双壳纲动物核糖体RNA 18S-ITS1序列及其在分子系统发育研究中的 应用18S-ITS1 Sequence of rRNA in Bivalves and its Application in Phylogenetic Analysis

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摘要

测定了双壳纲不同科、属、种及种内共11个个体的核糖体RNA 18S-ITS1序列。结果表明,该序列在种间存在很高 的多态性,长度从558 bp到784 bp不等,碱基差异百分比在10.7%~61.7%之间, ITS1序列同源性很低,有片段的 插入与缺失。种间18S部分序列碱基差异百分比在0.9%~23.7%之间,变化主要是碱基的转换。用邻接法(NJ)构建 ▶ 本刊中 包含 "ITS1"的 相关文章 了8个种的18S部分序列(约240 bp)的系统发育树,与传统形态学分类结果相符。马氏珠母贝(Pinctada martensi)4个不同地域个体间的序列差异百分比在0.6%~1.9%之间。分析指出:18S基因可以作为双壳纲动物高 阶元系统发育的分子标记; ITS1序列种间变化很大,可以应用于该纲物种的分类及鉴别,在亲缘关系相近种及种 内变异相对较小,但核苷酸变异位点信息量丰富,可用于属内种间、亚种和群体间的遗传多样性研究。Abstract: Bivalves constitute a dominant and divers group of marine animals in China, most of them are of major commercial important species, and studies of their genetic diversity are necessary for the sustainable exploitation and conservation of these bioresources. The objective of the present work is to explore the feasibility of using the ribosomal RNA as a molecular marker for studying the inerspecific and intraspecific genetic variations among bivalves. The 18S-ITS1 sequences of 11 individuals at differing taxonomic levels were determined. The sequence were found to exhibit a high degree of length polymorphism among different species, ranging from 558 bp in C.farreri to 784. bp in O.rivularis, mainly resulting from the variation of ITS1, and the percent divergence ranging from 10.7% to 61.7%. The NJ (neighbor-joining) tree inferred from 18S fragment agrees with the previous study based on morphologies and chemical analysis well. The sequence variation was found to vary among 4 individuals of P. martensi (0.6%~1.9%), collected from 4 geographical sites, which involved substitutions, transversion as well as insertions and deletions. All these results show that ITS1 is highly divergent among different species of bivalves and could be used in classification and distinguishing closely related species, and also could be used for molecular systematic studies at relative species, subspecies and population levels.

关键词 ITS1 18S RNA 遗传多样性 双壳纲Key words 18S RNA ITS1 genetic diversity Bivalves 分类号

Abstract

Key words

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