

实验研究

## 三地钉螺线粒体DNA两个分子的遗传变异研究

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摘要

目的 分析广西、云南、湖南三地钉螺线粒体DNA细胞色素C氧化酶 I (CO1)基因和细胞色素氧化酶b (Cytb)基因的遗传变异。方法 收集广西靖西、云南洱源和湖南岳阳三地钉螺, 提取其基因组DNA, PCR法扩增线粒体CO1和Cytb基因并测序。用Clustal W(1.82)软件对所测基因序列排序, 用MEGA (3.1)计算其碱基组成、转换及颠换; 用Kimura双参数法计算遗传距离, 用非加权组平均法(UPGMA)和最大简约法(MP)构建系统发生树。结果 PCR扩增获得CO1和Cytb基因大小分别约为700及600 bp(含两侧引物)。三地钉螺CO1基因中共检测到106个多态性位点, 约占核苷酸总数的15.9%, Cytb基因中多态性位点为165个, 约占核苷酸总数的28.5%。广西靖西与湖南岳阳、广西靖西与云南洱源的钉螺CO1基因和Cytb基因的遗传距离分别为0.051、0.158和0.031、0.405。根据CO1和Cytb的基因序列, 用上述两种方法构建的系统发生树结果均一致。广西靖西与湖南岳阳的钉螺同属一个支系, 云南洱源钉螺单独形成另一支系。结论 广西、湖南和云南的钉螺CO1和Cytb基因总体上具有相对丰富的多态性。

关键词 [钉螺](#) [细胞色素C氧化酶 I 基因](#) [细胞色素氧化酶b基因](#) [遗传变异](#)

分类号

## Genetic Variation of Two Mitochondrial DNA Molecules from Three Isolates of *Oncomelania hupensis*

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Abstract

Objective To study the genetic variation of two mitochondrial DNA molecules (CO1 and Cytb gene) of *Oncomelania hupensis* isolated from different areas. Methods Snails were collected from Jingxi of Guangxi, Yueyang of Hunan and Eryuan of Yunnan. Genomic DNA was extracted from the snails, Co1 and Cytb gene fragments were amplified by PCR, then purified and sequenced. Sequences of each isolates were edited by using Clustal W(1.82) software, and the nucleotide composition, transition and transversion were accounted by using MEGA(3.1) software. The genetic distances were computed with Kimura method and phylogenetic trees were constructed with UPGMA and MP method respectively. Results CO1 and Cytb gene fragments were about 700 bp and 600 bp(including 2 primers) respectively. A total of 106 mutation spots (15.9%) were tested in CO1 homological nucleotides, and 165 mutation spots (28.5%) were tested in Cytb homological nucleotides. The distance matrix between Guangxi isolate and Hunan isolate was 0.051 and 0.031 for CO1 gene and Cytb gene respectively; while that between Guangxi and Yunnan isolates was 0.158 and 0.405 respectively. Phylogenetic trees constructed by UPGMA and MP took on the similar topo-structure: isolates of Guangxi and Hunan clustered into one group, while the Yunnan isolate exhibited as another group. Conclusion *Oncomelania hupensis* in Guangxi, Hunan and Yunnan are of relatively rich polymorphism in CO1 and Cytb genes in general.

Key words [Oncomelania hupensis](#); [CO1 gene](#); [Cytb gene](#); [Gene variation](#)

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