA). Unless noted, all supplies were purchased through Fisher Scientific. The brain, liver, and gonad tissue stored at −80°C were transferred directly to 1 ml cold TRIzol (Invitrogen) and homogenized twice for 30 s each using a Psychotron NIT-ON, NS 310E (Microtec Co., Ltd, Chiba, Japan). Following homogenization, 200 µl of hydrated chloroform was added and the samples were vortexed and incubated at 4°C for 30 min. Samples were centrifuged and the aqueous phase was transferred to another tube containing 500 µl of isopropanol, vortexed, and incubated at 4°C for 30 min. The supernatant was removed and 500 µl of 80% ethanol was added to precipitate total RNA. Total RNA was purified with RNAeasy mini kit following the manufacturer’s instructions (Qiagen), quantified using a DU640 spectrophotometer (Beckman Coulter, Fullerton, CA, USA), and adjusted to a final concentration of 0.1 µg/µl. An aliquot of purified RNA was run out on 1% agarose gel to assure quality.

Total RNA (1-0 µg/µl) was processed by attaching poly dT-linked primers (Invitrogen) to the poly (A) end of the mRNA following the manufacturer’s instructions. cDNA was synthesized with SuperScript II RNase H reverse transcriptase (Invitrogen) and dNTP mix (Invitrogen) for 10 min at room temperature, 90 min at 42°C, and 10 min at 70°C. To run QPCR, SYBR Green PCR Master Mix, forward and reverse primers, and water were combined and gently vortexed. cDNA standards of 2 µl (for each gene at 125, 25, 5, and 1 µg/µl) or samples were combined with 48 µl SYBR Green PCR Master Mix, forward and reverse primers, and water. Into each well of a MicroAmp 96-well reaction plate (Applied Biosystems), 15 µl of this mixture was pipetted in triplicate for both standards and samples. QPCR cycles were as follows: 50°C for 2 min, 95°C for 10 min, and 40 cycles of 95°C for 15 s and 60°C for 1 min. The primers were chosen to amplify short PCR products (<100 bp) with the assistance of Primer Express software (Applied Biosystems) and primer sequences were synthesized by Qiagen (Table 1). Melting curve analysis using ABI Prism 5700 Sequence Detection System software was performed to confirm the primer efficiency.

Data analysis

All sequences were searched for similarity using BLASTN and BLASTP of the National Center of Biotechnology Information. Multiple sequence alignments and construction of unrooted phylogenetic trees were performed using the CLUSTALW (Thompson et al. 1994) and TREEVIEW programs (Page 2000).

Estrogen receptor and aromatase gene expression were normalized by the expression of ribosomal protein L8. Data were checked for homogeneity of variance, transformed where necessary, and retested. Normalized gene expression in the hermaphrodite and the male
tissues were compared using the $t$-test or where data remained heteroscedastic, using the Mann–Whitney $U$-test (StatView, v 5.0, Cary, NC, USA).

Results

Cloning and sequencing of ER$\alpha$ and ER$\beta$ genes

To understand the effects of estrogens on the differentiation of rivulus, we tried to isolate the cDNA clone of ER. Using PCR techniques, partial DNA fragments were amplified from the rivulus gonad RNA. DNA fragments were obtained and sequence analysis showed that the fragments were classified into two kinds of clones, one similar to ER$\alpha$ and the other to ER$\beta$ (data not shown). Next, using the RACE technique, we were able to clone the full-length rivulus ER$\alpha$ and ER$\beta$ cDNA in the 5′ and 3′ directions, including the ATG start site and the TGA (ER$\alpha$), or TAG (ER$\beta$) termination signals (Fig. 2; GenBank accession nos AB251458 and AB251457 for ER$\alpha$ and ER$\beta$ respectively). Rivulus ER$\alpha$ has a 1743 bp open reading frame with 5′ and 3′ untranslated regions of 358 and 853 bp respectively (Fig. 2, data not shown). The deduced protein is 580 amino acids (aa) with a calculated molecular mass of 61 868·3 Da. ER$\beta$ has a 1653 bp open reading frame with 5′ and 3′ untranslated regions of 783 and 779 bp respectively (Fig. 1, data not shown). The deduced protein is 550 aa with a calculated molecular mass of 61 268·2 Da.

Amino acid sequences of rivulus ER$\alpha$ and ER$\beta$ show an overall homology of 35%. Using the nomenclature of Krust et al. (1986), rivulus ER$\alpha$ and ER$\beta$ sequences can be divided into four domains based on their sequence homology to other steroid hormone receptors. Full-length amino acid sequences were used to derive phylogenetic tree data. The two ERs share 5% homology in the A/B domain, 95·4% in the C domain (the DNA-binding domain), 10·9% in the D domain, 51·8% in the E domain (the ligand-binding domain), and 11·1% in the F domain (Fig. 2A). Thus, domains C and E are highly conserved between rivulus ER$\alpha$ and ER$\beta$, whereas A/B, D and F domains show greater variability. The overall comparison of both rivulus ER amino acid sequences with those of other fishes revealed that they were most similar to the ER sequences of the mummichog (*Fundulus heteroclitus*) at 78·7% for ER$\alpha$ and 83·0% for ER$\beta$ and medaka (*O. latipes*) at 80·3% for ER$\alpha$ and 76·1% for ER$\beta$ (data not shown).

Based on the alignment results, phylogenetic analyses were carried out and a phylogenetic tree of ER$\alpha$ and ER$\beta$ proteins was constructed using the Neighbor-Joining method (Fig. 2B) (Saitou & Nei 1987). The unrooted ER distance analysis grouped the ER$\alpha$ and ER$\beta$ homologs on separate clades and both rivulus ERs with the corresponding orthologous ER protein of other teleost fish, with high bootstrap supports for both the ERs (Felsenstein 1985). The phylogenetic tree revealed that both ER$\alpha$ and ER$\beta$ were most closely related to the mummichog and medaka ERs.

Cloning and sequencing of AroA and AroB genes

To isolate AroA and AroB cDNAs from rivulus, PCR-based amplification techniques were used. DNA fragments were obtained and sequence analysis showed that the fragments were classified into two kinds of clones: one is similar to AroB, and the other to AroA (data not shown). Next, using the RACE technique, we tried to clone the full-length rivulus AroA and AroB. We could obtain the AroB cDNA in the 5′ and 3′ directions including the ATG start site and the TAA termination signal (Fig. 3; GenBank accession no. AB251459). Rivulus AroB has a 1509 bp open reading frame with 5′ and 3′ untranslated regions of 815 and 218 bp respectively (Fig. 3A, data not shown). The deduced protein is 502 aa with a calculated molecular mass of 57 097·3 Da. We could also determine the terminal signal (TGA) and 3′ untranslated region of AroA. Unfortunately, however, we could not determine the ATG start site by 5′ RACE. Partial sequence of AroA has a 1293 bp open reading frame with 3′ untranslated region of 419 bp (GenBank accession no. AB251460, Fig. 3B, data not shown).

Table 1 Quantitative PCR primer pairs for estrogen receptors, gonadal and brain aromatase, and the ribosomal protein L8 (normalizing) genes

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Abbreviation</th>
<th>Forward</th>
<th>Reverse</th>
</tr>
</thead>
<tbody>
<tr>
<td>Estrogen receptor-α</td>
<td>ER$\alpha$</td>
<td>5′-CCCAGCGACCAAA TCAGTGTA-3′</td>
<td>3′-TTGCCGACACCT CCTTTC-5′</td>
</tr>
<tr>
<td>Estrogen receptor-β</td>
<td>ER$\beta$</td>
<td>5′-TAAACGAACTTT CACCACCA-3′</td>
<td>3′-CAGCTCTTCTAC GTCCCT-5′</td>
</tr>
<tr>
<td>Aromatase-ovarian</td>
<td>AroA</td>
<td>5′-TGAGTGTTCTGG AGAGTTCA-3′</td>
<td>3′-TGAAGCGGCTGA TGATGTCA-5′</td>
</tr>
<tr>
<td>Aromatase-brain</td>
<td>AroB</td>
<td>5′-GTGATGTCCTTC ACGATGCGT-3′</td>
<td>3′-TGCTAAGGCCA AGGGTG-5′</td>
</tr>
<tr>
<td>Ribosomal protein (normalizing gene)</td>
<td>L8</td>
<td>5′-TGATAAGCCCAT CCGTCAAGG-3′</td>
<td>3′-TGCTAAGGCCA TGATGTC-5′</td>
</tr>
</tbody>
</table>
The deduced amino acid sequences of the rivulus aromatase genes were compared with other fishes (Fig. 4). The overall homology between rivulus AroA and AroB is 57%.

The homologies between AroA in rivulus and those of other fishes, medaka, mummichog, roach (*Rutilus rutilus*), zebrafish (*Danio rerio*), goldfish (*Carassius auratus*), and catfish (*Ictalurus punctatus*) are 83%, 83%, 63%, 62%, 59%, and 59% respectively.

The homologies between the AroB in rivulus and those of other fishes, medaka, mummichog, roach, zebrafish, and catfish are 84%, 46%, 26%, 26%, 22%, and 22% respectively.

**Figure 2** Nucleotide sequences of the rivulus ERα (A) and ERβ (B), and the deduced amino acid sequences.
goldfish, and catfish, are 74.7, 74.0, 57.1, 57.9, 57.1, and 54.4% respectively. Based on the alignment results, phylogenetic analyses were carried out and a phylogenetic tree of AroA and AroB proteins was constructed using the Neighbor-Joining method (Fig. 4B; Saitou & Nei 1987). The unrooted aromatase distance analysis grouped the AroA and AroB homologs on separate clades and both rivulus aromatase genes with the corresponding orthologous aromatase protein of other teleost fish, with high bootstrap support for both aromatase genes (Felsenstein 1985). The phylogenetic tree revealed that both AroA and AroB were most closely related to the corresponding medaka and mummichog aromatase genes as with the ER genes (Fig. 5).

**Discussion**

We tested the hypothesis that gene expression would differ between rivulus hermaphrodites and males and that expression would reflect the presence of ovarian tissue in the hermaphrodites. In this paper, we show reproductive morph- and tissue-specific differences since hermaphrodites had increased ERα, ERβ, AroA, and AroB gene expression in the liver, gonad, gonad, and brain respectively, compared to males.

In contrast to mammals, which have two ERs, there are three known ERs in teleost fishes (Hawkins et al. 2000). These include ERα and two isoforms of ERβ: ERβ1 (ERβα or Esr2b) and ERβ2 (also ERββ or Esr2a), and formerly ERγ; Filby & Tyler 2005, Hawkins et al. 2005, Pinto et al. 2006). The two ERβ isoforms arose from a gene duplication following the split between tetrapods and teleosts (Hawkins et al. 2000).

ERβ expression has been measured in a number of species, including Atlantic croaker, zebrafish, sea bream (Sparus auratus), and the fathead minnow (Pimephales promelas) (Menuet et al. 2002, Filby & Tyler 2005, Hawkins et al. 2005, Pinto et al. 2006). In this study, expression of ERβ in rivulus was strongest in the liver and this finding is in agreement with the previous studies. ERβ has a strong affinity for estradiol and is upregulated in the liver by estradiol in females and estrogen-exposed male fish, where it induces vitellogenin synthesis (Filby & Tyler 2005). Given the presence of ovarian tissue, the increased expression of hepatic ERβ in the hermaphrodites compared to the males makes sense.

ERβ1 and ERβ2 expression has also been characterized in the Atlantic croaker, zebrafish, sea bream, and the fathead minnow (Menuet et al. 2002, Filby & Tyler 2005, Hawkins et al. 2005, Pinto et al. 2006). In this study, gonadal ERβ expression was upregulated in the hermaphrodite compared to the male rivulus. Again, these results are consistent with other studies, where 17β-estradiol synthesized mainly by the ovarian follicular granulosa cells has a stimulatory effect through the
ER on the ovarian development, oogenesis, and seasonal ovarian recrudescence (Devlin & Nagahama 2002). Both isoforms of ER are known in the gonads of both sexes in fishes and mammals and there is no general agreement at this time about the relative importance of one isoform over another. All three isoforms of ER are known to be expressed in various brain regions and expression patterns differ in the Atlantic croaker compared to the zebrafish. Using both an analysis of nucleic and amino acid sequences, as well as the immunolocation of ER\(\alpha\), ER\(\beta_1\), and ER\(\beta_2\) transcripts to distinct regions of the brain (preoptic area, hypothalamus, and cerebellum) in the Atlantic croaker (Micropterus undulatus) and distinctly overlapping brain regions in the zebrafish gives support to the hypothesis that these three forms of ER have specialized functions and enable different regulatory roles of reproduction and behavior (Menuet et al. 2002, Hawkins et al. 2005). In this study, there was no difference in the expression of ER\(\beta_2\) in the brain and we were not able to find evidence of a third ER in rivulus.

Figure 4 Nucleotide sequences of rivulus brain-type aromatase (A), ovarian-type aromatase (B) and the deduced amino acid sequences.
Figure 5 Alignment of the amino acid sequence (A) and phylogenetic tree of rivulus aromatase genes (B), AroA and AroB.
In contrast to most mammals, which have a single aromatase gene, there are two isoforms of aromatase in most teleosts and these are thought to be the result of gene duplication (Simpson et al. 1994, Callard et al. 2001, Pellegrini et al. 2005). As with the ERs, aromatase expression occurs in many tissues including brain, pituitary, gonads, and adipose tissue. However, ovarian aromatase, AroA, is predominantly expressed in the ovary, and brain aromatase, AroB, in the brain. Also unique to teleosts is the magnitude (2–3 orders of magnitude greater than in mammals) of AroB expression and activity in the telencephalon, preoptic area, and hypothalamus of the teleost brain (Callard et al. 1978, Pellegrini et al. 2005). In the brain, furthermore, AroB expression typically exceeds the expression of AroA (Callard et al. 2001).

In this study, we isolated two aromatase cDNAs, encoding AroA and AroB. AroA cDNA of rivulus was cloned by PCR-based method; it encodes a protein of 430 amino acids with molecular mass of 57 kDa. In addition, the full-length AroB cDNA was isolated from brain RNA using the RACE technique, and the deduced protein was 502 amino acids with a calculated molecular mass of 58.6 kDa. All fish AroB proteins reported so far have a range of 488–508 amino acid sequences (Gelinas et al. 1998, Halm et al. 2001, Valle et al. 2002). The amino acid sequence of rivulus AroB has no signal peptide; however, this amino acid sequence is of a membrane protein, which has a transmembrane helix in the N-terminal region (GQTVVSCLSEVTSLLLLFLIT). This transmembrane domain is found in wrasse AroB.

### Table 2 Normalized expression of estrogen receptors and ovarian and brain aromatase genes for brain, gonad, and liver

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Abbreviation</th>
<th>Tissue</th>
<th>Normalized gene expression mean (S.E.M.)</th>
<th>Herm versus male</th>
</tr>
</thead>
<tbody>
<tr>
<td>Estrogen receptor-α</td>
<td>ERα</td>
<td>Brain</td>
<td>0·021(0·005)</td>
<td>NS</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Gonad</td>
<td>0·186(0·168)</td>
<td>NS</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Liver</td>
<td>1·904(0·392)</td>
<td>P=0·0004</td>
</tr>
<tr>
<td>Estrogen receptor-β</td>
<td>ERβ</td>
<td>Brain</td>
<td>0·220(0·055)</td>
<td>NS</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Gonad</td>
<td>1·702(0·135)</td>
<td>P=0·0002</td>
</tr>
<tr>
<td>Aromatase-ovarian</td>
<td>AroA</td>
<td>Brain</td>
<td>0·043(0·008)</td>
<td>NS</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Gonad</td>
<td>1·670(0·145)</td>
<td>P&lt;0·0001</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Liver</td>
<td>0·002(0·0004)</td>
<td>NS</td>
</tr>
<tr>
<td>Aromatase-brain</td>
<td>AroB</td>
<td>Brain</td>
<td>4·536(1·01)</td>
<td>P=0·007</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Gonad</td>
<td>0·776(0·268)</td>
<td>NS</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Liver</td>
<td>0·005(0·001)</td>
<td>NS</td>
</tr>
</tbody>
</table>

P values as shown and NS, non-significant, values at P > 0.05.
(VTVFLLLMVLLLFT; Choi et al. 2005). Unfortunately, we could not determine the full sequence of AroA of rivulus. With the information of the full-length sequence, we will be able to better understand the functional structure and evolution of aromatase.

Alignment results of each aromatase subtype showed that the rivulus aromatase shared the highest homology with Cyprinodontiformes aromatases, such as mummi-chog and medaka. All compared aromatase sequences have higher conservation in functional regions common to both aromatase subtypes. Phylogenetic analysis shows that teleost group separates into two clear clusters, one of them containing the AroA and the other AroB. Rivulus aromatases also belong to each cluster form and this result is consistent with other teleost phylogenetic analysis, such as rainbow trout (Valle et al. 2002) and wrasse (Choi et al. 2005).

In rivulus, we measured greater AroA expression in the gonad of the hermaphrodite compared to the male gonad. These data are in agreement with research on other species and makes sense given the presence of ovarian tissue in the hermaphrodite (Callard et al. 2001). In goldfish and zebrafish, AroA expression was greater in the ovary compared to the testis. Japanese eels (Anguilla japonica) have only one aromatase gene (Jeng et al. 2005). Although making a direct comparison to rivulus is difficult due to this fact, it is interesting to note that the male eels have no measurable aromatase expression in the testis compared to the ovary, where expression is measurable.

The results discussed thus far are in accord with the findings of labs investigating other species. It is comforting to know that, in this initial study of gene expression in rivulus, data from the ERs and AroA genes are consistent with gene expression data reported for other species in the same tissues. Interestingly, the data from this study document the elevated expression of AroB in the hermaphrodite versus male brain.

The functional significance of the dimorphic expression of AroB is unclear at this time. The elevated expression of AroB in hermaphrodites compared with males may be due to different regulatory requirements of an organism with an ovotestis or simply a testis. Most of the hermaphrodites studied in detail are sequential, which are similar to gonochores in that temporally they have functional ovaries that transition into functional testes and vice versa. Prior to these data on rivulus, what we know about the endocrine control of reproductive physiology and/or ethology of simultaneous hermaphroditic fish is found in one published study on the belted sandfish (Serranus subligarius; Cheek et al. 2000). This study was limited to measuring the circulating concentrations of sex steroids during the reproductive season, daily spawning cycles, and contains no information regarding the expression of ERs or aromatase enzyme genes. Nothing is known about the mechanisms regulating simultaneous development of ova and spermatozoa in the same gonad. Sex-specific brain differences in the regulation of gametogenesis are thought to be ultimately modulated by neurotransmitters upstream of GnRH-secreting neurons, i.e., to be controlled by the frequency and amplitude of GnRH release, but there are few published data for this hypothesis in gonochores or sequential hermaphrodites (Parhar et al. 2001, Miranda et al. 2003). Clearly, more research needs to be done to examine the differential expression of AroB and its potential role in the regulation of gametogenesis in the rivulus.

In mammals, aromatase is expressed in the neurons (Balthazart et al. 2003). In teleosts, AroB is known to be synthesized in the radial glial cells of the midshipman (Porichthys notatus), rainbow trout (Oncorhynchus mykiss), and zebrafish (Forlano et al. 2001, Menuet et al. 2002, 2003). Radial glial cells have been shown to play a role in neurogenesis and local synthesis of estradiol has been hypothesized to regulate neurogenesis in adult electric fish (Apteronotus leptorhynchus) and threespine sticklebacks (Gasterosteus aculeatus; Pellegrini et al. 2005). While co-localization of ER and AromB would seem logical, thus far, these functionally related proteins are co-localized to brain/pituitary regions, but have not been found in the same cells (Menuet et al. 2002, 2003). The high levels of AroB in the teleost brain have been hypothesized to enable cell proliferation necessary for requisite sex-specific behaviors and gametogenesis during recrudescence in seasonal reproduction (Pellegrini et al. 2005). It seems unlikely that self-fertilizing rivulus hermaphrodites would have these requirements. In transitioning sequential hermaphrodites, elevated AroB levels may enable cellular proliferation in sex-specific neurons of the new sex (Pellegrini et al. 2005). Secondary male rivulus, which transition from functional selfing hermaphrodites to functional males at 28 °C might experience an increase in AroB to enable this new brain architecture. The thought that all the hermaphrodites in this experiment were undergoing transition to secondary males is also untenable, given the young age of these fishes and the temperature at which they were housed (24 ± 1 °C).

One of the weaknesses of the study was the lack of aromatase activity data, i.e., we have no knowledge of the amount of functional enzyme. Future research should examine the aromatase protein catalytic activity together with brain aromatase mRNA quantity to conclude a dimorphism in neuroestrogon synthesis and the potential regulatory role it may play in the reproductive ethology and physiology of the rivulus.
In conclusion, this is the first study to examine gene expression in the only self-fertilizing vertebrate hermaphrodite known, the mangrove rivulus, *Rivulus marmoratus*. Rivulus is an exciting model for studies on sex determination and sexual differentiation because of the uniqueness of its reproductive biology. This research has laid the groundwork for future investigations of the role of sex steroid hormones in the differentiation of the brain, pituitary, liver, and gonad in the various and intriguing reproductive morphs of this model system.

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Animal care and use statement

All research contained in this manuscript was conducted in full compliance with the Florida Atlantic University Institutional Animal Care and Use Committee (permit #A0601).

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