

论著

我国五省斯氏并殖吸虫群体DNA序列分析的研究

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摘要

目的 主要研究我国五省(广东、福建、云南、湖北、四川)斯氏并殖吸虫各群体之间的遗传差异以及四川并殖吸虫独立性问题,并探讨异盘、宫崎、泡囊并殖吸虫在并殖属中的分类地位。方法 以GNT-K法抽提基因组DNA后,用特异引物,PCR扩增ITS2和部分CO1基因,将PCR扩增产物纯化后直接进行测序或克隆后测序,分析序列的同源性,并构建种系发生树。结果 从DNA序列结果来看,5省斯氏并殖吸虫群体之间存在的遗传性差异较小,其中四川并殖吸虫与斯氏并殖吸虫之间存在的遗传性差异亦小。遗传关系均比较接近。泡囊并殖吸虫在种系发生树上位于斯氏并殖吸虫各地域株之间。在种系发生树上,日本的宫崎并殖吸虫亦位于斯氏并殖吸虫各地域株之间,并且与福建地域株最为接近。异盘并殖吸虫在种系发生树上虽与斯氏并殖吸虫各地域株之间距离较远,但相对卫氏并殖吸虫而言,仍与斯氏并殖吸虫遗传距离较近。结论 广东、福建、云南、湖北和四川5省斯氏并殖吸虫群体均属斯氏并殖吸虫同一虫种,由于受地理因素影响,种内存在着不同的地域株。四川并殖吸虫与斯氏并殖吸虫系同种异名。泡囊并殖吸虫与日本的宫崎并殖吸虫很可能是斯氏并殖吸虫的同种异名。异盘并殖吸虫在形态上与种系发生树上,与斯氏并殖吸虫亲缘关系近于卫氏并殖吸虫,分类地位处于两

关键词 [斯氏并殖吸虫](#) [四川并殖吸虫](#) [地域株](#) [分类学](#) [DNA序列分析](#)

分类号

Study on DNA Sequences of Paragonimus skrjabini Populations from Five Provinces in China

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Abstract

Objective To study differences among Paragonimus skrjabini populations from five provinces (Guangdong, Fujian, Yunnan, Hubei, Sichuan) and Paragonimus szechuanensis and to analyze the taxonomic status of P. heterotremus and P. veocularis in the Genus Paragonimus Braun, 1899. Methods DNA sequences were obtained from the ITS2 and CO1 genes and phylogenetic trees were built. Results Difference of the DNA sequences among P. skrjabini populations from five provinces were minor. P. veocularis and P. skrjabini were similar in DNA sequences. There were also some resemblances between P. miyazakii from Japan and the Fujian isolates of P. skrjabini. In addition, P. heterotremus was found to be closer to P. skrjabini and quite a distance from P. westermanni in the phylogenetic tree. Conclusion All studied populations can be regarded as different strains of P. skrjabini; P. szechuanensis is not a separate species, but possibly a geographical strain of P. skrjabini. Also found was that P. veocularis and P. miyazakii may be the synonyms of P. skrjabini. As a separate species, P. heterotremus was found to be closer to P. skrjabini and quite a distance from P. westermanni in the genetic relationship.

Key words [Paragonimus skrjabini](#) [Paragonimus szechuanensis](#) [geographical strain](#) [taxonomy](#) [DMA sequences](#)

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