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论著

杜氏利什曼原虫平原和荒漠疫区分离株LACK基因克隆及序列分析

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摘要

目的 测定我国平原疫区和荒漠疫区杜氏利什曼原虫分离株活性蛋白激酶 C受体同源物 (L ACK)基因序列 ,并与山丘疫区分离株及国外利什曼原虫分离株进行比较。 方法 应用 RT- PCR扩增 L ACK基因 ,将其克隆入p UC18载体后用双脱氧链末端终止法测序 ,并与 Gen Bank中相关数据进行比较。 结果 用 RT- PCR成功扩增出约95 0 bp的 L ACK基因片段 ,测序结果表明其片段大小均为 94 2 bp,与Gen Bank中多种利什曼原虫 L ACK基因的核苷酸序列一致性达 97%以上。我国山丘、平原和荒漠 3个不同疫区杜氏利什曼原虫分离株的 L ACK基因序列的一致性达95 %以上。 结论 获得了我国平原和荒漠疫区杜氏利什曼原虫 L ACK基因序列。我国 3个不同疫区杜氏利什曼原虫分离株的 L ACK基因具有高度同源性。

关键词 利什曼原虫 LACK 克隆 序列分析

分类号

Cloning and Sequence Analysis of LACK Gene of Leishmania Donovani Isolates from Plain and Desert Foci of China

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Abstract

Objective To determine the nucleotide sequence of the LACK (Leishmania homologue of receptors for activated protein kinase C) gene of Leishmania donovani isolates from plain foci (L.d SD1) and desert foci (L.d XJ771) of China, and to find out the difference of the sequence of LACK gene with other Leishimania spp. and also the isolate from hill foci of China.. Methods. The LACK genes of L.d SD1 and L.d XJ771 were amplified by RT-PCR and cloned into pUC18 vector respectively, sequenced by the dideoxy chain termination method, then analyzed and compared with that of other isolates.. Results . The LACK genes of the two isolates were successfully cloned. Both of the 2 fragments were 942 bp in length. Comparison of the two nucleotide sequences with that of other Leishmania spp. in GenBank showed that the identities were more than 97%, and the identities of the nucleotide sequences of LACK genes of the three L.d isolates from plain, desert and hill foci of China were more than 95%.. Conclusion . High identities exist among the nucleotide sequences of LACK genes of the three L.d isolates from the three foci of China.

Key words Leishmania donovani LACK gene cloning gene sequencing

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