Differential evolution of duplicated medakafish *mitf* genes

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**Supplementary figure legends**

**Figure S1. Nucleotide and deduced amino acid sequence of medaka *mitf1* and *mitf2*.** (A) *mitf1*. (B) *mitf2*. Start codon and stop codon are shown in bold. Broken and solid arrows depict sequences of primers for PCR analysis and cDNA cloning, respectively. Sequences are deposited in GenBank under accession numbers KC249979 (*mitf1*) and KC249980 (*mitf2*).

**Figure S2. Mitf protein sequence alignment.** Common species names, Mitf proteins or isoforms and percentage sequence similarity values compared to the medaka Mittf1 and Mitf2 are seen. The basic helix-loop-helix leucine zipper sequences are indicated. For accession numbers see Figure 1B.

**Figure S3. Phylogentic tree construction by maximum likelihood.** For accession numbers and more details, see the legend to Figure 1B.

**Figure S4. Phylogentic tree construction by minimum evolution.** For accession numbers and more details, see the legend to Figure 1B.
Figure S1. Nucleotide and deduced amino acid sequence of medaka mitf2
<table>
<thead>
<tr>
<th>Species</th>
<th>Mitf1</th>
<th>Mitf2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Medaka 1</td>
<td>100%</td>
<td>61%</td>
</tr>
<tr>
<td>Stickleback 2</td>
<td>83%</td>
<td>59%</td>
</tr>
<tr>
<td>Xiphophorus</td>
<td>93%</td>
<td>59%</td>
</tr>
<tr>
<td>Zebrafish b</td>
<td>81%</td>
<td>67%</td>
</tr>
<tr>
<td>Human A</td>
<td>76%</td>
<td>59%</td>
</tr>
<tr>
<td>Human M</td>
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<td>60%</td>
</tr>
<tr>
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<td>67%</td>
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<tr>
<td>Xiphophorus M</td>
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<tr>
<td>Stickleback 1</td>
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<td>75%</td>
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<tr>
<td>Medaka 2</td>
<td>61%</td>
<td>100%</td>
</tr>
</tbody>
</table>

**Figure S2.** Mitf protein sequence alignment.
Figure S3. Phylogenetic tree construction by maximum likelihood.
Figure S4. Phylogenetic tree construction by molecular evolution.