

动物遗传学

鳊类鱼类的线粒体DNA控制区结构及其系统发育分析

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摘要

鳊类为低等鲈形目鱼类, 是东亚特有类群。然而, 关于其系统位置、分类以及一些物种的有效性等尚有争议。采用PCR扩增直接测序的方法, 获得了鳊、大眼鳊、斑鳊、暗鳊、波纹鳊、长体鳊、中国少鳞鳊线粒体DNA控制区基因的序列。对比其他已报道鱼类控制区的结构识别序列, 对鳊类鱼类控制区的结构进行了分析, 识别了终止序列区、中央保守区和保守序列区, 并找到了DNA复制终止相关的序列ETAS和中央保守区的保守序列CSB-F、CSB-E、CSB-D以及保守序列区的保守序列CSB1、CSB2、CSB3。几种鳊鱼间共有191个变异位点, 其中, 终止序列区的变异最高, 占总变异的61.3%, 中央保守区和保守序列区占总变异的38.7%。这一结果可为全面了解鱼类线粒体DNA控制区的结构特征提供资料。同时, 利用高度变异的控制区序列, 以鲈科和鲈科作为外群, 使用邻接法和最大简约法构建了这几种鳊鱼的系统发育树。结果表明: 鳊类为一单系类群, 鳊、大眼鳊、斑鳊、暗鳊、波纹鳊、长体鳊构成一支鳊鱼群, 其中, 鳊与大眼鳊为姐妹种; 中国少鳞鳊为另一支少鳞鳊群; 长体鳊未单独成一支, 而是聚入鳊鱼群内, 应更名为*Siniperca roulei*。研究结果支持将现生鳊类分为两个类群的观点。

关键词

鳊类; mtDNA控制区; 结构; 系统关系

分类号

Structure of the Mitochondrial DNA Control Region of the Siniperine Fishes and Their Phylogenetic Relationship

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Abstract

<P>The mitochondrial DNA control region of *Siniperca chuatsi*, *S. kneri*, *S. scherzeri*, *S. obscura*, *S. undulata*, *Coreosiniperca roulei* and *Coreoperca whiteheadi* were amplified by PCR amplification and directly sequenced. The mtDNA control region of the siniperine fishes could be separated into three domains, namely, the terminal associated sequence domain, the central conserved sequence domain and the conserved sequence block domain. The extended terminal associated sequence (ETAS), three conserved sequence blocks (CSB-F, CSB-E, CSB-D) in the central conserved sequence domain and three conserved sequence blocks (CSB1, CSB2, CSB3) in the conserved sequence block domain were also identified. The phylogenetic relationships among these siniperine fishes were constructed through neighbor-joining and maximum parsimony methods using Percidae and Serranidae as outgroups. Results showed that siniperine fishes were a monophyletic group, with *Siniperca* forming one group, and *Coreoperca* forming another group. *Coreosiniperca roulei* did not form an independent group but was merged into the genus *Siniperca*. Thus it should be renamed as *Siniperca roulei*.</P>

Key words

[Siniperine fishes; mitochondrial DNA control region; structure; phylogenetic relationship](#)

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