

动物遗传学

# 帘蛤科贝类rDNA内转录间隔区序列的研究

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## 摘要

根据18S rDNA、5.8 S rDNA和28 S rDNA保守序列设计引物, 应用聚合酶链式反应(PCR)扩增了文蛤(*Meretrix meretrix* L.)、青蛤(*Cyclina sinensis* G.)、硬壳蛤(*Mercenaria mercenaria* L.)和江户布目蛤(*Protothaca jedoensis* L.) 4种帘蛤科贝类的第一内转录间隔区(ITS1)和第二内转录间隔区(ITS2)序列, 并进行了测序。结果表明, 文蛤、青蛤、硬壳蛤和江户布目蛤的ITS1扩增产物大小分别为978 bp、663 bp、757 bp和942 bp, GC含量分别为61.55%、60.78%、62.48%和64.86%~64.97%, 其中ITS1序列长度分别为900 bp、585 bp、679 bp和864 bp, 是迄今已报道双壳贝类中变化范围最大的, GC含量分别为61.67%、61.03%、63.03%和65.51%~65.62%, 江户布目蛤种内ITS1序列有个体差异; ITS2扩增产物大小分别为644 bp、618~620 bp、593 bp和513~514 bp, GC含量分别为61.18%、61.29%~61.81%、62.73%和61.48%~61.60%, 其中ITS2序列长度分别为412 bp、386~388 bp、361 bp和281~282 bp, GC含量分别为65.29%、65.21%~66.06%、67.87%和67.38%~67.62%, 青蛤和江户布目蛤种内ITS2序列有个体差异。4种蛤ITS1和ITS2序列种间差异很大, 有明显的长度多态性, ITS2种间序列相似度73.0%~89.1%, 与ITS1的种间序列相似度48.7%~81.5%相比略高。此外, 在4种蛤ITS1和ITS2序列中各发现2个与rRNA加工有关的保守区。通过对ITS1和ITS2序列的组装获得了4种蛤5.8S rRNA基因完整序列, 序列长度都是157 bp, GC含量57.96%~58.60%, 4种蛤5.8S rRNA基因相对保守, 种间序列差异度0~6.0%, 共有10个变异位点, 其中转换4处, 颠换6处, 硬壳蛤和江户布目蛤5.8S rRNA基因序列完全相同。以ITS2序列(包含5.8S rRNA和28S rRNA基因部分序列)为标记, 调用北极蛤科的*Arctica islandica*相应序列数据作外群, 构建了帘蛤科贝类的系统发育树, 其拓扑结构显示江户布目蛤与硬壳蛤亲缘关系最近, 青蛤与其他3物种的亲缘关系最远。

## 关键词

帘蛤科; 核糖体DNA; 内转录间隔区; 5.8S rRNA基因; 系统发育分析; 物种鉴定

## 分类号

# Study on Sequences of Ribosomal DNA Internal Transcribed Spacers of Clams Belonging to the Veneridae Family (Mollusca: Bivalvia)

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## Abstract

<P>The first and second internal transcribed spacer (ITS1 and ITS2) regions of the ribosomal DNA from four species, *Meretrix meretrix* L., *Cyclina sinensis* G., *Mercenaria mercenaria* L., and *Protothaca jedoensis* L., belonging to the family Veneridae were amplified by PCR and sequenced. The size of the ITS1 PCR

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amplification product ranged from 663 bp to 978 bp, with GC contents ranging from 60.78% to 64.97%. The size of the ITS1 sequence ranged from 585 bp to 900 bp, which is the largest range reported thus far in bivalve species, with GC contents ranging from 61.03% to 65.62%. The size of the ITS2 PCR amplification product ranged from 513 bp to 644 bp, with GC contents ranging from 61.29% to 62.73%. The size of the ITS2 sequence ranged from 281 bp to 412 bp, with GC contents ranging from 65.21% to 67.87%. Extensive sequence variation and obvious length polymorphisms were noted for both regions in these species, and sequence similarity of ITS2 was higher than that of ITS1 across species. The complete sequences of 5.8S ribosomal RNA gene were obtained by assembling ITS1 and ITS2 sequences, and the sequence length in all species was 157 bp. The phylogenetic tree of Veneridae clams was reconstructed using ITS2-containing partial sequences of both 5.8S and 28S ribosomal DNA as markers and the corresponding sequence information in *Arctica islandica* as the outgroup. Tree topologies indicated that *P. jedomensis* shared a close relationship with *M. mercenaria* and *C. sinensis*, a distant relationship with other species.

**Key words**

[Veneridae; rDNA; internal transcribed spacer; 5.8S rRNA gene; phylogenetic analysis; species identification](#)

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