

实验报道

日本血吸虫线粒体DNA两个分子的遗传变异

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摘要

目的 从线粒体DNA的2个分子,探讨我国日本血吸虫的遗传变异。方法 试剂盒抽提基因组总DNA后,以特异性引物对线粒体还原型烟酰胺腺嘌呤二核苷酸(NADH)脱氢酶1(ND1)和细胞色素c氧化酶I(COI)进行PCR扩增,将PCR产物分别测序,并以生物信息学方法加以比较,构建系统进化树。结果 序列系统进化树显示日本血吸虫中国大陆株与中国台湾株之间差异较大,在树状图中可归为2类;中国大陆山区型地域株,即云南洱源和四川天全在树状图中归为1类;中国大陆湖沼洲滩型地域株,即湖南岳阳、江西新建和安徽贵池3个地域株在树状图中处于并列位置;湖北省境内不同地域株在树状图中归为1类。结论 我国各地日本血吸虫存在不同程度的遗传变异,各地域株间亲缘关系密切,存在共同的起源

关键词 [日本血吸虫](#) [地域株](#) [线粒体NADH脱氢酶1](#) [细胞色素c氧化酶I](#) [遗传变异](#) [系统进化树](#)

分类号

Studies on the Genetic Variation of Two Mitochondrial DNA Molecules of *Schistosoma japonicum*

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Abstract

Objective To study the variation of *Schistosoma japonicum* through two mitochondrial DNA molecules. Methods Genomic DNA was isolated with kit, and the mitochondrial NADH dehydrogenase 1(ND1) and cytochrome c oxidase I(COI) gene fragments were amplified by polymerase chain reaction(PCR) and sequenced. The gene trees were constructed and the acquired data were analyzed with the help of bioinformatics. Results The gene trees showed that the Taiwan isolate and the mainland isolates can be divided in two groups: a group from the hilly region (Yunnan and Sichuan), another group from the lake region (Hunan, Jiangxi and Anhui); isolates from Hubei are at a different position on the gene trees. Conclusion There are variations among the geographic isolates of *Schistosoma japonicum* in China, nevertheless, they have close kinship.

Key words [Schistosoma japonicum](#) [Geographic isolate](#) [Mitochondrial NADH dehydrogenase 1](#) [Cytochrome c oxidase I](#) [Genetic variation](#) [Gene trees](#)

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