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论著

我国内脏利什曼病山丘疫区与平原疫区利什曼原虫SSUrDNA多变区序列分析

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摘要

[目的]分析我国内脏利什曼病 (VL)山丘疫区与平原疫区利什曼原虫 (L .d)分离株小亚基核糖体DNA (SSUrDNA)多变区的序列差异。 [方法]nDNA进行PCR扩增 ,将扩增出的SSUrDNA基因的特异片段克隆于 pGEMR TEasyVector上 ,采用通用引物M 13进行PCR扩增 ,全自动测序仪测序。 [结果]序列分析显示 ,扩增的 5株利什曼原虫SSUrDNA序列大小均为 392bp ;序列差异均发生在两个独特序列区(UQ Ⅰ和UQ Ⅱ) ;山丘疫区L .d甘肃分离株和四川分离株均在UQ Ⅱ区上有 2个相同的碱基突变 ,L .d甘肃分离株UQ Ⅰ区上有 1个碱基突变 ;无移码突变。 [结论]山丘疫区分离株与平原疫区分离株之间的碱基序列有差异 ,平原疫区L .d山东分离株与婴儿利什曼原虫 (L .infantum)的碱基序列相同

关键词 利什曼原虫 小亚基核糖体核酸基因 聚合酶链反应 克隆 序列分析 基因变异

分类号

SEQUENCE ANALYSIS OF SSU rDNA VARIABLE REGIONS OF LEISHMANIAISOLATES FROM HILLY FOCI AND PLAIN FOCI OF CHINA

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Abstract

Objective] To analyze the sequence difference of the SSU rDNA variable regions of Leishmania isolates from hilly foci and plain foci of China. [Methods] Specific SSU rDNA fragments from nuclear DNA of five Leishmania species and isolates were amplified by PCR. The amplified DNA fragments were cloned into pGEM R-T Easy vector. The specific fragments were sequenced by the automated DNA sequencer. [Results] Sequence analysis showed that the amplified DNA fragments of five Leishmania species and isolates were all 392 bp in length, point mutations were located in the two unique sequence (UQ-Ⅰ and UQ-Ⅱ); L.d.SC10 and L.d.GS7 had two same point mutations in UQ-Ⅱ, only L.d.GS7 had one in UQ-Ⅰ; no insertion/deletion. [Conclusion] Sequence difference of the SSU rDNA variable region existed between Leishmania isolates from hilly foci and plain foci; The sequences of the SSU rDNA variable regions of L.d. SD2 isolate and L.infantum were identical.

Key words Leishmania small subunit ribosomal DNA polymerase chain reaction cloning sequence analysis genetic variation

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