**Introduction**

The important role of ABC transporters in tissue defense is reflected by their tissue distribution. Numerous studies revealed the highest expression of transporters from the ABCB, ABCG and ABCD subfamily in important physiological and/or pharmacological barriers of mammalian[1-3]. On the contrary, detailed studies of ABC transporter genes expression and function in aquatic animals are scarce[4]. Consequently, the main goals of our study were: (1) gene expression analysis of ABC transporters (abcb1, abcb11, abcc1-5 and abcg2) implicated in disposition of various xenobiotics in rainbow trout tissues (brain, gills, liver, kidney, gonads, distal tubule), (2) to determine functional activity of target ABC transporters in rainbow trout cell lines (R1) after 24 h exposure to various xenobiotics. 

**Results**

1. **Conclusions**

a) **Tissue RNA distribution**

- Constitutive expression of all tested transporters throughout the tissues with high expression of abcb1, abcc3 and abcg2.
- Abcb11 expression is tissue specific for liver.
- Low transporters expression in gills

b) **Cell line RNA distribution (Figure 2)**

- Constitutive expression of all tested transporters with high expression of abcc1-3 and extremely low expression of abcb1, abcb11 and abcg2

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**Figure 1**. Tissue RNA distribution Relative expression levels of ABC transporter genes in trout tissue samples. Expression is presented relative to the housekeeping gene e18s RNA as mean ± SD obtained from 3 independent RNA isolations of each cell line. Elta RNA (e18s) is set to 10,000 in all cell lines.

**Table 1.** MOR assay – data are presented as ratios of maximal inhibitory effect (substrate accumulation) relative to control with Calcien-AM as fluorescent substrate

<table>
<thead>
<tr>
<th>Rainbow trout tissue distribution</th>
<th>B1</th>
<th>B2</th>
<th>C1</th>
<th>C2</th>
<th>C3</th>
<th>C4</th>
<th>C5</th>
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</table>

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**Figure 2**. Cell line RNA distribution Relative expression levels of ABC transporter genes abcb1, abcb11, abcc1-5 and abcg2 in permanent rainbow trout cell lines RTgill-W1, RTgut, R1, RTgill, RTbrain, RTgill-W1, RTgut, RTbrain and reverse transcribed to CDNA.

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**Gene expression was quantified using Sybr green absolute quantification. Data analysis was done with ABI SDS 2.0 software and GraphPad 5.0 software. Foldes were calculated according to qGene and Pfaffl equations.**

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**Table 2.** Cell line induction – data are presented as fold increase relative to control. Foldes were calculated according to Pfaffl equation.

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**References**


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