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论著

应用多重PCR技术鉴定我国6个旋毛虫地理株的研究

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摘要

目的 对我国猪源旋毛虫地理株进行鉴定和分类。 方法 根据旋毛虫rDNA扩展片段V区（expansion segment V region，ESV）和内转录间隔区（internal transcribed spacers，ITS）ITS1和ITS2基因序列合成5对特异性引物，以旋毛虫（*Trichinella spiralis*，T1）、乡土旋毛虫（*T. nativa*，T2）、布氏旋毛虫（*T. britovi*，T3）、伪旋毛虫（*T. pseudospiralis*，T4）及纳氏旋毛虫（*T. nelsoni*，T7）的国际参考株作为对照，应用多重PCR对我国6个猪源旋毛虫地理株（河南、云南、哈尔滨、黑龙江同江、湖北及天津）进行鉴定，并观察影响多重PCR扩增的因素。 结果 我国6个猪源旋毛虫地理株多重PCR扩增结果显示，均具1条与T1相同的条带（173 bp）。应用多重PCR对单条旋毛虫幼虫、不同保存条件的旋毛虫幼虫及含幼虫的新鲜小鼠肌肉提取液进行扩增，均得到173 bp的特异性条带。 结论 经多重PCR鉴定我国6个猪源旋毛虫地理株均为T1。

关键词 旋毛虫 中国地理株 多重PCR 鉴定

分类号

Identification of Six *Trichinella* Isolates from China by Multiplex PCR

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Abstract

Objective To identify and classify six isolates of swine-originated *Trichinella* from China. Methods Five specific pairs of primers were synthesized based on DNA sequence of expansion segment V region and internal transcribed spacers （ITS1 and ITS2） of ribosomal DNA repeat from Trichinella. International reference strains of five Trichinella species［*Trichinella spiralis* （T1）， *T. nativa* （T2）， *T. britovi* （T3）， *T. pseudospiralis* （T4） and *T. nelsoni*（T7）］ were used as control. Six swine *Trichienlla* isolates from Henan， Yunnan， Harbin， Tongjiang of Heilongjiang， Hubei and Tianjin were identified by multiplex PCR and its effecting factors of PCR amplification were observed. Results Electrophoresis results of multiplex PCR products of *Trichinella* larvae showed that the band （173 bp） of the six isolates was the same as *T. spiralis*（T1）. The specific band （173 bp） was detected by multiplex PCR through amplification from issues of single T. spiralis larva， the larvae conserved in 80% ethanol for 6 months， the larvae stored in 10% formaldehyde， in 0.05% formaldehyde， 0.2% sodium azide or 0.05% merthiotate for 2 weeks，or fresh mouse muscle with larvae. Conclusion All the six swine *Trichinella* isolates are identified as *T. spiralis* （T1） by multiplex PCR.

Key words *Trichinella* Chinese isolates Multiplex PCR Identification

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