

论文

肠道病毒71型分离株基因特征分析

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摘要:

目的 了解2009—2010年山东省临沂市肠道病毒71型(EV71)分离株的基因特征,初步探讨VP1区核苷酸或氨基酸变异与不同临床类型的关系。**方法** 从手足口病(HFMD)病例、重症病例和死亡病例的粪便标本中分离获得23株EV71病毒株,RT-PCR扩增VP1区,并进行序列测定和分析。**结果** 23株分离株与A、B基因型同源性较低;与C4亚型的C4a群代表株的核苷酸和氨基酸同源性分别达到92.8%~93.5%和98.3%~99.3%,明显高于其他亚型代表株的同源性;各分离株间的氨基酸序列比对显示无特征性改变。**结论** 2009—2010年临沂地区流行的EV71是C4亚型的C4a群,HFMD病例、重症病例和死亡病例分离株VP1区核苷酸序列和氨基酸序列无特征性差异。

关键词: 肠道病毒71型(EV71) VP1基因 基因特征

Genetic characteristics of enterovirus 71 strains isolated in Linyi, Shandong province, 2009-2010

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Abstract:

Objective To explore the genetic characteristics of VP1 gene of enterovirus 71 strains isolated in Linyi, Shandong province, 2009-2010 and to analyze the relationship between variations of VP1 gene and different clinical types. **Methods** The VP1 genes of 23 enterovirus strains isolated from stool and throat swab specimens of hadn-foot-and mouth disease(HFMD)cases were amplified with reverse transcription-PCR(RT-PCR)and their sequences were analyzed with DNASTAR 6 and MEGA 4. **Results** The homology between the 23 strains and the reference strains of subtype A and B was relatively low. The homologies of nucleotide and the amino acid of the 23 strains with the reference strains of group C4a were 92.8%-93.5% and 98.3%-99.3%, respectively, indicating that there was a close relationship between them. Comparisons of amino acid sequences among the 23 strains showed that there were no characteristic variations. **Conclusion** The enterovirus 71 strains isolated in Linyi, Shandong province belonged to the group C4a of subtype C4, and there were no characteristic variations in nucleotides or amino acids among HFMD cases, severe cases or death cases.

Keywords: enterovirus 71 VP1 gene genetic characteristics

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