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新疆羊狂犬病病毒的鉴定及N基因序列分析

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Identification and sequence analysis of the rabies virus N gene from sheep in Xinjiang Uygur Autonomous Region, China

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摘要 目的 诊断疑似羊狂犬病病例并分析其病原分子N基因遗传进化关系。方法 采集新疆阿勒泰地区疑似狂犬病羊脑组织, 以狂犬病病毒特异性目的基因(N基因)RT-PCR扩增和序列测定进行病毒鉴定;以DNAStar-Lasergene.v7.1 软件拼接测定序列, 应用BLAST软件分析N基因的遗传进化关系。结果 显示本研究鉴定的狂犬病毒阳性并获得了病毒全基因序列, 建立了其N基因的遗传进化关系树, 确定疑似的羊狂犬病病毒与狂犬病病毒基因Ⅰ型俄罗斯C群的遗传关系较近。结论 应用RT-PCR方法对羊源狂犬病进行实验室诊断, 获得该病原全基因序列, 明确了新疆狂犬病病原和流行地域分布, 为羊狂犬病毒分子流行病学研究奠定基础。

关键词: 羊 狂犬病病毒 N基因 进化树

Abstract: To diagnose suspected sheep rabies case and analyze molecular epidemiological characteristics of the pathogen, brain tissues

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of sheep with clinical symptom from a farm in Xinjiang Uygur Autonomous Region, China were used. Rabies virus (RV) in brain tissue was confirmed by specific nucleoprotein gene (N) RT-PCR amplification. The full-length gene sequence of RV from sheep was sequenced and assembled by DNAStar Lasergene.V7.1 based on N gene sequence of rabies virus, which was analyzed with phylogenetic tree. Results showed that the sheep disease case was caused by RV. And the full-length sequence of RV from sheep in Xinjiang was obtained. It was suggested that the RV had a closer genetic relationship with the genotype Ⅰ of Russia Group C by phylogenetic tree analysis. This study provided a basis for further study toward molecular epidemiology of sheep RV in China in the future.

Keywords： sheep rabies virus N gene phylogenetic tree
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