



Universidade Federal do Rio Grande  
Instituto de Ciências Biológicas  
Pós-graduação em Biologia de  
Ambientes Aquáticos Continentais



**Identificação do transcrito *CYP1A* no peixe  
*Phalloceros caudimaculatus* e resposta para a  
exposição a beta-naftoflavona e amostras  
ambientais de sedimento.**

**Roger Stacke Ferreira**

Orientador: Juliano Zanette

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Dissertação apresentada ao Programa de Pós-graduação em Biologia de Ambientes Aquáticos Continentais como requisito parcial para a obtenção do título de Mestre em Biologia de Ambientes Aquáticos Continentais.

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## RESUMO

Contaminantes orgânicos, como os hidrocarbonetos policíclicos aromáticos (HPAs), podem atingir corpos da água e possuem potencial para causar efeitos tóxicos em organismos. A exposição aos HPAs causa indução nos níveis de citocromo P450 1A (CYP1A) em peixes, e portanto, é utilizado como um biomarcador de contaminação ambiental. O guarú *Phalloceros caudimaculatus* ocorre naturalmente em ambientes aquáticos dulcícolas e mixohalinos na América do Sul. O presente estudo identificou a sequência nucleotídica do transcrito *CYP1A* de *P. caudimaculatus*, que codifica uma proteína com 521 aminoácidos, e que apresenta 91% e 70% de identidade com CYP1A de *killifish* e paulistinha, respectivamente. A partir desta sequência foi possível realizar a avaliação dos níveis de mRNA de *CYP1A* deste peixe por RTq-PCR. Foi realizada uma caracterização de sua indução órgão- e tempo-dependente frente a exposição ao HPA beta-naftoflavona (BNF) e ao elutriato preparado a partir de sedimento de dois corpos da água possivelmente contaminados com HPAs. Foi constatado um aumento significativo nos níveis de mRNA de *CYP1A* em fígado, brânquia, intestino, cérebro, nadadeira anal de macho adultos e em alevinos na primeira hora de exposição a 1  $\mu$ M de BNF, em relação ao grupo controle. O rim e as nadadeiras caudal e dorsal apresentaram indução de *CYP1A* após duas horas de exposição ao BNF. As maiores induções nos peixes dos grupos expostos ao BNF em relação ao controle foram de 176 no rim e 122 vezes no cérebro, observadas respectivamente após 8 e 48 horas de exposição. Os níveis de mRNA de *CYP1A* nos órgãos e tecidos de alevino, mantiveram-se induzidos pela exposição ao BNF até o final das 96 horas de exposição. A exposição dos peixes ao elutriato produzido a partir dos sedimentos coletados em dois locais potencialmente contaminados causou indução do *CYP1A* no fígado de 22 e 122 vezes em relação ao controle. Os resultados demonstram que a indução de *CYP1A* em *Phalloceros caudimaculatus* ocorre em tempos curtos de exposição, além da variação de acordo com o tempo de exposição e com o órgão analisado. Além disso, foi demonstrado que tecidos externos também podem ser utilizados para tais análises e que o elutriato feito a partir de sedimento de locais que recebem descargas de contaminantes podem causar indução de *CYP1A* nos organismos.

**Palavras-chave:** Ciprinodontiformes, citocromo P450, contaminação, guarú, elutriato.

## ABSTRACT

Organic contaminants, such as polycyclic aromatic hydrocarbons (PAHs), can reach water bodies and have the potential to cause toxic effects in organisms. Exposure to PAHs cause induction in the levels of cytochrome P450 1A (CYP1A) in fish and therefore is used as a biomarker of environmental contamination. The guppy *Phalloceros caudimaculatus* occurs naturally in freshwater and mixohaline aquatic environments in South America. This study identified the nucleotide sequence of *P. caudimaculatus* CYP1A transcript, which encodes a protein with 521 amino acids, and shows 91% and 70% identity with CYP1A of killifish and zebrafish, respectively. Based on this sequence it was possible to evaluate the CYP1A mRNA levels of this fish by RTq-PCR. A characterization of its organ- and time-dependent induction by exposure to PAH beta-naphthoflavone (BNF) and elutriate prepared from sediments of two bodies of water possibly contaminated with PAHs was carried out. A significant increase was seen in the CYP1A mRNA levels in liver, gill, gut, brain, anal fin of male adults and fingerlings in the first hour of exposure to 1  $\mu$ M of BNF in compared to control group. Kidney, caudal fin and dorsal fin presented CYP1A induction after two hours of exposure to BNF. The highest induction in fish exposed to BNF groups compared to the control were 176 times in the kidney and 122 times in the brain, observed respectively after 8 and 48 hours of exposure. The CYP1A mRNA levels in organs and fingerling, remained induced by exposure to BNF until the end of 96 hours of exposure. The fish exposure to elutriate produced from sediments collected in two potential contaminated sites caused CYP1A induction in liver of 22- and 122- fold control. The results demonstrate that induction of CYP1A in *Phalloceros caudimaculatus* occurs in short exposure time and there is variation according to the time of exposure and analyzed organ. Furthermore, it was demonstrated that external tissues can also be used for such analysis and elutriate made from sediment of sites that receive contaminant discharges induces CYP1A in those organisms.

**Key-words:** Cyprinodontiformes, cytochrome P450, contamination, guppy, elutriate.

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## **INTRODUÇÃO GERAL**

### **Os Ambientes Aquáticos Continentais**

Ambientes aquáticos continentais englobam vários ecossistemas, como lagoas de água doce e salobra; savanas, campos e florestas de inundação temporária ou permanente e os banhados (Maltchik et al., 2004). O estado do Rio Grande do Sul possui uma grande variedade de ambientes aquáticos, incluindo 3441 banhados que representam uma área total inundada de aproximadamente 30332 km<sup>2</sup> e ocupam aproximadamente 10,7% da área total do estado. Destes banhados, 72 % possuem uma área menor do que 1 km<sup>2</sup> (Maltchik et al., 2003; Rolon e Maltchik, 2006). Além dos banhados, o estado abriga o sistema da Lagoa dos Patos, considerada a maior lagoa costeira do mundo (Kjerfve, 1986). O sistema tem mais de 250 km de nordeste para sudoeste, com uma largura média de 40 km e profundidade média de 5 metros, com área de superfície de 10.360 km<sup>2</sup> e área estuarina de 900 km<sup>2</sup>. A lagoa faz contato com o Oceano Atlântico através de um canal de entrada com aproximadamente 20 km de comprimento e 1 km de largura (Fernandes et al., 2004, Janeiro et al., 2008).

Banhados são áreas alagadas de forma permanente ou temporária, alimentados pela água da chuva e pelo escoamento de águas superficiais ou subterrâneas. São considerados ilhas de biodiversidade, pois têm cadeias alimentares extensivas e uma rica biodiversidade. Logo, estes ecossistemas são locais importantes para a conservação (Getzner, 2002; Rolon e Maltchik, 2006). Porém, devido à ocupação humana os banhados estão desaparecendo e ocupando áreas cada vez menores (Gibbs, 2000).

Os estuários, como o do sistema da Lagoa dos Patos, estão entre os ambientes mais importantes da zona costeira, os quais constituem zonas de transição, onde a água doce da drenagem de rios se mistura com a água marinha, criando alguns dos habitats mais produtivos conhecidos (Kennish, 2002). Os estuários são importantes para o ciclo de vida de muitos organismos marinhos e suas áreas rasas são utilizadas como berçários para diversas espécies de peixes e camarões, pois oferece proteção de predadores. Além disso, os estuários apresentam importância ecológica e comercial pela sua alta produtividade e por possuir abundância de alimento para os animais que o habitam (Pearcy e Myers, 1974; Weinstein, 1979; Martins et al., 2007).

O estuário da Lagoa dos Patos é delimitado pelas cidades de São José do Norte e Rio Grande, sendo a última a principal cidade no estuário, e que nos últimos anos tem aumentado sua importância no contexto nacional e América do Sul devido ao Mercosul.

Rio Grande tem como suas principais atividades a pesca, o turismo, atividade portuária e instalações industriais, além de uma refinaria de petróleo (Janeiro et al., 2008).

### **Os Contaminantes Ambientais**

Compostos orgânicos naturais ou artificiais são aportados nos ecossistemas aquáticos por diversas formas, como por escoamento superficial, liberação de efluentes industriais e urbanos, derrames de combustíveis fósseis, deposição de partículas do ar (Neff, 1985; O'Malley et al., 1994; Garcia et al., 2010), e dispersados por movimento abióticos e bióticos, e transferência pela cadeia alimentar (Livingstone, 1998).

De maneira geral, os contaminantes estão presentes no ambiente fazendo parte de uma mistura de substâncias tóxicas, e possuem diferentes propriedades químicas, modos de toxicidade e potencial para interação com o ambiente e organismos. Além disso, os efeitos tóxicos de misturas não são a simples adição de toxicidades dos contaminantes individuais, o que torna a interpretação dos efeitos tóxicos causados por misturas na biota bastante complexa (Norwood et al., 2003). A cidade de Rio Grande carece de uma estrutura de tratamento de esgotos, o que resulta em uma descarga de esgotos para o estuário sem qualquer tipo de tratamento. As águas de escoamento urbano também são drenadas diretamente para o estuário. Estudo feito por Medeiros e colaboradores (2005) nos efluentes da região indicou pontos de contaminação por HPAs nos sedimentos perto da refinaria de petróleo e nos efluentes urbanos. Além disso, zonas de intensa navegação no estuário também são afetadas, superando o nível de contaminação em áreas rasas adjacentes da cidade e impactadas por efluentes industriais (Garcia et al., 2010).

Logo, o estuário da Lagoa dos Patos tem um histórico de contaminação antropogênica em pontos no Porto de Rio Grande, no pólo industrial, como na saída de efluentes industriais da refinaria de petróleo da região, produtoras de fertilizantes e da indústria pesqueira; e em saídas de efluentes urbanos não-tratados (Baisch et al., 1989). Estudo feito neste estuário demonstra que a contaminação da água e sedimento por metais pesados e contaminantes orgânicos dos efluentes industriais, urbanos e das atividades portuárias têm causado uma série de impactos sobre os ecossistemas abrigados pelo estuário (Tagliani et al., 2003).

### **Os Hidrocarbonetos Policíclicos Aromáticos**

Os hidrocarbonetos policíclicos aromáticos (HPAs) são compostos por dois ou mais anéis de benzeno fundidos, que podem ser alquilados ou não. De acordo com o

tamanho, estrutura e solubilidade, podem ser divididos em compostos carcinogênicos (ex. benzo[a]pireno), e não carcinogênicos (ex. beta-naftoflavona). Os HPAs são relativamente mais solúveis do que outros hidrocarbonetos que possuem o mesmo número de átomos de carbono (McAuliffe, 1987) e esta solubilidade dos HPAs é uma característica importante, considerando que muitos HPAs estão entre os componentes mais tóxicos do petróleo bruto (Ramachandran et al., 2006), representando um risco para a biota aquática (Kennish, 1992).

As fontes de entrada de HPAs de origem antropogênica no meio aquático são feitas por combustão de combustíveis fósseis, derrame de derivados do petróleo e emissão de resíduos domésticos, sendo estas entradas mais aparentes em locais associados com as atividades industriais, atividades de transporte de petróleo e efluentes de esgoto doméstico (Medeiros et al., 2005). Segundo a organização dos Estados Unidos que coleta, analisa e dissemina informações sobre fontes energéticas, a *U.S. Energy Information Administration*, foram extraídos mais de 90 milhões de barris de petróleo por dia no ano de 2013 e produzidos quase 8 milhões de toneladas de carvão em 2012. A exploração, o refino, o transporte e as operações de armazenamento do petróleo e de seus derivados podem ocasionar derramamentos acidentais levando a contaminação tanto de solos quanto de ambientes aquáticos (Andrade et al., 2010).

O petróleo e seus derivados são uma classe ampla de contaminantes ambientais que podem entrar no ambiente aquático através de descargas de efluentes industriais e urbanos, atividades de transporte, derrames de petróleo, queima de combustíveis fósseis e afloramentos naturais (Medeiros et al., 2005) e o desenvolvimento dos centros urbanos e industriais aumentou consideravelmente os níveis de produtos petroquímicos no ambiente, principalmente em estuários e zonas costeiras (Lima et al., 2007). A contaminação ambiental por HPAs tornou-se uma preocupação global e existem relatos de contaminação significativa não apenas em sistemas costeiros e marinhos, como em também em água doce (Curran et al., 2000; Donahue et al., 2006).

De forma geral, os HPAs são incorporados por organismos (ex.: plantas e peixes) por difusão passiva, isso ocorre devido à natureza apolar dos HPAs que lhe conferem a capacidade lipofílica para atravessar a membrana das células (Gauthier et al., 2014). Após a incorporação, o HPA e seus metabólitos podem aumentar a produção de espécies reativas de oxigênio por vários mecanismos, os quais podem conduzir a danos celulares por meio de oxidação de proteínas, peroxidação lipídica e danos de DNA (Altenburger et al., 2003). Para evitar essas lesões, sistemas antioxidantes são ativados pela célula para

eliminar espécies reativas de oxigênio estimuladas pelos contaminantes, permitindo que o organismo supere o estresse oxidativo em ambientes contaminados (Livingstone, 2001; Lima et al., 2007).

Para analisar a contaminação de ambientes aquáticos por HPAs são estudadas amostras da coluna d'água, de sedimentos e de organismos (Volkman et al., 1992). Porém, a contaminação do sedimento tem recebido mais atenção, pois os HPAs são compostos hidrofóbicos com baixa solubilidade em água, que se associam principalmente com o material particulado, como o sedimento (Readman et al, 1984; Neff, 1985), fazendo com que a concentração de HPAs encontrada no sedimento seja superior a da água no mesmo local (Li et al., 2010).

Na Lagoa dos Patos, o lodo coletado diretamente nos pontos de escoamento (industrial, esgoto urbano e misto) apresentou níveis altos de contaminação por HPAs, sendo quase 20 vezes maiores que as encontradas nas amostras de sedimentos mais afastadas dos locais de descargas de efluentes. As concentrações de HPAs encontradas nos pontos amostrados revelam que a Lagoa dos Patos assemelha-se à outros estuários com um nível de contaminação por HPAs moderada (Garcia et al., 2010). Dentre estes HPAs, o benzo[a]pireno (BaP) é um dos HPAs frequentemente utilizado por guias governamentais para indicar contaminação por HPAs, sendo estudado devido à sua propriedade carcinogênica e muito usado em experimentos com peixes como modelo para estudos que visam a compreensão do efeito de HPAs em vertebrados (Beyer et al., 1997). O BaP foi encontrado quase 100 vezes mais concentrado no lodo na saída do efluente do que no sedimento, demonstrando que a concentração dos contaminantes provenientes dos efluentes diminui drasticamente com o aumento da distância da fonte de contaminação (Medeiros et al., 2005; Garcia et al., 2010).

### **Remobilização de Contaminantes**

A remobilização de contaminantes provenientes dos sedimentos afeta a mobilidade dos contaminantes, pode aumentar a biodisponibilidade e os efeitos sobre os organismos no local. Logo, a remobilização de contaminantes deve ser monitorada adequadamente, especialmente quando atividades de dragagem são feitas, pois mesmo após o término da atividade a concentração dos contaminantes pode permanecer elevada na água (Bocchetti et al., 2008) e causar impactos tanto subletais quanto letais nos organismos (Kennish, 2002). A ressuspensão pode ocorrer tanto de modo natural, pelas tempestades, por grande aporte de água pluvial ou correntes de fundo, quanto por

atividades antrópicas, por operações de dragagem ou movimentação de barcos e navios (Bergen et al., 2005).

Para reprodução em laboratório de uma situação de ressuspensão dos contaminantes contidos no sedimento depositado no fundo de ambientes aquáticos, pode ser utilizado o elutriato (Bergen et al., 2005). A elutriação é feita pela a adição de água a uma substância sólida ou material solto (ex.: sedimentos, resíduos, lamas, lodos), as quais são misturadas por agitação ou aeração. Posteriormente é feita uma centrifugação, filtragem ou decantação do sobrenadante, sendo esta solução aquosa sobrenadante denominada elutriato, a qual é utilizada para os testes toxicológicos (EPA, 2001). A remobilização dos contaminantes do sedimento para a água ocorre em função do aumento do teor de água no sedimento e/ou mudanças nas condições de redução e oxidação (Di Toro et al, 1991;. Ankley et al., 1996).

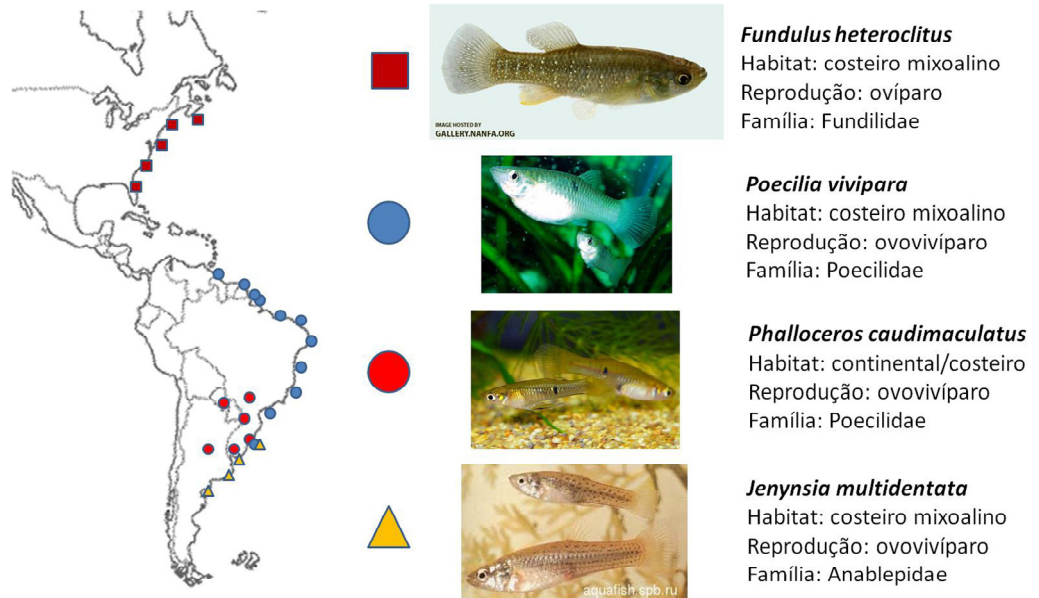
Além disso, a elutriação remobiliza para água qualquer contaminante que esteja na fase particulada, trazendo à tona não só hidrocarbonetos policíclicos aromáticos (HPAs), mas também outros contaminantes (EPA, 2001). Estes contaminantes remobilizados podem interagir ao mesmo tempo sobre o organismo, podendo influenciar no transporte, metabolismo e desintoxicação através de competição por sítios ou complexação dos mesmos. Assim o uso do elutriato para testes toxicológicos mostra não só os efeitos dos um contaminante contido no sedimento, mas sim a interação do conjunto total de contaminantes remobilizados (Gauthier et al., 2014).

### ***Phalloceros caudimaculatus*: um Potencial Biomonitor de Contaminação**

Ambientes aquáticos abrigam diversas espécies de plantas e animais, as quais entram em contato com os contaminantes carregados para os corpos d'água. As populações de peixes desempenham um papel importante na avaliação da contaminação aquática, pois algumas espécies respondem com sensibilidade a mudanças no ambiente aquático (Siroka e Drastichova, 2004).

A ordem Ciprinodontiformes é composta de diversas espécies de peixes, como os *killifish*, barrigudinhos e guarús. Têm de pequeno à médio porte (8 mm à 34 cm), são encontrados em ambientes de água doce e salobra. É considerada uma ordem cosmopolita (Parenti, 1981) e seus membros são conhecidos por sua tolerância a baixa qualidade da água (Araújo et al., 2007). Esta ordem tem entre seus representantes o *killifish Fundulus heteroclitus*, o qual vem sendo utilizado nos Estados Unidos como um modelo para o estudo de respostas adaptativas de organismos para a contaminação

ambiental (Burnett et al., 2007). *Poecilia vivipara* e *Jenynsia multidentata* também são representantes desta ordem que vem sendo utilizados para estudos de contaminação ambiental na América do Sul (Fig. 1).



**Figura 1.** Distribuição, habitat e reprodução de espécies de Ciprinodontiformes estudados na América do Norte e América do Sul (Froese e Pauly, 2003).

A ordem Ciprinodontiformes é subdividida em dez famílias, Anablepidae, Aplocheilidae, Cyprinodontidae, Fundulidae, Goodeidae, Nothobranchiidae, Poeciliidae, Profundulidae, Rivulidae e Valenciidae. Sendo que no estado do Rio Grande do Sul foi observada uma alta riqueza e abundância de Ciprinodontiformes, principalmente a família Poeciliidae, em habitats de área reduzida, baixa profundidade, susceptibilidade ao estresse hídrico e com alta densidade de macrófitas (Maltchik et al., 2014).

Espécies de Poeciliidae ocorrem em ambientes de água doce e salobra (Nelson, 1994), são caracterizados pelo pequeno porte, onivoria, ovovivipariedade, fecundação interna e pelo dimorfismo sexual acentuado, no qual a fêmea é maior que o macho, e o macho possui a nadadeira anal modificada para transferência de esperma durante a cópula (Betito, 2006). Estudos relatam uma maior abundância de fêmeas do que de machos e a capacidade de reter esperma de uma cópula para fecundações sucessivas sem a necessidade de cópula. Essa família possui cerca de 200 espécies em 16 gêneros, entre as quais está o guarú *Phalloceros caudimaculatus* (Fig. 2) (Parenti, 1981; Araujo et al., 2007).

Como já descrito para a ordem, o guarú *P. caudimaculatus* é conhecido por ter capacidade de prosperar em condições ambientais adversas, podendo ser utilizado como bioindicador de más condições de água em estudos de comunidades. Esta capacidade faz com que colonize zonas impactadas por efluentes industriais e domésticos, caracterizando-a como uma espécie oportunista (Araújo et al., 2007). Esta espécie está distribuída na área continental e costeira do sudeste do Brasil até o norte da Argentina (Froese e Pauly, 2003), sendo que estudos recentes a apontaram como uma das espécies mais abundantes e bem distribuídas nos banhados do estado do Rio Grande do Sul (Maltchik et al., 2014).



**Figura 2.** Guarú *Phalloceros caudimaculatus*, A) macho com 24,5 mm; B) fêmea com 36,8 mm (Lucinda, 2008)

Mudanças na faixa etária predominante e distribuição das espécies em uma população de peixes são bioindicadores gerais da contaminação da água, mas há também respostas específicas a produtos químicos estranhos ao organismo, conhecidos como xenobióticos (Siroka et al. 2004; Nebert e Dalton, 2006). Neste caso, os peixes podem ser utilizados como bioindicadores e biomonitores, pois os efeitos da exposição a xenobióticos podem ser medidos em respostas fisiológicas, bioquímicas ou moleculares (Mondon et al., 2001).

A análise química é capaz de medir quantitativamente uma ampla gama de contaminantes, porém somente estabelece a presença e concentração do que é possível detectar, sendo incapaz de revelar alterações biológicas nos organismos. A utilização de biomarcadores, bioquímicos e moleculares, cumpre esse propósito através da mensuração das respostas bioquímicas e/ou moleculares em organismos, podendo

demonstrar tanto que organismos estão sendo expostos a certas classes de contaminantes, como demonstrar a ocorrência dos efeitos tóxicos causados (Siroka e Drastichova 2004). Biomarcadores celulares e moleculares têm o potencial de antecipar mudanças em níveis mais elevados de organização biológica, servindo como um alerta precoce, permitindo que sejam tomadas medidas de biorremediação antes de ocorrer mudanças irreversíveis no ecossistema (Cajaraville et al., 2000).

### **Biomarcador CYP1A**

A biotransformação de xenobióticos e metabolização de substâncias endógenas podem ser divididas em três fases, a fase-I é conhecida pela introdução de um grupo funcional, como hidroxila (OH), carbonila (COOH) ou nitro (NO<sub>2</sub>), ou alteração de algum grupo funcional existente por reações químicas, como oxidação, redução, hidratação ou hidrólise. A fase-II é realizada pelas transferases, as quais anexam uma unidade polar (ex.: glutationa, sulfato e aminoácidos) a um grupo funcional da molécula parental. A fase-III é o transporte e excreção do xenobiótico (Livingstone, 1998). O objetivo das fases-I e -II é aumentar a hidrofiliabilidade dos xenobióticos e das substâncias endógenas, ou seja, aumentar a afinidade destas moléculas com a água. A fase-I é realizada principalmente por enzimas da superfamília citocromo P450 (CYP) (Myers et al., 2003) e a fase-II por enzimas como sulfotransferases e glutationa S-transferases (Xu et al., 2005). Atividades de regulação do sistema de biotransformação/metabolização de fase-I e -II têm sido utilizados para quantificar os efeitos de xenobióticos em espécies aquáticas. No entanto, as enzimas de fase-II são geralmente menos responsáveis do que os sistemas de fase-I (Holth et al., 2008).

CYP é uma superfamília de hemoproteínas presente em praticamente todos os tecidos, e em todos os organismos vivos. A ligação heme-tiolato no sítio ativo da enzima é responsável por diversas propriedades catalíticas desta superfamília de enzimas. O CYP representa um dos sistemas enzimáticos mais importantes na biotransformação de xenobióticos e metabolização de lipídios endógenos (Estabrook e Werringloer, 1978).

Enzimas CYP podem ser classificadas de acordo com a sua função em três classes, designadas por FC-E, FC-S, e FC-X, baseado nas características dos seus substratos e produtos. Enzimas FC-E são essenciais para a síntese e degradação de compostos endógenos, tais como hormônios e vitaminas, enzimas FC-X são as envolvidas na biotransformação de xenobióticos, e as enzimas FC-S participam na síntese e catabolismo de metabólitos secundários. Porém esta classificação não é rígida,



pois são conhecidas enzimas CYPs das famílias CYP1, CYP2, CYP3 e CYP4 que são associadas tanto com a biotransformação de xenobióticos, quanto com o metabolismo dos esteróides e eicosanóides em mamíferos (Gotoh, 2012). Logo, uma alteração na indução de enzimas CYP por xenobióticos para biotransformação pode alterar a dinâmica nas vias de degradação e síntese de compostos endógenos.

Dentre os compostos que são metabolizados pela superfamília CYP estão drogas, solventes, anestésicos, pesticidas, petróleo e seus derivados, HPAs, antioxidantes, corantes, aromatizantes, esteróides, ácidos graxos, hidroperóxidos de lípidos, vitaminas lipossolúveis, aminoácidos, eicosanóides e retinóides (Coon, 2005).

O aumento do conteúdo de enzimas CYP é proposto como um biomarcador de exposição a xenobióticos, como os HPAs (Porte et al., 2001). Além disso, vários estudos de campo têm demonstrado relação direta entre a indução de enzimas da superfamília CYP e as concentrações de HPAs e bifenilas policloradas no ambiente (Petushok et al., 2002). Os efeitos de HPAs em organismos aquáticos têm sido avaliados através da atividade enzimática de fase-I e os subseqüentes efeitos provocados por estes compostos, tais como a formação de aduto de DNA e lesões histopatológicas (Myers et al., 2003). A toxicidade dos HPAs é atribuída principalmente a biotransformação dos compostos originais em metabólitos reativos, e, portanto, a toxicidade destes compostos é mediada por membros da superfamília CYP (Nebert e Dalton, 2006).

Devido ao grande número de enzimas na superfamília CYP, é necessário um sistema de classificação, no qual as enzimas são distribuídas em famílias e subfamílias, com base na porcentagem de identidade obtida pelo alinhamento destas sequências. A constatação de 40% ou mais de identidade entre sequências polipeptídicas de CYPs, leva ao agrupamento em uma determinada família designada por um algarismo arábico (ex.: CYP1). A constatação de 55% ou mais de identidade entre as sequências de aminoácidos leva ao agrupamento em uma subfamília designada por uma letra (ex.: CYP1A), e caso haja mais de uma isoforma em uma dada subfamília, é adicionado mais um algarismo arábico (ex.: CYP1A1) (Nelson et al., 1996).

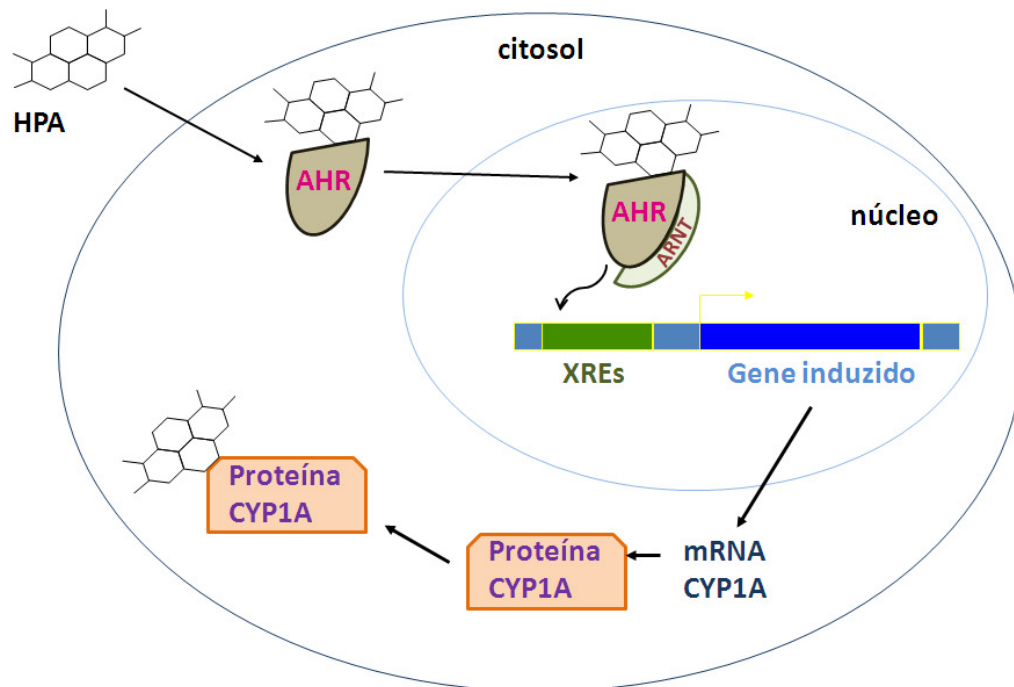
A biotransformação de HPAs tem recebido atenção devido a sua capacidade de alterar a via metabólica do CYP1, levando a indução de enzimas da família CYP1. Esta indução é mediada pelo receptor de hidrocarboneto aromático (AHR) (Hahn, 2002) que pode ser ativado pela ligação com HPAs, os quais podem ser agonistas do AHR, estimulando a biotransformação de HPAs pela indução da transcrição do gene *CYP1A* (Stegeman e Hahn, 1994; Hahn, 1998). Porém, existem HPAs que possuem pouca ou

nenhuma afinidade com o AHR, porém estes são considerados exceções (Van Tiem e Di Giulio, 2011; Wassenberg et al., 2005).

CYP é o principal complexo enzimático que atua na desintoxicação/bioativação de HPAs (Aas et al, 2000). Estudos feitos com paulistinha demonstraram que as diversas subfamílias de CYP1 diferem na magnitude da sua expressão basal e a expressão de CYPs varia entre órgãos e estágios de desenvolvimento (Jönsson et al., 2007; Goldstone et al., 2010), sugerindo que as diferentes enzimas CYP podem desempenhar diferentes papéis na susceptibilidade aos agonistas do AHR. Para mamíferos e peixes, quatro famílias de CYP são conhecidas por desempenhar um papel importante na biotransformação de xenobióticos, as famílias CYP1, CYP2, CYP3 e CYP4 (Stegeman e Hahn, 1994; Hahn, 1998; Nerbert e Dalton, 2006).

CYP1A é uma subfamília importante, em grande parte das classes de vertebrados, no processo de biotransformação de HPAs e outras substâncias agonistas dos AHR (Teramitsu et al., 2000). CYP1A é uma das formas de CYP muito estudada em peixes e vem sendo amplamente utilizada como biomarcador de contaminação aquática, pois é induzida por compostos tóxicos, como HPAs, bifenilas policloradas (PCB), dioxinas (TCDD) e furanos (TCDF) (Stegeman, 1993; Rattner et al, 1993; Bucheli e Fent, 1995).

De acordo com a revisão feita Kawajiri e Fujii-Kuriyama (2007) (Fig. 3), a ligação de compostos endógenos ou exógenos, tais como as dioxinas no AHR causa sua ativação, o que leva ao transporte nuclear do complexo AHR-agonista. Dentro do núcleo ocorre uma dimerização com o translocador nuclear do receptor de hidrocarbonetos (ARNT), formando um novo dímero, o AHR-ARNT, o qual reconhece regiões mediadoras conhecidas por elementos de resposta a xenobióticos (XREs). O dímero AHR-ARNT ligasse na região do XRE causando uma remodelação da cromatina, a qual aumenta a sensibilidade em um ponto próximo ao local de iniciação da transcrição do gene *CYP1A*. Assim, fatores de transcrição atuam no local sensibilizado fazendo a transcrição do gene em RNA mensageiro (RNAm), o qual é mobilizado para o citoplasma onde será traduzido na proteína CYP1A para biotransformação dos compostos.



**Figura 3.** Desenho esquemático da indução do gene *CYP1A* na presença de um hidrocarboneto policíclico aromático (HPA) (Kawajiri e Fujii-Kuriyama, 2007).

A carcinogênese acionada pelos metabólitos das reações feitas pelo complexo enzimático CYP é o mecanismo mais reconhecido pelo qual os HPAs exercem efeitos tóxicos (Baird et al., 2005). Porém, estudos sobre a toxicidade do benzo[a]pireno (BaP), um forte agonista do AHR, demonstrou a função protetora da biotransformação feita pela enzima *CYP1A* durante a embriogênese de peixes (Van Tiem e Di Giulio, 2011; Wills et al, 2009), e que a inibição da *CYP1A* leva a um aumento da toxicidade (Gauthier et al., 2014)

O *CYP1A* é geralmente determinado em microsomas hepáticos, sendo que agonistas do AHR como os HPAs, podem ser facilmente biotransformados em outros órgãos, como as brânquias, fazendo com que a atividade hepática não reflita com precisão a exposição total de agonistas do AHR (Jönsson et al., 2006). A utilização de medições das alterações biológicas induzidas por contaminação química em ambientes aquáticos, como a atividade enzimática de *CYP1A*, tem sido amplamente empregada em ecossistemas aquáticos na América do Norte e Europa, em programas de biomonitoramento para detectar a exposição a esses produtos químicos (Stegeman, 1993; Bourgeot et al., 1996).

A informação de seqüência nucleotídica pode ser usada para produzir iniciadores e anticorpos para quantificar a transcrição/expressão gênica do gene/proteína de interesse no organismo e usá-los como uma medida do efeito contaminante sobre o mesmo (Greytak et al., 2005). Porém a baixa similaridade de seqüência entre genes *CYP1A* resulta em baixa reatividade cruzada entre diferentes espécies para anticorpos de CYP1A (Cousinou et al., 2000). Sendo assim, é necessário obter a seqüência de *CYP1A* do novo organismo de testes, para a produção de iniciadores e anticorpos específicos para analisar a transcrição/expressão gênica (Lee et al., 2005). A transcrição gênica de biomarcadores foca na etapa anterior, medindo a quantidade de RNAm, o qual codifica proteínas ou enzimas, sendo que na maioria dos casos, mas não todos, ambos os tipos de biomarcadores, transcrição gênica e ensaio enzimático/quantificação protéica estão mutuamente correlacionados (Piña et al., 2007). O estudo feito por Quirós e colaboradores (2007) demonstrou uma correlação positiva entre a atividade enzimática EROD, a qual o CYP1A é uma das principais enzimas associadas, com a transcrição gênica de *CYP1A*. Transcrição gênica de biomarcadores também pode ser destinada para avaliação de efeitos de contaminação observada nos organismos expostos ou para fornecer um aviso prévio nos casos de suspeita de impacto antropogênico no ambiente. A principal limitação do seu desenvolvimento é a falta de conhecimento sobre aspectos fisiológicos, genéticos, embriológicos, e, em geral, a biologia da biota impactada (Piña et al., 2007)

A mudança na transcrição gênica antecede as mudanças nos processos celulares, os quais podem afetar em nível de população, servindo de alerta anterior às mudanças em níveis mais complexos (Myers et al., 2003; Holth et al., 2008). Além disso, o custo de uma reação para análise de transcrição gênica é relativamente baixo, e um grande número de amostras pode ser analisada em um único ensaio. Além de ser um método relativamente rápido e preciso, após a otimização dos iniciadores, o qual não necessita de muito material biológico (Piña et al., 2007).

Neste estudo foi identificado o RNAm que codifica a enzima CYP1A em *Phalloceros caudimaculatus*. Foram avaliadas as respostas órgão-específicas e tempo-dependentes ocorridas nos níveis de RNAm de *CYP1A* frente a exposição ao HPA beta-naftoflavona (BNF) no fígado, intestino, cérebro, brânquia, rim, nadadeiras dorsal, caudal e anal e em alevinos. Avaliou-se também a resposta ocorrida nos níveis de RNAm de *CYP1A* de *P. caudimaculatus* expostos ao elutriado feito a partir dos sedimentos de locais possivelmente contaminados com HPAs, com a finalidade de demonstrar a

utilização potencial deste biomarcador no monitoramento ambiental. A hipótese foi de que o HPA BNF causaria aumento nos níveis de RNAm de *CYP1A* em alguns órgãos e em pelo menos algumas das janelas temporais testadas. E de que a mistura de contaminantes contidos nos sedimentos dos locais potencialmente contaminados também causariam aumento nos níveis de RNAm de *CYP1A* no guarú *Phalloceros caudimaculatus*.

## **OBJETIVOS**

### **Objetivo geral**

Demonstrar o potencial do guarú *Phalloceros caudimaculatus* para utilização como bioindicador e biomonitor de ambientes contaminados por agonistas do receptor de hidrocarbonetos aromáticos (AHR) através da mensuração dos níveis de RNAm de *CYP1A* e a utilização das nadadeiras como um método não-invasivo para mensuração dos níveis de RNAm de *CYP1A*.

### **Objetivos específicos**

- Identificar a sequência nucleotídica do transcrito *CYP1A* em *P. caudimaculatus*
- Avaliar os níveis de expressão de RNAm de *CYP1A* em fígado, intestino, cérebro, brânquia, rim, nadadeiras dorsal, caudal e anal e tecidos de alevinos de *P. caudimaculatus* expostos a 1 µM de BNF por 1, 2, 4, 8, 24, 48 e 96 horas.
- Avaliar os níveis de expressão de RNAm de *CYP1A* em fígado de *P. caudimaculatus* expostos por 8 horas aos elutriados feitos a partir de sedimentos de dois locais possivelmente contaminados, e outro não contaminado.

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## CAPÍTULO ÚNICO - MANUSCRITO

**New cytochrome P450 1A transcript in the guppy *Phalloceros caudimaculatus*  
and *CYP1A* response to beta-naphthoflavone and environmental samples**

(Manuscrito a ser submetido para a revista Aquatic Toxicology).

New cytochrome P450 1A transcript in the guppy *Phalloceros caudimaculatus* and  
*CYP1A* response to beta-naphthoflavone and environmental samples

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1 **ABSTRACT**

2           The cytochrome P450 1A (CYP1A) in fishes is induced in the transcriptional  
3 level by agonists of the aryl hydrocarbon receptor (AHR), such as the environmental  
4 contaminants polycyclic aromatic hydrocarbons (PAHs), polychlorinated biphenyl  
5 (PCBs) and dioxins. Here we cloned the *CYP1A* gene from the guppy *Phalloceros*  
6 *caudimaculatus*, a potential model for toxicological studies in South America. The *P.*  
7 *caudimaculatus* *CYP1A* encodes a protein with 521 amino acids that shared 96%,  
8 91% and 70% identity with CYP1A of the fishes *Poecilia vivipara*, *Fundulus*  
9 *heteroclitus* and *Danio rerio*, respectively. The characterization of organ- and time-  
10 dependent induction of *CYP1A* by waterborne exposure to the model CYP1A inducer  
11 beta-naphthoflavone (BNF) was carried out by RT-qPCR. The minimum exposure  
12 time that elicited significant *CYP1A* transcriptional induction was 1 h for liver, gill,  
13 gut, brain, anal fin and fingerlings; 2 h for dorsal fin; and 4 h for kidney and tail fin.  
14 In most of the organs *CYP1A* tends to reach the greatest induction in the first few  
15 hours (1 to 8 h) of experiment and *CYP1A* mRNA levels remained elevated until the  
16 end of the experiment (96 h; with water renewing every 24 h). This information  
17 could be important planning toxicological assays using fish. In addition, fins that has  
18 regeneration capacity, could also be used for such analyzes which could favor for the  
19 use of non-lethal biopsy for the use of *CYP1A* biomarker in guppies. Validation of  
20 *CYP1A* gene biomarker in fish was done by exposing *P. caudimaculatus* to elutriate  
21 made from sediment of three streams located in adjacent areas of the Patos Lagoon  
22 Estuary in Rio Grande city, RS, Brazil. There was a *CYP1A* induction by elutriates  
23 made from sediment from urban and industrial areas (22- and 122-fold control); and  
24 absence of induction by elutriate from an area located 22 Km away from the  
25 populated area of the city (reference site). The results suggest that two of the streams  
26 were potentially contaminated by organic contaminants that are AHR agonists. The  
27 responsiveness of *CYP1A* to BNF and elutriate from urban areas indicates that the  
28 guppy *P. caudimaculatus* could be used as model for environmental toxicology and  
29 monitoring of AHR agonist compounds.

30

31 **Keywords:** Cyprinodontiformes, guppy, contamination, cytochrome P450, PAH.

32



33 **1. INTRODUCTION**

34

35         The cytochrome P450 of family 1 and sub-family A (CYP1A) is a member of  
36 the CYP super family and play critical roles in the biotransformation of drugs,  
37 environmental contaminants and endogenous compounds (Livingstone, 1998;  
38 Schober et al., 2006). *CYP1A* is highly inducible by environment contaminants via  
39 aryl hydrocarbon receptor (AHR)-mediated gene transcription (Kawajari and Fujii-  
40 Kuriyama, 2007) and is used as a biomarker for the environmental exposure to  
41 contaminants in fish (Behnisch et al., 2001).

42         The environmental contaminants that induces *CYP1A* includes planar  
43 polychlorinated biphenyl (PCBs), dibenzo-p-dioxin (PCDD), dibenzofuran (PCDF),  
44 halogenated aromatic hydrocarbons (HAHs) and polycyclic aromatic hydrocarbons  
45 (PAHs) (Hahn, 2002; Nebert and Russell, 2002). These compounds are highly  
46 associated with particulate matter, e.g. sediment and soil, due to the hydrophobic  
47 nature of these compounds (Readman et al, 1984). The resuspension of compounds  
48 associated with the sediment can be done in laboratory by elutriation, which  
49 simulates a real situation of dredging, storm or intake of large volumes of rainwater  
50 that can make a fraction of the compounds bioavailable (EPA, 2001).

51         The guppy *Phalloceros caudimaculatus* (Cyprinodontiformes; Poeciliidae;  
52 Hensel, 1868) is widespread in contaminated and pristine freshwater and estuarine  
53 environments of South American countries, e.g. Brazil, Argentina, Paraguay and  
54 Uruguay, and has been introduced in countries from other continents too, e.g.  
55 Malawi and New Zealand (Froese and Pauly, 2003; Lucinda, 2008). Similar to other  
56 cyprinodontiforme fishes, including guppies and killifishes (e.g. *Poecilia reticulata*  
57 and *Fundulus heteroclitus*, respectively) *P. caudimaculatus* present characteristics

58 that favor the use as a model in environmental toxicology studies, to understand  
59 mechanisms of resistance to live in contaminated environments and to be employed  
60 as a biomonitor in environment monitoring (Aluru et al., 2011).

61 Enzymatic assay and/or gene expression in fishes have been used as  
62 biomarkers for biomonitoring different contaminants, such as PAHs, in the aquatic  
63 environment (Payne et al., 1996; Jönsson et al., 2010). The analysis of *CYP1A*  
64 mRNA levels by real time PCR has showed a positive correlation to traditional  
65 methods that evaluates the levels of CYP1A protein and activity (e.g., Western blot  
66 and EROD, respectively) (Piña et al., 2007). *CYP1A* transcript expression was  
67 demonstrated to reach a peak before the EROD activity, which could be due to lag  
68 between mRNA and protein synthesis (Gao et al., 2011).

69 The present study aimed to: (1) identify the full-length sequence of *P.*  
70 *caudimaculatus* *CYP1A* transcript; (2) analyze the expression in liver, gut, brain, gill,  
71 kidney, dorsal fin, tail fin, anal fin and fingerlings in a time course exposure to 1  $\mu$ M  
72 of beta-naphthoflavone (BNF), a synthetic derivated of a natural flavonoid  
73 compound, which strongly induces *CYP1A1/2* in mammals and is a strong non-  
74 genotoxic inductor (Digiovanni, 1990); and (3) analyze the induction of *CYP1A*  
75 mRNA levels by exposure to elutriate made from sediments of reference and  
76 contaminated sites. The results aims to elucidate if the guppy *Phalloceros*  
77 *caudimaculatus* can be used for biomonitoring of AHR agonists in the aquatics  
78 environments. The investigation of responses in different exposure times can be  
79 useful for planning future toxicological tests with this specie and different organs

80

## 81 **2. MATERIAL AND METHODS**

### 82 **2.1. Identification of *CYP1A* Transcript in *P. caudimaculatus***

83 Liver was excised from one wild male *Phalloceros caudimaculatus* (2 cm;  
84 0.2 g) collected using fishing net in a watercourse at Cassino Beach (Rio Grande, RS,  
85 Brazil). The liver was placed in TRIzol Reagent (Life Technologies, Carlsbad, CA,  
86 USA) and then stored at – 20 °C. Total RNA was isolated using TRIzol Reagent and  
87 cDNA was synthesized using a High-Capacity cDNA Reverse Transcription Kit  
88 (Applied Biosystems, Foster City, CA, USA) with random hexamer primer (provided  
89 in the reverse transcriptase kit) and RNaseOUT Recombinant Ribonuclease Inhibitor  
90 (Invitrogen, Carlsbad, CA, USA). Degenerate primers were designed using highly  
91 conserved regions of previously known *CYP1A* sequences from *Fundulus*  
92 *heteroclitus* (Cyprinodontiformes), Japanese medaka *Oryzias latipes* (Beloniformes)  
93 and stickleback *Gasterosteus aculeatus* (Gasterosteiformes) (GenBank accession  
94 numbers AF026800, NM\_001105087, and HQ202281, respectively) and avoiding  
95 conserved regions present in other CYP1 subfamilies, i.e. CYP1B, CYP1C and  
96 CYP1D. The forward and reverse degenerate primers used are presented in Table 1  
97 and the PCR reactions were performed using the following PCR conditions: 95 °C  
98 for 3 minutes, 35 cycles of 95 °C for 30 seconds, 45 °C for 30 seconds and 72 °C for  
99 1 minute and a final extension of 72 °C for 10 minutes. Primers were obtained from  
100 IDT Integrated DNA Technologies. PCR products were resolved on a 1% agarose gel  
101 and then isolated and purified using Illustra GFX PCR DNA and Gel Band  
102 Purification Kit (GE Healthcare, Buckinghamshire, UK). Partial sequences were  
103 obtained using an ABI Prism 3130xl Platform (Applied Biosystems). The sequence  
104 then was used to design specific primers with Primer3 (Rozen and Skaletsky, 2000)  
105 for Real-time qualitative PCR (RTq-PCR) and for the SMARTer™ RACE cDNA  
106 Amplification Kit (Clontech, Mountain View, CA, USA) (Table 1). The full-length  
107 sequence of *P. caudimaculatus* *CYP1A* was cloned using the SMARTer™ RACE

108 cDNA Amplification Kit and sequenced using an ABI Prism 3130xl Platform. The  
109 full nucleotide sequence was translated to the predicted amino acid sequences and  
110 aligned with other CYP1 family members using Sequence Identity Matrix tool,  
111 Bioedit Sequence Alignment Editor Software (Hall, 1999). Calculation of identities  
112 among *P. caudimaculatus*, *Danio rerio* and *F. heteroclitus* nucleotide and amino acid  
113 predicted sequences was performed using the Multiple Sequence Alignment tool,  
114 Clustal Omega (Sievers et al., 2011). Substrate recognition sites were located based  
115 on those indicated by Gao et al. (2011) and Dorrington et al. (2012).

116

## 117 **2.2. Fish Collection and Maintenance**

118 Pregnant females and adult *P. caudimaculatus* were caught at the same place  
119 and collection process described in the item 2.1 in September 2012 and May 2013,  
120 respectively. The pregnant females (n = 10) were transferred to the laboratory and  
121 acclimated for two weeks at 20 °C in 100 L aquaria with dechlorinated freshwater,  
122 constant aeration and fed twice a day with Alcon BASIC MEP 200 Complex *ad*  
123 *libitum* (Alcon, Camboriú, SC, Brazil), until the birth of the fingerlings. The born  
124 fingerlings were immediately separated from the females to a 20 L aquarium to  
125 prevent predation and were maintained under the same conditions as described above  
126 until the exposure experiment described in the item 2.3. Adult males of *P.*  
127 *caudimaculatus* (n = 140, length: ~2 cm) were transferred to the laboratory and  
128 acclimated for two weeks at the same conditions of water quality and feeding as  
129 described above and used for the beta-naphthoflavone (BNF) exposure experiment as  
130 described in the item 2.3.

131 Adult males of *P. caudimaculatus* (n = 56, length: ~2 cm) were caught at the  
132 same place and collection process described in the item 2.1 in August 2013,

133 transferred to the laboratory, acclimated for two weeks at the same conditions of  
134 water quality and feeding as described above and used for the elutriate exposure  
135 experiment as described in the item 2.5.

136 The collection of the wild fish to use in scientific activity have the  
137 authorization from SISBIO (process number: 24486-3) and the procedures used in  
138 these experiments were approved by the Animal Care and Use Committee (CEUA)  
139 at the Universidade Federal do Rio Grande (FURG).

140

### 141 **2.3. BNF Exposure Experiment and Quantification of *CYP1A* mRNA levels**

142 Adult *P. caudimaculatus* (n = 70, length: ~2 cm) were waterborne exposed to  
143 1 µM of beta-naphthoflavone (BNF) (Sigma–Aldrich Co., St. Louis MO, USA)  
144 dissolved in DMSO (to reach 20 ppm in the final volume) in a glass aquarium. Adult  
145 *P. caudimaculatus* were also kept in a second glass aquarium with an equivalent  
146 concentration of DMSO in the water (control group; n=70; length: ~2 cm). The  
147 selection of the waterborne BNF concentration was based on Jönsson et al. (2007)  
148 and Kim et al. (2008) that showed strong induction of *CYP1A* mRNA levels. Fish  
149 were kept without food in the aquarium with aerated water and temperature 20 °C for  
150 24 h before the exposure experiment and no food was supplied during the exposure  
151 experiment. The proportion of five fish per liter of water in both aquariums (BNF  
152 and control) was maintained along the period of the experiment and the water was  
153 renewed every 24 h to maintain the BNF and DMSO concentration during the 96-h  
154 experiment. The same exposure procedures described using adult *P. caudimaculatus*  
155 was conducted for the fingerlings BNF exposure. Fingerlings with five to eight days  
156 of age were used and the exposure was performed with 10 fingerlings per 200 mL of  
157 water.

158 Adult fish and fingerlings, from BNF exposed or control group, were  
159 randomly sampled at 1, 2, 4, 8, 24, 48 and 96 h of exposure, immersed in ice water  
160 and euthanized by cervical transaction. Liver, gut, brain, gill, kidney, dorsal fin, tail  
161 fin and anal fin were dissected from the adult fish and immediately placed in  
162 RNAlater (Ambion, Austin, TX, USA). Each fingerling was collected as a whole  
163 sample. The samples were held for 24 h at 4°C, and then stored at -20 °C according  
164 to the RNAlater manufacturer's instructions.

165 Total RNA was extracted from adult fish organs and fingerlings. The cDNA  
166 was synthesized (n = 6 per experimental group) as described in the item 2.1. *P.*  
167 *caudimaculatus* specific primers (Table 1) were used to quantify *CYP1A* and *β-actin*  
168 mRNA levels by real-time PCR (RTq-PCR). The RTq-PCR runs were performed in  
169 duplicate using GoTaq qPCR Master Mix (Promega, Madison, WI, USA) according  
170 to the manufacturer's instructions and a 7300 Real-Time PCR System (Applied  
171 Biosystems) using the program: 50 °C for 2 minutes, 95 °C for 2 minutes, and 40  
172 cycles of 95 °C for 15 seconds and 60 °C for 30 seconds. Melting-curve analysis was  
173 performed on all the PCR products at the end of each RTq-PCR run to verify the  
174 amplification of a single product. The  $2^{-\Delta Ct}$  method described by Schmittgen and  
175 Livak (2008) was employed to calculate *CYP1A* relative mRNA levels of individual  
176 samples, using *β-actin* as a housekeeping gene.

177

#### 178 **2.4. Sediment Sampling**

179 Sediment samples used to produce the elutriate to the fish exposure  
180 experiment (see item 2.5) were collected at no more than 1 m depth in three sites.  
181 The site S1 (32°01'49.35"S, 52°06'31.15"W) was a watercourse in the middle of the  
182 urban area that receive domestic and urban sewage discharges; the site S2

183 (32°02'56.48"S, 52°05'06.98"W) was nearby the petro distributor of the city in a  
184 watercourse close to the loading terminal of tank trucks; and the reference site (REF)  
185 (32°33'32.48"S, 52°23'54.59"W) was a watercourse 22 km south-west from the  
186 closer urban area at Cassino beach. The locations were selected to represent sites  
187 with different kinds and degrees of contamination. The sites (S1 and S2) were close  
188 to places that have historically received effluent of domestic and industrial activities,  
189 S2 site was close to a contaminated site with PAHs, being reported as moderately  
190 contaminated with PAH and S1 to a less PAH contaminated site but was more  
191 contaminated than the reference site for PAH levels (Medeiros et al., 2005; Garcia et  
192 al., 2010). One sediment sample of 500 ml was collected for each place. The  
193 sampling of surface sediment (0-10 cm) was performed using a stainless steel Ekman  
194 grab and the material was stored for less than 20 days at -20 °C until the preparation  
195 of the elutriate solution.

196

## 197 **2.5. Exposure to Elutriate and Quantification of *CYP1A* mRNA levels**

198 Elutriate was obtained by mixing 300 ml of sediment and 1200 ml of  
199 dechlorinated water (ratio 1:4 v/v) inside a glass container. Detritus (i.g. small rocks  
200 and plant roots) were manually removed from sediment using forceps. The mix was  
201 maintained under vigorous agitation for 1 h, followed by a settling down process for  
202 at least 8 h (EPA, 2001). Afterwards, 1 L of the supernatant fraction was placed in  
203 glass aquariums for the fish exposure.

204 Adult *P. caudimaculatus* (n = 56, ~2 cm) were kept without food with aerated  
205 freshwater and temperature 20 °C for 24 h before the exposure experiment and no  
206 food was supplied during the exposure. The exposure was held with 1 L of  
207 concentrated elutriates (100%). Elutriates made with sediments of REF site, S1 site

208 and S2 site were placed in aquarium with constant aeration. Groups of fourteen adult  
209 fish were added to each of the experimental aquaria. A control group (n = 14) was set  
210 in a separate aquarium containing the same freshwater that was used to prepare  
211 elutriates. Fish from the four experimental aquaria were sampled after 8 hours of  
212 exposure, anesthetized by immersion in a tricaine solution (150  $\mu\text{g}\cdot\text{ml}^{-1}$ ) for ~2.5 min  
213 (Sigma, St Louis, MO, USA) and euthanized by cervical transection. The use of  
214 anesthetic procedure in this experiment was implemented, as this procedure  
215 apparently did not alter significantly the *CYP1A* mRNA levels in guppy (Pinto et al.,  
216 2015). The liver was dissected and immediately placed in RNAlater and stored. The  
217 reverse transcription and quantification of the *CYP1A* mRNA levels was done as  
218 described in the item 2.1.

219

## 220 **2.6. Statistical Analyses**

221 Statistical analyses for both experiments were performed using Past software  
222 (version 2.17) (Hammer et al, 2001). No difference in the *CYP1A* mRNA levels in  
223 different organs and fingerlings were found between the control groups for different  
224 times of exposure and the data from control groups were pooled for the subsequent  
225 analyses. All data was log-transformed and ANOVA assumptions were verified. For  
226 the BNF exposure experiment a one-way ANOVA for repeated measures was  
227 performed to test the differences among treatments. For the elutriate exposure  
228 experiment a one-way ANOVA was performed to test for differences among the four  
229 experimental groups. Tukey's *post hoc* test was performed for both analyses to  
230 identify differences between groups. The significance level for all analyses was  $p \leq$   
231 0.05.

232



233 **3. RESULTS**

234 **3.1. Identification of *CYP1A* mRNA Sequence in *P. caudimaculatus***

235         The first fragment achieved using the degenerate primers was 534 base pair  
236 long with 89% of identity with predicted *Fundulus heteroclitus* CYP1A amino acid  
237 sequence. Using SMARTer<sup>TM</sup> RACE cDNA Amplification Kit, one sequence with  
238 391 base pairs and another with 1516 base pairs were obtained, corresponding to the  
239 3' and 5' cDNA ends of the *P. caudimaculatus* *CYP1A*, respectively. The contig of  
240 those three sequences revealed a 1750 bp nucleotide sequence containing the *P.*  
241 *caudimaculatus* *CYP1A* complete open reading frame with 1566 base pairs coding  
242 for a 521 amino acid protein. The obtained sequence also contained 130 bp in the 5'  
243 untranslated region (UTR) and 54 bp in the 3' UTR. The 3' UTR was apparently  
244 incomplete since no poly-A tail was found. The *CYP1A* nucleotide sequence of *P.*  
245 *caudimaculatus* and the predicted translated amino acid sequences were aligned with  
246 other CYP1A sequences from *Poecilia vivipara*, *F. heteroclitus* and *Danio rerio*  
247 (Fig. 1). The percent identities between those sequences and other CYP1 sequences  
248 of *F. heteroclitus* are shown in the Table 2. The *P. caudimaculatus* CYP1A amino  
249 acid sequence was 96%, 91% and 70% identical to the *P. vivipara*, *F. heteroclitus*  
250 and *D. rerio* CYP1A sequences, respectively. CYP1B1, CYP1C1 and CYP1D1  
251 amino acid sequences showed less than 55% of identity with the *P. caudimaculatus*  
252 new sequence. The alignment of Fig. 1 showed that amino acid sequences were  
253 identical in *P. caudimaculatus* and *P. vivivapara* for the substrate recognition sites  
254 SRS 1, SRS 5, SRS 6 and the heme binding domain. Between *P. caudimaculatus* and  
255 *F. heteroclitus* sequences, SRS 3, SRS 4, SRS 5, SRS 6 and the heme binding  
256 domain were identical, and the SRS 6 was identical for all fishes in the alignment.  
257

258 **3.2. *CYP1A* mRNA levels in *P. caudimaculatus* Exposed to BNF**

259 No mortality was observed for adult fish and fingerlings in the control or  
260 BNF exposed groups. The *CYP1A* mRNA level was induced in all organs of the adult  
261 fish and in fingerlings (Fig. 2) of *P. caudimaculatus* exposed to 1  $\mu$ M of BNF in  
262 comparison to the respective controls. Liver, gill, gut, brain, anal fin and the  
263 fingerlings showed increased *CYP1A* mRNA level after one hour of BNF exposure;  
264 dorsal fin showed *CYP1A* induction after two hours, and kidney and tail fin showed  
265 *CYP1A* induction after four hours. In the first few hours (1 to 8 h), gill, gut, kidney of  
266 adult fish, and the fingerlings reached the highest mean value of *CYP1A* mRNA  
267 levels, while the remaining organs reached the highest mean value of *CYP1A* mRNA  
268 levels after 24 h.

269 The mean of the induction of *CYP1A*, compared to control group, ranged  
270 between 4- and 27-fold in the liver, 7- and 39- fold in gill, 21- and 97- fold in gut, 8-  
271 and 122- fold in brain, 19- and 176- fold in kidney, 14- and 45- fold in dorsal fin, 4-  
272 and 112- fold in tail fin, 8- and 64-fold in anal fin and 4- and 46- fold in fingerlings  
273 (data not shown). The highest mean inductions of *CYP1A* mRNA levels were  
274 observed in kidney at 8 h of BNF exposure (176 fold) and brain at 48 h of BNF  
275 exposure (122 fold). At 96 h after the beginning of BNF exposure the *CYP1A* level in  
276 all organs of the adult fish and in the fingerlings remained induced.

277

278 **3.3. *CYP1A* mRNA levels in *P. caudimaculatus* Exposed to Elutriate**

279 Mortality of three individuals was observed in response to the exposure to  
280 elutriate from the sediment of the site S1. The results of *CYP1A* mRNA levels for  
281 fish livers are presented in figure 3. Elutriate made of sediment from the REF site  
282 showed no difference comparing to the control water. The elutriate from S1 site was

283 different from the control water, but not from the REF site, inducing the *CYP1A*  
284 mRNA levels 22 times in comparison to the control water. The elutriate from the S2  
285 site was significantly different from all others sites and control water, with an  
286 induction of 122 times in comparison to the control water.

287

#### 288 **4. DISCUSSION**

289 The guppy *P. caudimaculatus* possess characteristics that are desired for use  
290 as a model in environmental and mechanistic studies in toxicology, since it is  
291 widespread in geographic areas of South America and potentially possess unique  
292 adaptation to survive in habitats with adverse conditions, e.g. high levels of  
293 contaminants, high turbidity and low oxygen (Froese and Pauly, 2003; Pinto and  
294 Araújo, 2007; Araújo et al., 2009). In the present study, the nucleotide sequence of  
295 CYP1A, a well established biomarker in fish, was identified in *P. caudimaculatus*,  
296 permitting the characterization of *CYP1A* mRNA induction by BNF in different  
297 exposure times and organs. We were able to show for the first time that *P.*  
298 *caudimaculatus* has a fast transcriptional response (few hours) to AHR agonists in  
299 many organs, including fins, and that *CYP1A* mRNA is strongly induced by exposure  
300 to elutriate made from environmental samples. The results presented here could favor  
301 for the use of this organism in ecotoxicology studies in the South American  
302 subtropical environment.

303 The newly identified CYP1A predicted protein showed identity higher than  
304 70 % with the CYP1A sequences of cyprinodontiformes *Poecilia vivipara* and  
305 *Fundulus heteroclitus*; and the cypriniform *Danio rerio*. As the identity is greater  
306 than 55% the new sequence should be classified in the family 1 and subfamily A  
307 (CYP1A) according to the current classification criterion for CYP nomenclature

308 (Nelson et al., 1996). The higher similarity found to CYP1D1 than the other CYP1s  
309 (CYP1B1, 1C1, 1C2) from *F. heteroclitus* was expected as the CYP1A and CYP1D1  
310 have been show to group together in one clade in fishes, while CYP1B1 and CYP1Cs  
311 are in another, according to previous molecular phylogenetic analysis (Zanette et al.,  
312 2009). The high identity and high similarity among the substrate recognition sites  
313 (SRSs) and the full-sequence between the CYP1A amino acid sequences of *P.*  
314 *caudimaculatus*, *P. vivipara* and *F. heteroclitus* suggest these enzymes possibly  
315 catalyzes similar compounds (Gotoh, 1992) as substantial similarity in the size and  
316 shape of the crystal structure of the protein between isoforms and even different  
317 subfamilies corresponds to the overlapping substrate profiles (Dong et al., 2012).

318         The *CYP1A* mRNA levels in *P. caudimaculatus* showed an increasing  
319 response to BNF waterborne exposure. BNF treatment is known to enhance the  
320 expression of *CYP1A* as the carcinogenics PAHs such as 3-methylcholanthrene and  
321 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD) (Nebert and Gonzalez, 1987).  
322 Fingerlings and eight organs from adult fish were select for the expression of  
323 *CYP1A*, five organs were removed with an invasive process: liver, gill, gut, brain and  
324 kidney; and three organs removed with a non-invasive process: dorsal, tail and anal  
325 fins; and the fingerlings. All adult fish organs and fingerlings showed *CYP1A*  
326 induction to BNF exposure.

327         Previous studies demonstrated that *CYP1A* levels are induced in fish exposed  
328 to PCBs and BNF, which are AhR agonists, i.g. *F. heteroclitus* (Elskus, 1999) and  
329 *Jenynsia multidentata*, and in the same family (Poecillidae), i.g. *Poecilia vivipara*  
330 (Ferreira et al., 2012). The induction of *CYP1A* mRNA levels by BNF was expected  
331 in all organs, especially in the main detoxification organs, liver and intestine, which  
332 both showed a fast induction (1 h). *CYP1A* expression was observed in the liver and

333 gill of several fishes, i.g. *F. heteroclitus*, *Danio rerio*, *P. vivipara*, *J. multidentata*  
334 exposed to AHR agonists, gill showed a higher increase than liver in *F. heteroclitus*,  
335 *D. rerio* and *P. vivipara*, and a higher increase in liver than gill was seen in *J.*  
336 *multidentata* (Jönsson et al., 2007; Zanette et al., 2009; Ferreira et al., 2012). The  
337 same pattern, higher induction of *CYP1A* mRNA level in gill over liver, can be seen  
338 for *P. caudimaculatus*. Since the liver is known to have a high basal level of *CYP1A*  
339 in some species of fish, e.g. *Danio rerio* and *Fundulus heteroclitus* (Jönsson et al.,  
340 2007; Zanette et al., 2009), it was possible that the expression could not increase  
341 much over the basal level (Gao et al., 2011).

342         Several studies were done to evaluate induction level of *CYP1A* over time  
343 course exposures and single time exposure to low concentrations of AHR agonists,  
344 e.g., PCB126, 3-methylcholanthrene, benzo[a]pyrene and BNF. Short time exposures  
345 ranged from 2 h to 24 h (Chung-Davidson et al., 2004; Kim et al., 2008; Gao et al.,  
346 2011; Ferreira et al., 2012), going to long time exposures that could take more than  
347 one week (Schlezinger et al., 2006; Gao et al., 2011; Holth et al., 2014) but time-  
348 course studies of *CYP1A* induction with lake trout and pufferfish show raise in the  
349 mRNA levels of *CYP1A* after 4 and 6 hours of exposure, respectively (Chung-  
350 Davidson et al., 2004; Kim et al., 2008). A recent study with *Jenynsia multidentata*  
351 (Pinto et al., 2015) analyzed gill, liver and anal fin demonstrating an increase in the  
352 mRNA levels of *CYP1A* after only one hour of exposure to BNF. *P. caudimaculatus*  
353 mRNA levels of *CYP1A* are different from the control group in the first hour of  
354 exposure. The raise of the mRNA levels of *CYP1A* in *P. caudimaculatus* and *J.*  
355 *multidentata* (Pinto et al., 2015) after only one hour of exposure to 1  $\mu$ M of BNF in  
356 several organs and in the fingerlings suggests that the *CYP1A* induction, which is

357 mediated by the AHR, in this Cyprinodontiformes occurs rapidly and can provide an  
358 early warning about AHR agonists in the environment.

359 *P. caudimaculatus* *CYP1A* mRNA levels reached a great induction in the first  
360 hours (1 to 8 h) of experiment, this corroborates with Pinto et al. (2015), which  
361 showed great inductions in the *CYP1A* mRNA levels of *Jenynsia multidentata*  
362 between 1 to 8 h too. *P. caudimaculatus* *CYP1A* mRNA levels remained elevated  
363 until the end of the experiment (96 h; with water renewing every 24 h) but Kim et al.  
364 (2008) showed a decrease, even reaching a level similar to the control, in the *CYP1A*  
365 mRNA levels, this could be due to the decay of the BNF in the water, as the BNF  
366 was dissolved in the water once at the beginning of the experiment. This information  
367 could be important to plan toxicological assays using fish.

368 Liver and gills have been used to analyze enzymatic and mRNA levels of  
369 *CYP1A* (Jönsson et al., 2007; Curtis et al., 2011; Dorrington et al., 2012) but for this  
370 methodology the death of the fish is required and actually there is a growing ethical  
371 concern about the use of animals for research. The use of fins in this study  
372 demonstrates that these organs that can be removed with a non-lethal procedure can  
373 be used for analysis of mRNA levels of *CYP1A*. Besides this, the fins have a  
374 regeneration capacity (Offen et al., 2008), which reinforces the utility for studies of  
375 biomonitoring. Dorsal and tail fin showed an increase in the *CYP1A* mRNA levels  
376 after two and four hours of exposure, respectively. Both fins increased and sustained  
377 high mRNA levels of *CYP1A*, with the tail fin reaching 112 fold induction in 24  
378 hours of exposure. While for the anal fin *CYP1A* mRNA levels was observed an  
379 induction in the first hour of exposure like the one seen in liver, gill, gut, brain and  
380 fingerlings. Different magnitudes and patterns of *CYP1A* mRNA levels during the  
381 exposure among the fins could be associated with the histological composition of

382 each fin, as the dorsal and tail fins have more dermal skeleton, which is similar to  
383 scales, than the anal fin (Kuntz, 1914; Ogino et al., 2004; Zauner et al., 2003).  
384 Biopsied fins of *Jenynsia multidentata* exposed to BNF and showed induction of  
385 *CYP1A* mRNA levels (Pinto et al., 2015), this procedure does not expose the fish to  
386 the contaminants and could be used with *P. caudimaculatus*.

387 CYP1A have been showing induction after exposure to many different  
388 chemical in laboratory with the help of carriers (Gao et al., 2011; Ferreira et al.,  
389 2012; Dorrington et al., 2012) but this is not an approach that simulate a real  
390 condition. PAHs are hydrophobic compounds with low water solubility, which  
391 associate primarily with the particulate phase (Readman et al, 1984). The exposure to  
392 sediments and elutriates can be used to simulate real situations, e.g. dredging and  
393 intense storms, helping to understand the dynamic of the several contaminants that  
394 are remobilized to the water column (Bergen et al., 2005).

395 As expected, there was no statistical difference between the REF site and the  
396 control water, demonstrating that the elutriate method and exposure do not induced  
397 *CYP1A* mRNA levels in *P. caudimaculatus*. The higher expression of *CYP1A* mRNA  
398 levels, which are involved in biotransformation pathways, in *P. caudimaculatus*  
399 exposed to elutriate made from possibly contaminated S2 site sediment may be due  
400 to a higher concentration of contaminants present in the sediment that were  
401 resuspend by the elutriate method. Ribecco et al. (2012) performed a exposure of  
402 juvenile of the fish *Solea solea* to a sediment contaminated with pesticides, PCBs,  
403 HPA and heavy metals, which was considered moderately contaminated, after 96  
404 hours all the biomarkers analyzed, in which was *CYP1A* and *CYP3A*, were up  
405 regulated, being considered an early response to contamination..

406 In conclusion, this study showed that *Phalloceros caudimaculatus* respond to  
407 AHR agonist inducing *CYP1A* mRNA levels in all organs analyzed and fingerlings.  
408 This information can be used for toxicological purposes, such as the use of *P.*  
409 *caudimaculatus* for monitoring AhR agonist in environmental samples and the use of  
410 fins as sample material for *CYP1A* mRNA analysis, as the excision of these organs  
411 do not implies the death of the fish.

412

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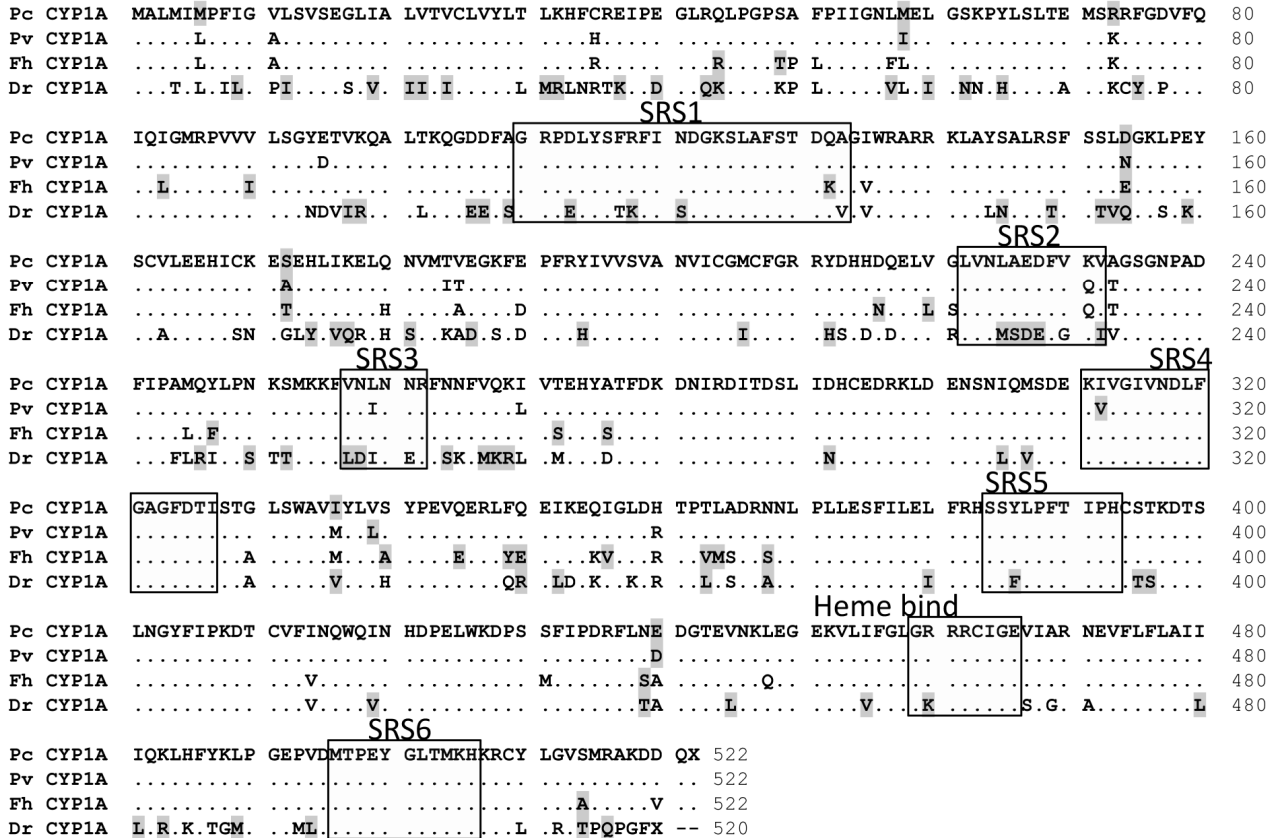
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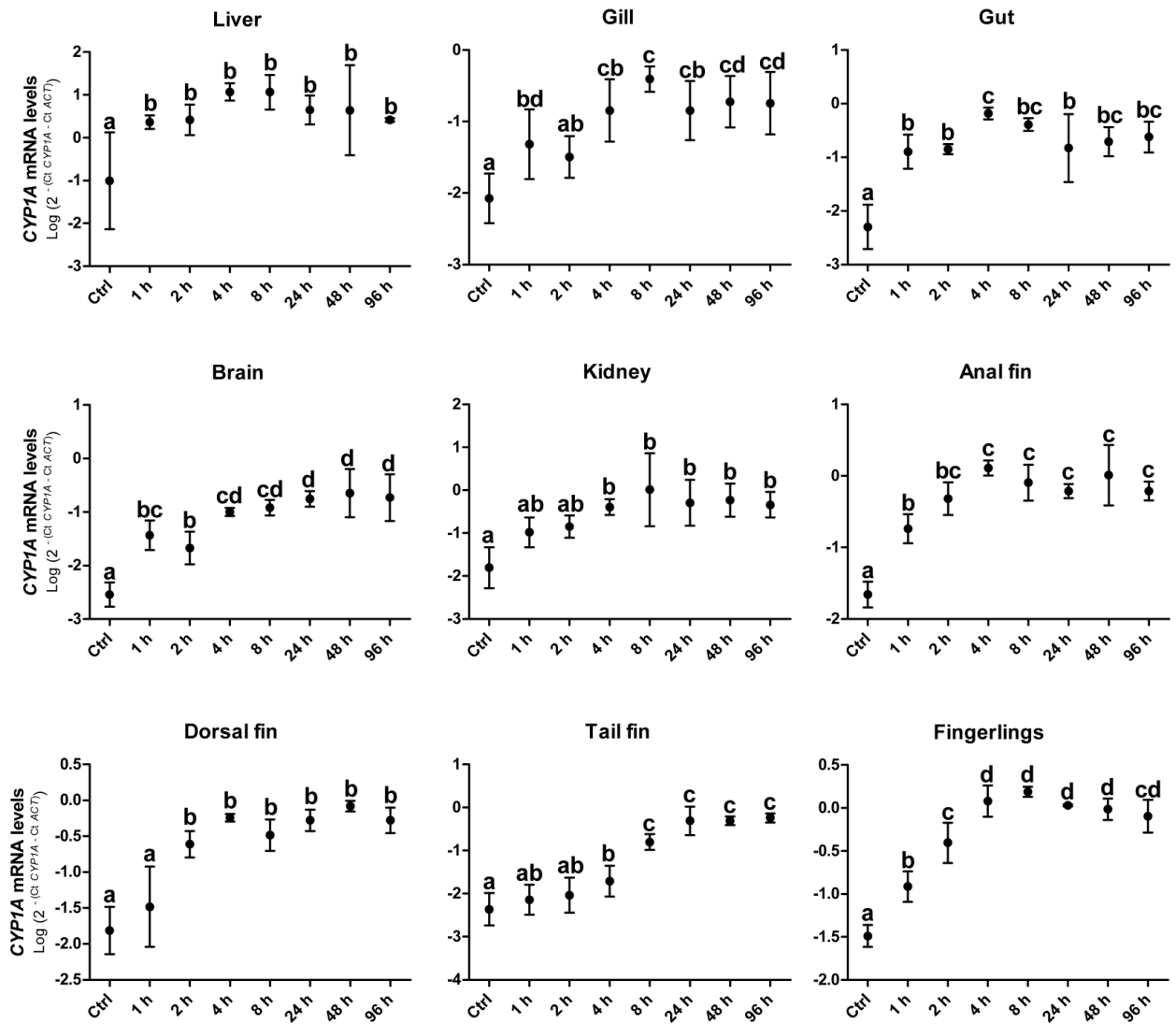
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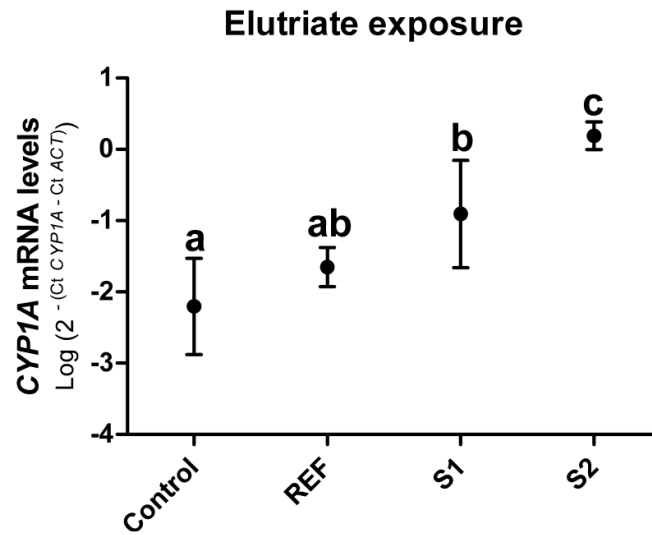
## FIGURES



**Fig. 1.** Alignment of the CYP1A amino acid sequences of guppy *P. caudimaculatus* (Pc), guppy *Poecilia vivipara* (Pv), killifish *Fundulus heteroclitus* (Fh) and zebrafish *Danio rerio* (Dr). Identical and similar amino acids are represented by dot and gray background, respectively, comparing to Pc CYP1A sequence. The substrate recognition sites (SRS 1-6) and the heme binding site are indicated by boxes.



**Fig. 2.** CYP1A mRNA levels in liver, gill, gut, brain, kidney, anal fin, dorsal fin, tail fin and fingerling of *P. caudimaculatus* exposed to 1 μM BNF during 1, 2, 4, 8, 24, 48 and 96 h. Differences between groups were determined by one-way ANOVA for repeated measures followed by Tukey's *post hoc* test ( $p < 0.05$ ,  $n = 6$ ). Dots in the figures represent means  $\pm$  SD.



**Fig. 3.** *CYP1A* mRNA levels in adult *P. caudimaculatus* liver exposed for 8 hours to the control water, elutriate from the sediment reference site, domestic waste site and petrochemical pole site. Differences between groups were determined by one-way ANOVA followed by Tukey's *post hoc* test ( $p < 0.05$ ,  $n = 10$ ). Dots in the figures represent means  $\pm$  SD.



## TABLES

**Table 1.** Degenerate and specific primers employed in the *CYP1A* identification and in the *CYP1A* and *B-actin* RTq-PCR analysis in *P. caudimaculatus*.

Primer name	Sequence (5'-3')
CYP1A_degenerate_F	CAACCCWGCAGAYTTCATCCCTGC
CYP1A_degenerate_R	GGGTCRTGGTTTATYTGCCACTGG
CYP1A_RACE_F1	CCCTGCTATGCAGTATCTTCCCAAC
CYP1A_RACE_R1	GTCTGTGATGTCACGGATGTTGTCC
CYP1A_RACE_F2	GAGGACCGGAAGCTGGATGAGAA
CYP1A_RACE_R2	GCCCATGACAAACCAGTAGAGATGG
CYP1A_qPCR_F	GAGGACCGGAAGCTGGATGAGAA
CYP1A_qPCR_R	GCCCATGACAAACCAGTAGAGATGG
$\beta$ -ACT_qPCR_F	ACCATCACCGGAGTCCATGACGA
$\beta$ -ACT_qPCR_R	ATGTACGTTGCCATCCAGGCCGT

**Table 2.** Identities between nucleotide sequences (in the left-bottom) and amino acid sequences (right-top) among *P. caudimaculatus* (Pc), *Poecilia vivipara* (Pv) and zebrafish *Danio rerio* (Dr) CYP1As and *Fundulus heteroclitus* (Fh) CYP1A, 1B1, 1C1 and 1D1 sequences.

	Pc_CYP1A	Dr_CYP1A	Pv_CYP1A	Fh_CYP1A	Fh_CYP1B1	Fh_CYP1C1	Fh_CYP1D1
Pc_CYP1A		70	96	91	39	37	43
Dr_CYP1A	68		71	71	40	39	44
Pv_CYP1A	97	68		91	40	39	43
Fh_CYP1A	90	69	90		39	38	44
Fh_CYP1B1	49	49	49	49		49	37
Fh_CYP1C1	49	47	49	47	57		39
Fh_CYP1D1	55	54	54	54	50	48	

Accession numbers: NM\_131879.1 (Dr\_CYP1A); JX027071.1 (Pv\_CYP1A); AF026800.1 (Fh\_CYP1A); FJ786959.1 (Fh\_CYP1B1); FJ786960.1 (Fh\_CYP1C1); FJ786961.1 (Fh\_CYP1D1)

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