New Primers Reveal the Presence of a Duplicate Histone H3 in the Marine Turtle Leech Ozobranchus branchiatus


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New primers reveal the presence of a duplicate histone H3 in the marine turtle leech *Ozobranchus branchiatus*

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**Introduction**

Marine leeches, specifically *Ozobranchus branchiatus*, have been studied for their role in the spread of fibropapillomatosis (FP), a pandemic marine turtle disease. Historically, FP has been a significant threat to marine turtle conservation efforts due to its rapid spread and high mortality rates. The disease is caused by a viral agent that infects marine turtles, leading to severe skin lesions and often resulting in death. Understanding the genetic diversity of the leech population is crucial for effective disease management and conservation strategies.

**Methods**

New primers were designed using Primer3 (Rozen & Skaletsky, 2000) and hybridized to existing sequences obtained from GenBank. The primers were used in polymerase chain reaction (PCR) reactions to amplify genetic markers from marine leeches. The PCR products were sequenced using BigDye Terminator v3.1 cycle sequencing and analyzed using Sequencher software.

**Results and Conclusions**

The new primers revealed the presence of a duplicate histone H3 (H3R1 and H3R2) in *O. branchiatus*. These markers were specifically associated with the Indian River Lagoon and Big Cypress National Preserve in Florida, indicating potential differences in genetic diversity between these regions. The duplication event occurred within the Ozobranchidae lineage, suggesting a recent evolutionary event.

**Acknowledgements**

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**References**


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**Table 1**

<table>
<thead>
<tr>
<th>Region</th>
<th>H3R1</th>
<th>H3R2</th>
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</thead>
<tbody>
<tr>
<td>Florida Lagoon</td>
<td>0.044</td>
<td>0.044</td>
</tr>
<tr>
<td>Big Cypress</td>
<td>0.312</td>
<td>0.312</td>
</tr>
<tr>
<td>St. Lucie</td>
<td>0.038</td>
<td>0.038</td>
</tr>
</tbody>
</table>

Conducted in MEGA6 (Tamura et al. 2011) using the Fitch parsimony model (Fitch 1971) with a gamma distribution shape parameter. *H* is a test of 176 included sequences (292 base pair sequence) and the association was assessed by visual inspection of the phylogram.