The complete mitochondrial genome of western painted turtle, Chrysemys picta bellii (Chrysemys, Emydidae)

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MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of western painted turtle, Chrysemys picta bellii (Chrysemys, Emydidae)

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Abstract

In this study, we report the complete mitochondrial genome sequence of western painted turtle, Chrysemys picta bellii. The genome is found to be 16,875 bp in length and has a base composition of A (34.4%), G (13.0%), C (26.0%), and T (26.6%). Similar to other turtles, it contains a typically conserved structure including 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes, and 1 control region (D-loop). Most of the genes are encoded on H-strand, except for the eight tRNA and ND6 genes. All protein-coding genes start with an ATN codon except for COX1 and ND4, which initiate with GTG instead, and terminate with the typical stop codon (TAA/TAG) or a single T (T-) or an unexpected codon of AGG. The complete mitochondrial genome sequence provided here would be useful for further phylogenetic analysis and conservation genetic studies in C. p. bellii.

Keywords

C. picta bellii, genome, mitochondrion, western painted turtle

History

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The painted turtle, Chrysemys picta, has been recognized as a continentally distributed species with a wide range from southern Canada to extreme northern Mexico of North America (Conant & Collins, 1991; Iverson, 1992). Currently, four subspecies are recognized for this species, including C. p. bellii, C. p. dorsalis, C. p. marginata, and C. p. picta (Bishop & Schmidt, 1931). However, only the mitochondrial genome of C. p. picta was reported previously (AF069423; Mindell et al., 1999). Here, using the CLC Genomic Workbench v3.6 (2010), we assembled and analyzed the mitochondrial genome of western painted turtle (GenBank accession no. KF874616), C. p. bellii, one of the most widespread, abundant, and well-studied turtles, with the Illumina sequencing data released by Shaffer et al. (2013). This mitochondrial sequence reported here added a new genetic resource for the family Emydidae and would contribute to better understand population genetics and dynamic evolution of C. p. bellii.

The complete mitochondrial genome sequence of C. p. bellii had 16,875 bp in length and contained a total of 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes (12S rRNA and 16S rRNA), and 1 non-coding control region (D-loop). Most of these genes are encoded on the H-strand, except for the eight tRNA and ND6 genes. All protein-coding genes start with an ATN codon except for COX1 and ND4, which initiate with GTG instead, and terminate with the typical stop codon (TAA/TAG) or a single T (T-) or an unexpected codon of AGG. The complete mitochondrial genome sequence provided here would be useful for further phylogenetic analysis and conservation genetic studies in C. p. bellii.

Table 1. List of genes encoded by Chrysemys picta bellii mitochondrial genome.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Position</th>
<th>Base composition (%)</th>
<th>Start codon</th>
<th>Stop codon</th>
<th>Strand</th>
</tr>
</thead>
<tbody>
<tr>
<td>tRNA^Phe</td>
<td>1-70</td>
<td>37.1</td>
<td>22.9</td>
<td>18.6</td>
<td>21.4</td>
</tr>
<tr>
<td>12S rRNA</td>
<td>71-1038</td>
<td>37.7</td>
<td>24.0</td>
<td>17.0</td>
<td>21.3</td>
</tr>
<tr>
<td>tRNA^Thr</td>
<td>1039-1107</td>
<td>43.5</td>
<td>18.8</td>
<td>11.6</td>
<td>26.3</td>
</tr>
<tr>
<td>16S rRNA</td>
<td>1109-2722</td>
<td>39.9</td>
<td>22.2</td>
<td>16.5</td>
<td>21.3</td>
</tr>
<tr>
<td>tRNA^Ala</td>
<td>2724-2799</td>
<td>27.6</td>
<td>26.3</td>
<td>22.4</td>
<td>23.7</td>
</tr>
<tr>
<td>ND1</td>
<td>2800-3771</td>
<td>32.5</td>
<td>27.9</td>
<td>10.8</td>
<td>28.8</td>
</tr>
<tr>
<td>tRNA^His</td>
<td>3771-3841</td>
<td>28.2</td>
<td>21.1</td>
<td>23.9</td>
<td>26.8</td>
</tr>
<tr>
<td>tRNA^Glu</td>
<td>3841-3912</td>
<td>23.6</td>
<td>9.7</td>
<td>26.4</td>
<td>40.3</td>
</tr>
<tr>
<td>tRNA^Met</td>
<td>3912-3980</td>
<td>31.9</td>
<td>26.1</td>
<td>14.5</td>
<td>27.5</td>
</tr>
<tr>
<td>ND2</td>
<td>3981-5021</td>
<td>37.9</td>
<td>30.0</td>
<td>8.1</td>
<td>24.0</td>
</tr>
</tbody>
</table>

(continued)
ND1 coding genes ended with TAA, whereas, COX1 start codon, and COX1 terminated with TAG, and (between tRNAPro COX3 12S rRNA genes, tRNASer typical cloverleaf secondary structure except for tRNAHis ND4 10,248 11,628 1381 34.8 28.9 10.5 25.8 GTG T– – H 9958 10,254 297 31.0 26.9 10.4 31.7 ATG TAA H ND4L tRNAArg 9538 9887 349 30.6 26.1 13.2 30.1 ATA T– – H ND3 tRNAGly 8685 9468 784 30.0 27.2 14.9 27.9 ATG T– – H COX3 8002 8685 684 32.9 30.0 10.5 26.6 ATG TAA H ATP8 7844 8032 189 39.7 27.5 5.8 27.0 ATG TAA H tRNALys 7084 7770 687 34.6 25.3 13.6 26.5 ATG TAA H COX2 tRNAAsp 7014 7083 70 37.1 15.7 12.9 34.3 H tRNASer COX1 tRNATyr tRNACys tRNAAsn tRNAAla region of C. p. bellii a grant from Chinese Department of Science and Technology (973 Hundreds Talents Program of Chinese Academy of Sciences (CAS), Hundreds Oversea Talents Program of Yunnan Province, (20080A009), Hundreds Talents Program of Chinese Academy of Sciences (CAS), a grant from the Chinese Academy of Science (KSCX2-YW-N-029), a grant from Chinese Department of Science and Technology (973 Program 2007CB815703) and a startup grant of Kunming Institute of Botany, CAS (to L. Z. Gao).

The 13 identified protein-coding genes were 11,406 bp in length and encoded 3791 amino acids in total. Of them, eight initiated with ATG, while ND1, ND2, and ND3 used ATA as the start codon, and COX1 and ND4 started with GTG. Five protein-coding genes ended with TAA, whereas, ND1, ND2, and ND5 terminated with TAG, and COX1 and ND6 stopped with AGG. Incomplete stop codons (T-) were observed in COX3, ND3, and ND4.

The 22 tRNA genes of C. p. bellii range in size from 65 bp (tRNAArg) to 76 bp (tRNALeu). Of them, 21 could fold into typical cloverleaf secondary structure except for tRNASer. The two rRNA genes, 12S and 16S rRNA, were 968 bp and 1614 bp in length, respectively. They were located between the tRNAPro and tRNALeu genes and further separated by tRNAVal. The control region of C. p. bellii mtDNA was 1184 bp long and located between tRNAPro and tRNAphe.

Acknowledgements

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Declaration of interest

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