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论著

中国大陆两种东毕吸虫rDNA-LSU基因的序列分析

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摘要

目的 测定程氏东毕吸虫、土耳其斯坦东毕吸虫结节变种rDNA LSU基因序列 ,并对照已发表的土耳其斯坦东毕吸虫同一基因序列 ,比较三者的差异 ,探讨东毕吸虫虫种分类问题。 方法 收集两虫种成虫 ,GNT K法抽提基因组DNA ,PCR扩增目的基因 ,并将其产物克隆入质粒再次扩增 ,提取质粒DNA ,以M13(F/R)作为测序引物进行测序。从GenBank获得土耳其斯坦东毕吸虫rDNA LSU基因序列 ,用BioEdit软件将 3种血吸虫基因序列排序并比较分析。 结果 程氏东毕吸虫、土耳其斯坦东毕吸虫结节变种的LSU序列完全一致 ,与土耳其斯坦东毕吸虫rDNA LSU基因序列仅相差一个碱基 ,同源性高达 99.99%。结论 γDNA LSU基因序列分析结果不支持程氏东毕吸虫为独立种 ,土耳其斯坦东毕吸虫结节变种可能是土耳其斯坦东毕吸虫的同种异名。

关键词 rDNA-LSU 东毕吸虫 序列分析

分类号

Sequence Analysis of rDNA-LSU Gene of Orientobilharzia turkestanicum from Mainland of China

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Abstract

Objective To classify the taxonomic status of O.cheni in relation to O.turkestanicum var. tuberculata from the mainland of China by comparing their nucleotide sequences of nuclear ribosomal partial large subunit gene (LSU). Methods The genomic DNA of adult worms were extracted by the GNT-K method. The target gene was amplified by PCR using specific primers. The PCR products were purified before ligation into the plasmid PCR-blunt (Invitrogen). Recombinant plasmids were amplified in E.coli , extracted and purified using routine methods and then sequenced using M13 primers (F/R) on a Licor long-read auto-sequencer. Sequences of O. turkestanicum was retrieved from GenBank and aligned with our data in BioEdit. Results The nucleotide sequences of LSU between O.turkestanicum var. tuberculata and O.cheni was 100% identical, and 99.99% identical between O.turkestanicum var. tuberculata and O.turkestanicum . Conclusion This study demonstrated high similarity in LSU nucleotide sequences, and the results do not support O.cheni as an independent species. O.cheni may be a synonym of O.turkestanicum var. tuberculata , and O.turkestanicum var. tuberculata is probably also a synonym of O.turkestanicum .

Key words rDNA-LSU Orientobilharzia sequence analysis

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