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研究报告

圆斑星鲽及相关种类线粒体DNA控制区结构分析

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摘要

采用PCR产物直接测序法测定了圆斑星鲽(*Verasper variegatus*)的24个个体的线粒体控制区(Control region)核苷酸全序列，并进行了结构分析。结果表明，圆斑星鲽线粒体控制区核苷酸全序列具有长度多态性，得到4种长度单元型，主要表现为控制区中的串联重复序列的长度不同。对鲽形目鱼类如鲽科的条斑星鲽(*Verasper moseri*)、黄盖鲽(*Limanda feruginea*)、马舌鲽 (*Reinhardtius hippoglossoides*)，美洲拟庸鲽(*Heppoglossoides platessoides*)和鲆科的牙鲆(*Paralichthys olivaceus*)以及鳎科的欧洲鳎(*Solea solea*)、塞内加尔鳎(*S. senegalensis*)和沙鳎(*S. lascari*)的控制区的比较研究发现，鲽形目鱼类的线粒体控制区均存在相似的结构，即线粒体控制区可分为终止相关序列区(ETAS)、中央保守区(包括CSB-A、CSB-B、CSB-C、CSB-D、CSB-E、CSB-F)以及保守序列区(CSB1、CSB2、CSB3)和重复序列区(Repeat region)4个区域。通过与脊椎动物各个纲线粒体控制区序列的比较分析，发现只有鲽形目(包括鲆、鲽类和鳎类)鱼类和两栖纲的无尾类在CSB-3之后存在相似的串联重复序列。

关键词 圆斑星鲽 线粒体控制区 串联重复序列 结构分化

分类号

Structure analysis of mtDNA control region of spotted halibut (*Verasper variegatus*) and its related species

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Abstract

<P>Spotted halibut (<EM>Verasper variegatus</EM>) is the only one species of GenusVerasper in China. The fish was naturally distributed in Yellow Sea and Bohai Sea in northern China and Kyushu in Japan and in Korean sea area. Using PCR product direct sequencing, mitochondrial control region sequences of 24 individuals of spotted halibut was confirmed and analyzed. 4 control region hyplotypes, resulting from length heteroplamy of the tandem repeat region, was obtained from these 24 fish. Sequence analysis demonstrated that there were four similar structures in the control region, i.e., extended terminal associ-ated sequences (ETAS), central conserved sequence block (CSB), conserved sequence block (CSB), and repeat region, in <EM>V. moseri, Limanda ferruginea, Reinhardtius hippoglossoides, Heppoglossoides platessoides, Paralichthys olivaceous, Solea solea, S. senegalensis,</EM> and <EM>S. lascari</EM>. By comparing with other vertebrates, we found that there were similar repeated sequences immediately after the CSB-3 in all of the anuran species.</P>

Key words Spotted halibut Verasper variegatus mtDNA control region tandem repeat structure analysis

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