

棕头鸥线粒体基因组全序列测定与分析

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- 摘要
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摘要 基于长距PCR扩增及保守引物步移法测定并注释了棕头鸥(*Larus brunnicephalus*)的线粒体基因组全序列。结果表明,棕头鸥线粒体基因组全长16 769 bp, GenBank登录号 JX155863。基因含量和排列次序与红原鸡一致,包含13个蛋白编码基因、22个tRNA、2个rRNA和一个D-loop区(控制区)。除COI基因以GTG、ND3基因以ATT为起始密码子外,其余11个蛋白质编码基因均以ATG起始。11个蛋白质编码基因以典型的完全终止密码子AGG、TAG、TAA或AGA终止,COIII和ND4基因因为不完全终止密码子T。预测了22个tRNA基因的二级结构,发现tRNA^{Ser}(AGN)缺少DHU臂,tRNA^{Phe}的TψC臂出现第4种排列形式。预测的棕头鸥12S和16S rRNA二级结构分别包括4个结构域47个茎环和6个结构域60个茎环。其他鸟类控制区发现的F-box、E-box、D-box、C-box、B-box、Bird similarity-box和CSB-boxes(1-3)也存在于棕头鸥中,预测了控制区H链复制起始序列O_H和双向复制起始序列LSP/HSP。系统发育分析支持将棕头鸥划归为面具鸥族(Masked gulls)。

关键词: 棕头鸥 线粒体基因组 RNA二级结构 控制区结构

Abstract: The complete sequence of mitochondrial genome of *Larus brunnicephalus* was determined using long PCR and conserved primers walking approaches. The results showed that the entire mitochondrial genome of *L. brun-nicephalus* is 16,769 bp in length, which has been deposited in GenBank with the accession number JX155863. The mitochondrial genomic organization and gene order of *L. brunnicephalus* were consistent with that of *Gallus gallus*, which contains 13 protein coding genes (PCGs), 22 tRNA, 2 rRNA, and a control region. Except for COI gene using GTG and ND3 gene with ATT as the initiation codon, all other 11 PCGs of the mtDNA in *L. brunnicephalus* started with the typical ATG codon. AGG, TAG, TAA, or AGA were used in 11 PCGs as usual termination codons, except for COIII and ND4 genes with incomplete termination codon (T). The secondary structures of 22 tRNAs were predicted and it is found that the tRNA^{Ser}(AGN) lacks DHU arm and tRNA^{Phe} contains the fourth types of permutation in the TψC arm. It is predicted that the secondary structures of 12S rRNA and 16S rRNA include 4 structural domains with 47 helices and 6 domains with 60 helices, respectively. F-box, E-box, D-box, C-box, B-box, Bird similarity-box, and CSB-boxes (1-3), which were found in the control regions of other bird species were also present in *L. brunnicephalus*. The sequence in the starting regions of H-strand replication (O_H) and the bidirectional light and heavy-strand transcription promoters (LSP/HSP) in the control region were also predicted. Result of phylogeny analysis supports that *L. brunnicephalus* should be categorized into the Masked gulls species.

Keywords: *Larus brunnicephalus*, complete mitochondrial genome, RNA secondary structure, control region structure

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



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