

论文

肠道病毒71型山东临沂分离株3D区遗传进化分析

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摘要:

目的 构建肠道病毒71型(EV71)山东临沂分离株3D区的系统进化树,进行遗传进化分析,探讨3D区与神经毒力的关系。**方法** 于2009—2010年在山东省临沂市人民医院采集手足口病(HFMD)患儿的粪便标本和咽拭子标本107份,进行EV71的分离;用Bioedit和MEGA 4对EV71山东临沂分离株SDLY1、SDLY11、SDLY48、SDLY96、SDLY107的3D区进行序列分析,参比序列选自GenBank。**结果** 3D区的系统发生树分析结果显示,5株临沂分离株在发生树上比较集中,SDLY11、96、107的3D区同源性最高,与CoxA16原型株G-10的系统发生关系较近,与EV71原型株BrCr/70的系统发生关系较远;3D区碱基构成比和氨基酸构成比分析显示,含量最高的碱基为A(29%),含量最高的氨基酸为亮氨酸(>10%);基因序列比对和氨基酸序列比对分析结果显示,碱基突变较多,但大多为静默突变,临沂分离株与CoxA16 G-10之间的氨基酸突变中有很大一部分是赖氨酸与精氨酸之间的突变,在SDLY107的3D区发现了3个特有的氨基酸突变:N37S、K142R、G261E。**结论** EV71山东临沂分离株3D区的进化可能与CoxA16 G-10有关,突变N37S、K142R、G261E可能与EV71的神经毒力有关。

关键词: 手足口病(HFMD) 肠道病毒71型(EV71) 3D区 遗传进化分析

Evolution of 3D region of enterovirus 71 strains isolated in Linyi, Shandong province, China

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Abstract:

Objective To establish a phylogenetic tree of enterovirus 71 strains isolated in Linyi, Shandong province based on the changes of 3D region to reveal the relationship between EV71 3D and neurovirulence. **Methods** Enterovirus 71 strains were isolated from 107 stool and throat swab specimens collected from Linyi People's Hospital. The nucleotide and amino acid sequences of 3D region of the strains SDLY1, SDLY11, SDLY48, SDLY96, and SDLY107 were aligned using Bioedit and MEGA 4. The phylogenetic tree, gene distance, nucleotide composition, amino acid composition, nucleotide sequence alignment, and amino acid sequence alignment were determined. **Results** Phylogenetic analysis of 3D region showed that the phylogeny was close within Linyi strains, especially within SDLY11, 96, 107, and the phylogeny was closer between Linyi strains and CoxA16 G-10 than that between Linyi strains and standard strain BrCr/70. Analysis of nucleotide composition and amino acid composition showed that composition of nucleotide A or leucine was the highest. Alignment of nucleotide and amino acid demonstrated some mutations of K and R, and 2 specific mutations for strain SDLY107, E947D and K1873R. **Conclusion** Evolution of 3D region of enterovirus 71 strains isolated in Linyi may be relevant to CoxA16 G-10, and two mutations of N37S and K142R may be related to the neurovirulence of EV71.

Keywords: hand, foot and mouth disease enterovirus 71 3D evolution analysis

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参考文献:

[1] Agut H,Kean KM,Fichot O,et al.A point mutation in the poliovirus polymerase gene determines a complementable temperaturesensitive defect of RNA replication[J].Virology,1989,168(2): 302-311.

[2] 温红玲,郝树彬,高峰,等.肠道病毒71型山东临沂分离株全基因组序列分析[J].中华微生物学和免疫学杂志,2011,32 (7): 603-608.

[3] Cardosa MJ,Perera D,Brown BA,et al.Molecular epidemiology of human enterovirus 71 strains and recent outbreaks in the Asia-Pacific region:comparative analysis of the VP1 and VP1 genes[J].Emerg Infect Dis,2003,9(4): 461-468.

[4] Lin TY,Twu SJ,HoM S,et al.Enterovirus 71 outbreaks,Taiwan: occurrence and recognition[J].Emerg Infect Dis,2003,9(3): 291-293.

[5] 郭淑珍,孙渡,王淑萍,等.哈尔滨市手足口病重症病例212例分析[J].中国公共卫生,2011,27(10):1353.

[6] 赵生仓,张世杰,岳建宁,等.西宁市儿童人肠道病毒71型血清学调查[J].中国公共卫生,2011,27(3):361-362.

[7] Simmonds P,Welch J.Frequency and dynamics of recombination within different species of human enteroviruses[J].J Virol,2006, 80(1): 483-493.

[8] Huang SC,Hsu W,Wang HC,et al.Appearance of intratypic recombination of enterovirus 71 in Taiwan from 2002 to 2005[J]. Virus Res,2008,131(2):250-259.

[9] Arita M,Ami Y,Wakita T,et al.Cooperative effect of the attenuation determinants derived from poliovirus sabin1 strain is essential for attenuation of enterovirus 71 in the NOD/SCID mouse infection model[J].J Virol,2008,82(4): 1787-1797.

[10] Chang GH,Lin L,Luo YJ,et al.Sequence analysis of six enterovirus 71 strains with different virulences in humans[J].Virus Res,2010,151(1): 66-73.

[11] Kung YH,Huang SW,Kuo PH,et al.Introduction of a strong temperature-sensitive phenotype into enterovirus 71 by altering an amino acid of virus 3D polymerase[J].Virology,2010,396(1): 1-9.

[12] 张慧娟,朱汝南,钱渊,等.2008—2009年北京分离的肠道病毒71型基因组3'末端序列分析[J].中华微生物学和免疫学杂志,2010,30(5): 392-398.

[13] Chan YF,Sam IC,AbuBakar S.Phylogenetic designation of enterovirus 71 genotypes and subgenotypes using complete genome sequence[J].Infect Genet Evol,2010,10(3): 404-412.

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1. 马建敏, 黄学勇, 吴妮莉.手足口病常规检测方法改进分析[J]. 中国公共卫生, 2013,29(5): 754-757
2. 司鲁莹, 高峰, 温红玲, 赵丽, 宋艳艳, 许洪芝, 袁晓晶, 王志玉.肠道病毒71型分离株基因特征分析[J]. 中国公共卫生, 2012,28(11): 1446-1448
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5. 温红玲(综述), 王志玉(审校).肠道病毒71型致中枢神经系统感染研究进展[J]. 中国公共卫生, 2012,28(9): 1249-1252
6. 梁英, 范荣军, 怀清杰, 张炳丽, 梁爽, 任莉娜, 李晓鹏, 王建.哈尔滨市肠道病毒71型VP1区基因序列分析[J]. 中国公共卫生, 2012,28(8): 1108-1111

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