

研究报告

青蟹线粒体COI假基因的分离和特征分析

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收稿日期 2004-11-17 修回日期 2005-2-26 网络版发布日期 接受日期

摘要

线粒体DNA标记在遗传结构和系统进化研究中得到广泛应用, 然而核假基因的存在对此有很大威胁。本文以中国东南沿海的青蟹(*Scylla paramamosain*)为研究对象, 利用线粒体COI基因的通用引物和特异性引物进行扩增, 分别得到34个假基因(nuclear mitochondrial pseudogenes, Numts)和5个线粒体COI基因序列。在所获得的34个假基因中共定义了29种单倍型, 根据序列的相似度, 这些假基因可以分为2类, 每类假基因都有各自保守的核苷酸序列。第I类假基因存在2处插入序列和1处8 bp的缺失序列, 这些位点导致了整个阅读框的移位; 在第II类假基因和5个线粒体COI序列中只有碱基替换, 未发现插入和缺失序列。实验结果分析表明, 这两类假基因分别代表了2次核整合事件, 即核转移事件的最低值。研究结果提示了

关键词 [青蟹; 细胞色素氧化酶亚基I基因; 线粒体假基因](#)

分类号 [S917, Q523+.8](#)

Separation and Characterization of Mitochondrial COI Pseudogenes in *Scylla paramamosain*

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Abstract

Mitochondrial DNA marker has been applied in genetic structure and phylogenetic analysis, but the differences between nuclear mitochondrial pseudogenes (Numts) and mitochondrial DNA complicate phylogenetic analysis. Using the universal and special primers, 34 pseudogene sequences (Numts) and 5 real mtDNA *COI* sequences were amplified respectively from 34 individuals of *Scylla paramamosain* from the coast of southeast China. Twenty-nine haplotypes were identified and two groups (Group I and Group II) were determined according to the homology of the 34 pseudogene sequences. Two insertions and an 8-bp deletion were found in some sequences of Group I, but no indel (insertion and deletion) was found in Group II. Compared to mtDNA *COI* sequences, the two groups had their conservative sites respectively. At least two independent nuclear transfer events are required to explain the codon position biases revealed through the pairwise comparisons of the 34 Numts, one for Group I and one for Group II. The results showed the necessity of great care in interpreting PCR-generated mtDNA sequences using universal primers when used in population or evolutionary studies in genus *Scylla*.

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Key words [Scylla paramamosain](#) [cytochrome oxidase I \(COI\) gene](#) [nuclear mitochondrial pseudogenes](#)

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