#### 生命科学

# 三种蝙蝠线粒体解偶联蛋白2(UCP2)基因的克隆和进化分析

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收稿日期 2008-12-26 修回日期 2009-2-9 网络版发布日期 2009-11-24 接受日期 2009-3-12

摘要 根据几种哺乳动物UCP2基因的保守区设计一对简并引物,扩增马铁菊头蝠(Rhi nol ophus ferrumequi num)、长翼蝠(Mini opterus ful i gi nosus)和犬蝠(Cynopterus sphi nx)的UCP2基因的全部编码区序列. 测序结果表明,三种蝙蝠UCP2编码区全长930 bp,编码309个氨基酸,推测的氨基酸序列包含线粒体内膜载体蛋白的3个特征结构及解偶联蛋白(UCPs)的特征序列. 序列分析表明,蝙蝠与其它哺乳动物UCP2的氨基酸推导序列有很高的同源性,为90. 6%~97. 0%. 进化分析表明,UCP2基因在哺乳动物中进化过程中非常保守,受到强烈的纯化选择压力作用( $\omega$ =0. 063). Branch-specific 模型分析表明,UCP2基因在蝙蝠支系与其它不能飞行的哺乳动物、冬眠蝙蝠与非冬眠蝙蝠的进化过程所受到的选择压力无明显差异(P>0.05). 这说明在整个哺乳动物进化过程中UCP2对其能量代谢的调控均起到了重要作用. 然而,UCP2如何参与哺乳动物能量调控仍有待于进一步研究.

关键词 蝙蝠;能量代谢;进化; UCP2

分类号 0785

# Cloning and evolutionary analysis of *UCP2* in bats (Chinese)

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#### **Abstract**

A pair of degenerated primers was designed based on the conserved region of UCP2 among human, mouse, horse and dog. Then, cDNA fragments encoding the complete coding domain sequence (CDS) of UCP2 were amplified from three bat species (orders), Rhinolophus ferrumequinum (Rhinolophidae), Miniopterus fuliginosus (Miniopteridae) and Cynopterus sphinx (Pteropodidae). The CDS of UCP2 from three different bat species contain 930 bp encoding 309 amino acids. The deduced amino acid sequence of bat UCP2 consist three signature motifs of mitochondrial transporter protein and UCP-specific sequences. Our results showed that UCP2 gene of bats and other mammals shared high homology (90.6% to 97.0%). Evolutionary analysis indicated that UCP2 gene is highly conserved and has undergone strong purifying selected pressure during the evolution of mammals ( $\omega$ =0.063). In addition, by comparing the difference of selected pressure on UCP2 between bats and other mammals, non-hibernating bats and hibernating bats, no significant difference was identified (P>0.05). Taken together, all these data proved that UCP2 has an effect on the regulation of energy metabolism of mammal evolution. The mechanism of metabolic regulation of UCP2, however, remains unclear and further investigation is needed to clarify this process.

Key words <u>bats</u> <u>energy metabolism</u> <u>evolution</u> <u>UCP2</u>

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