

论著

山东省汉坦病毒分子流行病学研究

张晓梅¹, 宋绍霞¹, 翟文济¹, 王梅¹, 李小娟¹, 王志强¹, 李德新², 张全福²

1 山东省疾病预防控制中心传染病防制所 (济南 250014);

2 中国疾病预防控制中心病毒病预防控制所

摘要:

【摘要】 目的 探讨山东省汉坦病毒(HV)的分子流行病学特点。方法 用反转录-聚合酶链反应(RT-PCR)及核苷酸序列测定技术,对肾综合征出血热(HFRS)监测点的阳性鼠肺标本进行目的基因扩增并测序,与国内外的HV毒株进行同源性分析及系统发生树分析。结果 有15份标本扩增出汉城(SEO)型S、M片段,对其中10份扩增片段进行序列分析认为均为SEO型HV, S片段之间的同源性≥96.3%,其推导的氨基酸序列同源性(JN5?153S和DY1S除外)≥96.8%; M片段之间及与山东省以往分离的ZB8同源性≥97.5%,其推导的氨基酸序列同源性为98.6%~100%。结论 近年来山东省流行的HV仍以SEO型S3亚型为主。同一地区或地理位置相邻的地区病毒基因组同源性较高,具有明显的地区聚集性,基因型别较为稳定。

关键词: 汉坦病毒 反转录-聚合酶链反应 同源性 系统发生树

Molecular epidemiological investigation of Hantavirus isolated from Shandong province

ZHANG Xiao-Mei, SONG Chao-Xia, ZHAI Wen-Ji, WANG Mei, LI Xiao-Juan, WANG Zhi-Qiang, LI De-Xin, ZHANG Quan-Fu

Shandong Center for Disease Control and Prevention, Jinan 250014, Shandong Province, China

Abstract:

【Abstract】 Objective To investigate molecular epidemiological characteristics of Hantavirus(HV) isolated from Shandong province. Methods A total of 48 lung tissues positive to HV antigens detected by immunofluorescence technique were amplified by RT-PCR with HV specific primers and the products were sequenced. The PCR products were analyzed in homology and phylogenetics with the known HV. Results Partial SEO S and M fragments were amplified from 15 HV antigen-positive Rattus norvegicus, and 10 strains of HV isolated were SEO. The nucleotide sequence homology of S segments was more than 96.3%, and the deduced amino acid sequence (exclude JN5?153S and DY1S) homology was more than 96.8%. The homology of M segments among those 10 strains of hantaviruses and ZB8 isolated in Shandong province was more than 97.5%, and the deduced amino acid sequence homologies were 98.6%-100%. Conclusion The HV isolated in Shandong province are mainly SEO?3 subtype. The nucleotide homology of SEO type of HV in the same or nearby area is higher and the viruses are highly conserved.

Keywords: Hantavirus RT-PCR Homology Phylogenetics

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通讯作者: 王志强, Email: wzq3678@126.com

作者简介: 张晓梅(1971-), 女, 硕士, 主管医师, 从事传染病防治工作。

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