

动物遗传学

鸮形目4种鸟类线粒体调控区全序列的测定与比较研究

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摘要

利用Long-PCR和Primer Walking的方法对鸮形目的短耳鸮、长耳鸮、纵纹腹小鸮、灰林鸮4种鸟类的线粒体调控区进行了全序列测定。结果表明:短耳鸮的调控区长度为3 290 bp;长耳鸮为2 848 bp;纵纹腹小鸮为2 444 bp;灰林鸮为1 771 bp。短耳鸮的调控区长度是4种鸮中最大的,并且是目前已知最大的鸟类线粒体调控区。这4种鸮类调控区的基本结构和其他鸟类相似,按照碱基变化速率的不同可以分为3个区:碱基变化速率较快的外围区域I、III和保守的中间区域II。这4种鸟类调控区的3'端均存在大量的串联重复序列,短耳鸮为126 bp单元重复7次和78 bp单元重复14次;长耳鸮为127 bp单元重复8次和78 bp单元重复6次;纵纹腹小鸮有3个重复单元,分别为89 bp单元重复3次、77 bp单元重复4次和71 bp单元重复6次;灰林鸮仅有1个单元的串联重复为78 bp重复5次。调控区中串联重复序列可能是由链的滑动错配产生,另外这些重复序列都能形成热力学稳定的多重茎环二级结构,而且在重复序列中还发现一些保守基序,这说明重复序列可能具有一定的生理功能,影响调控区的调控功能从而影响线粒体基因组的复制和转录。

关键词 [鸮形目](#); [线粒体基因组](#); [调控区](#); [重复序列](#)

分类号

Comparative Analysis of Complete Mitochondrial DNA Control Region of Four Species of Strigiformes

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Abstract

<P>The sequence of the whole mitochondrial (mt) DNA control region (CR) of four species of Strigiformes was obtained. Length of the CR was 3 290 bp, 2 848 bp, 2 444 bp, and 1 771 bp for *Asio flammeus*, *Asio otus*, *Athene noctua*, and *Strix aluco*, respectively. Interestingly, the length of the control region was maximum in *Asio flammeus* among all the avian mtDNA control regions sequenced thus far. In addition, the base composition and organization of mtDNA CR of *Asio flammeus* were identical to those reported for other birds. On the basis of the differential frequencies of base substitutions, the CR may be divided two variable domains, I and III, and a central conserved domain, II. The 3' end of the CR contained many tandem repeats of varying lengths and repeat numbers. In *Asio flammeus*, the repeated sequences consisted of a 126 bp sequence that was repeated seven times and a 78 bp sequence that was repeated 14 times. In *Asio otus*, there were also two repeated sequences, namely a 127 bp sequence that was repeated eight times and a 78 bp sequence that was repeated six times. The control region of *Athene noctua* contained three sets of repeats: a 89 bp sequence that was repeated three times, a 77 bp sequence that was repeated four times, and a 71 bp sequence that was repeated six times. *Strix aluco*, however, had only one repeated sequence, a 78 bp sequence that was repeated five times. The results of this study seem to indicate that these tandem repeats may have resulted from slipped-strand

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mispairing during mtDNA replication. Moreover, there are many conserved motifs within the repeated units. These sequences could form stable stem-loop secondary structures, which suggests that these repeated sequences play an important role in regulating transcription and replication of the mitochondrial genome.</P>

Key words [Strigiformes](#); [mitochondrial DNA](#); [control region \(CR\)](#); [tandem duplication](#); [molecular evolution](#)

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