

研究报告

## 暗纹东方鲀线粒体COI及其侧翼tRNA基因的克隆与序列分析

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**摘要** 以暗纹东方鲀(*Takifugu fasciatus*)肝脏的线粒体DNA为模板, 按照红鳍东方鲀线粒体DNA序列设计合成特异引物进行PCR扩增, 克隆并测定了线粒体细胞色素氧化酶I亚基(COI)及其侧翼tRNA基因的全序列, 结果显示, 克隆了暗纹东方鲀COI基因1546bp及其5'端上游的tRNATyr基因和3'端下游的tRNASer基因序列共1766bp。用DNA分析软件对暗纹东方鲀与GenBank中10个目13种鱼类的COI序列进行比较分析, 显示暗纹东方鲀与这些鱼类的COI基因具有较高的同源性, 与同属红鳍东方鲀的同源性最高为97.6%, 与同目不同科的矛尾翻车鲀和翻车鲀的同源性为76.5%和75.4%。根据暗纹东方鲀与其他13种鱼的COI基因序列同源性所建立的进化树, 与传统的分类地位基本吻合。推定的这二种tRNA的二级结构都具有典型的三叶草型结构。

**关键词** [暗纹东方鲀](#); [mtDNA](#); [COI](#); [系统学](#)

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## Charactreization and phylogenetic analysis of the CytochromOxidase Subunit I gene of Mitochondrial Genome from *Takifugu fasciatus*

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### Abstract

The *Takifugu fasciatus* mitochondrial cytochrome Oxidase I gene (COI) and its connected tRNA genes were sequenced by PCR. The open reading frame of COI gene contains 1546bp nucleotides, encoding a putative protein 515 amino acids. The pattern of codon usage of the COI gene is less biased of A+T. The COI gene of *Takifugu fasciatus* was proved to have good homology with the other 13 species of fish recorded in the GenBank and it has 97.6% homology with *Takifugu rubripes*. The phylogenetic trees show that the relationships based on the homology is consistent with the morphological taxonomic results. Assumed secondary structures of tRNA genes suggest that they have the classical cloverleaf structures.

**Key words** [Takifugu fasciatus](#); [mtDNA](#); [Cytochrome Oxidase I](#); [Molecular evolution](#)

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