

论著

黑龙江林区野鼠中斑点热群立克次体的核酸检测与序列分析

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摘要: 目的: 了解黑龙江林区野鼠中斑点热群立克次体的感染情况。方法: 运用聚合酶链反应方法对黑龙江地区采集的啮齿动物标本扩增斑点热群立克次体外膜蛋白A(OmpA)基因。阳性标本送测序并应用Mega5.0 软件进行序列分析。结果: 共检测鼠标本514 份,斑点热群立克次体的阳性率为9.3%(95%CI: 7.1%~12.2%),牡丹江、绥芬河、同江和东宁四个地区斑点热群立克次体的阳性率分别为12.4%(39/314),5.3%(3/57),2.0%(1/51),5.4%(5/92),地区间阳性率差异有统计学意义( $P=0.023$ )。感染斑点热群立克次体的有仓鼠、大仓鼠、大林姬鼠、褐家鼠、黑线姬鼠、红背鼠平、鼯鼠、棕背鼠平、东方田鼠、明纹花松鼠10 种,鼠种间阳性率差异有统计学意义( $P=0.002$ );棕背鼠平的阳性率最高,为22.1%(21/95)。测序结果显示鼠感染的斑点热群立克次体基因型是黑龙江立克次体基因型和一种新的未定种基因型。结论: 黑龙江地区存在鼠感染黑龙江立克次体,同时可能存在未定种新的斑点热群立克次体。

关键词: 斑点热群立克次体 OmpA基因 序列分析

DNA detection and sequence analysis of spotted fever group Rickettsiae in rodents from Heilongjiang forest region

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Abstract: Objective: To investigate the infection in spotted fever group Rickettsiae (SFGR) in wild rodents from Heilongjiang, China.

Methods: Polymerase chain reaction (PCR) was used to detect the OmpA gene of SFGR in rodents collected in Heilongjiang. The PCR products amplified from rodent specimens were sequenced and compared with the corresponding part of the sequences deposited in the GenBank. Phylogenetic trees were constructed with Mega 5.0 software.

Results: A total of 514 rodents were collected from Heilongjiang during 2009-2011 and 11 species were included. The infection rate of SFGR in the rodents was 9.3% (95% CI: 7.1%-12.2%). Statistical analysis showed a significant difference in different areas of Heilongjiang ( $P=0.023$ ). The highest prevalence was observed in Mudanjiang area (12.42%). There were significant differences in different species of rodents ( $P=0.002$ ). The infection rate of SFGR determined in *Clethrionomys rufocanus* was the highest (22.1%). Sequence analysis revealed SFGR belonged to *R.heilongjiangensis* and a new unknown rickettsia genotype.

Conclusion: *R.heilongjiangensis* has been presented in rodents in Heilongjiang, and a new SFGR genotype different from other rickettsiae genotypes may exist in this area.

Keywords: spotted fever group Rickettsiae OmpA gene sequence analysis

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