

论著

## 牛羊源土耳其斯坦东毕吸虫ITS和28S rDNA-LSU序列分析

仇建华, 李利, 王春仁\*, 陈佳, 陈爱华, 翟延庆

黑龙江八一农垦大学动物科技学院, 大庆 163319

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摘要

目的 探讨牛羊源土耳其斯坦东毕吸虫 (*Orientobilharzia turkestanicum*) 核糖体内转录间隔区 (ITS) 和28S核糖体大亚基序列 (rDNA-LSU) 的差异。方法 粪便检查、剖杀自然感染东毕吸虫的绒山羊、山羊、绵羊和黄牛, 收集虫体, 形态学鉴定为土耳其斯坦东毕吸虫。抽提成虫基因组DNA, 扩增其ITS (包括ITS-1、5.8S rDNA和ITS-2) 和28S rDNA-LSU序列, 测序并分析以上序列, 以及28S rDNA-LSU序列RNA二级结构。结果 牛、羊源土耳其斯坦东毕吸虫的ITS-1、5.8S rDNA、ITS-2和28S rDNA-LSU序列分别长384、159、331和1 304 bp。牛源和羊源的ITS-1和5.8S rDNA序列完全相同; 黄牛源、绵羊源和绒山羊源的ITS-2序列完全相同, 与山羊源存在1个碱基的差异; 绵羊源和绒山羊源的28S rDNA-LSU序列完全相同, 与牛源和山羊源分别有2个碱基的差异。绵羊源和绒山羊源的28S rDNA-LSU序列RNA二级结构相同, 与山羊源存在微小差异, 但牛源与羊源存在较大差异。结论 不同终末宿主源土耳其斯坦东毕吸虫的核糖体序列存在不同程度的差异, 羊源28S rDNA-LSU序列的RNA二级结构相同或相似, 但与牛源存在较大差异。

关键词 [土耳其斯坦东毕吸虫](#); [核糖体内转录间隔区](#); [5.8S核糖体DNA](#); [28S核糖体DNA大亚基序列](#); [序列分析](#)

分类号

## ITS and 28S rDNA-LSU Sequence Analysis of *Orientobilharzia turkestanicum* from Bovine and Caprine Hosts

QIU Jian-hua, LI Li, WANG Chun-ren\*, CHEN Jia, CHEN Ai-hua, ZHAI Yan-qing

College of Animal Science and Technology, Heilongjiang August-First Land Reclamation University, Daqing 163319, China

Abstract

Objective To explore sequence differentiation of ITS and 28S rDNA-LSU of *Orientobilharzia turkestanicum* from bovine and caprine hosts. Methods Adult worms of *O. turkestanicum* from the naturally infected cattle, sheep, cashmere goat and goat were collected and identified morphologically as *O. turkestanicum* according to existing keys and descriptions. The genomic DNA was extracted from parasites of different hosts. The internal transcribed spacer (ITS, contains ITS-1, 5.8S nuclear ribosomal DNA, ITS-2) and 28S nuclear ribosomal DNA-LSU were amplified by PCR, sequenced and analyzed by Chromas and DNASTAR softwares, and the RNA secondary structure of 28S rDNA-LSU was analyzed by DNAMAN software. Results ITS-1, 5.8S rDNA, ITS-2 and 28S rDNA-LSU of *O. turkestanicum* from bovine and caprine hosts were 384, 159, 331 and 1 304 bp, respectively. ITS-1 and 5.8S rDNA of *O. turkestanicum* from different definitive hosts were identical; ITS-2 of *O. turkestanicum* from cattle, sheep and cashmere goat were identical, with one nucleotide variation compared with that of goat; 28S rDNA-LSU of *O. turkestanicum* from sheep and cashmere goat were identical, with two nucleotides variation compared with that of cattle and goat. The RNA secondary structure of 28S rDNA LSU of *O. turkestanicum* from caprine hosts were identical or similar, but with large variation compared with that of cattle. Conclusion The rDNA sequence from different definitive hosts shows nucleotide variations to some extent and the RNA secondary structure of 28S rDNA-LSU from caprine hosts shows large variation in comparison to that of bovine.

Key words [Orientobilharzia turkestanicum](#); [ITS](#); [5.8S rDNA](#); [28S rDNA-LSU](#); [Sequence analysis](#)

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