The complete mitochondrial genome of *Pelecanus occidentalis* (Pelecaniformes: Pelecanidae) and its phylogenetic analysis

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The specimen was collected from southeastern United States and stored at Hunan Engineering Research Center for Internet of Animals, China. The total mitochondrial DNA was extracted from the muscle tissue using a DNeasy Plant Mini Kit (Qiagen, Valencia, CA), and sequenced by using the Illumina Miseq Platform (Illumina, San Diego, CA). Adapters and low-quality reads were removed using the NGS QC Toolkit (Patel and Jain 2012). The genome was annotated using the MITOS WEB Server (Bernt et al. 2013). Each of the annotated protein-coding genes (PCGs) were compared with published sequences of other vertebrate species using DOGMA (Wyman et al. 2004). Drawing a circular map of the mitochondria referred to Zhang’s method (Zhang et al. 2017) by using OGDRAW (Lohse et al. 2007). Phylogenetic tree of the relationships among Pelecaniformes and its related orders were presented using 13 shared PCGs among 18 species by Neighbour-joining (NJ) analyses using MEGA 7.0 software with 1000 bootstrap replication (Kumar et al. 2016). The complete mitochondrial genome of *P. occidentalis* was submitted to the NCBI database under the accession number MH041272.

The complete mitochondrial genome of *P. occidentalis* was 17,315 bp in length. A total of 36 mitochondrial genes were identified, including 13 protein-coding genes (PCGs), 21 transfer RNA (tRNA) genes, two ribosomal RNA (rRNA) genes, and one non-coding control region (D-loop). Among these genes, ND6 and eight tRNAs (tm\textsubscript{Glu}, tm\textsubscript{Ala}, tm\textsubscript{Asn}, tm\textsubscript{Cys}, tm\textsubscript{Gln}, tm\textsubscript{Tyr}, tm\textsubscript{Ser}, tm\textsubscript{Pro}, and tm\textsubscript{Gln}) were located on the light strand (L-strand), while all of the remaining genes were located on the heavy strand (H-strand). The overall base composition of *P. occidentalis* mitogenome was 30.1% for A, 23.7% for T, 31.5% for C, and 14.6% for G, with a GC content of 46.1%. The phylogenetic tree confirmed that *P. occidentalis* was sister to *C. boyciana* (Ciconiiformes), and Ardeidae and Threskiornithidae were both monophyletic group. This information will be useful in the current understanding of the phylogeny and evolution of Pelecaniformes.
All of the nodes were inferred with strong support by the NJ analysis. Our results confirmed that *P. occidentalis* (Pelecaniformes) was sister to *C. boyciana* (Ciconiiformes), and Ardeidae and Threskiornithidae were both monophyletic group. In all, the mitochondrial genome reported here would be useful in the current understanding of the phylogeny and evolution of Pelecaniformes.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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