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论文

甲型H1N1流感病毒抗原HA基因进化分析

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摘要：

目的 分析甲型H1N1流感病毒抗原HA基因的突变和分子进化树.方法 由河南省各市(地)疾病预防控制中心和流感监测哨点医院采集流感患者咽拭样本,从咽拭样本中分离甲型H1N1流感病毒毒株,选择20株提取病毒RNA,设计引物运用逆转录-聚合酶键反应(RT-PCR)技术扩增编码HA蛋白的基因序列,测序分析核酸和编码的蛋白序列突变位.结果 分离到51株新型H1N1流感病毒;扩增20株HA编码基因,18株成功扩增到HA编码基因,2部分基因片段分别为1 024 bp和654 bp,与预期大小相符;BLAST分析结果显示,在中国多个地区分布有甲型H1N1流感病毒HA基因433 T/C(N端145 S/P)突变株,进化树分析结果显示,这一位点的突变有可能是来自于猪-人之间相互感染.结论 甲型H1N1流感病毒抗原HA基因在中国内地传播期间个别氨基酸位点发生了突变,但是抗原性未改变.

关键词： 甲型H1N1流感病毒 病毒分离 基因测序 HA基因突变

Genetic and phylogenetic characterization of influenza A(H1N1) virus hemagglutinin

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Abstract:

Objective To analyze in fluenza A(H1N1) virus hem agglutin in(HA) antigengene mutations and molecular phylogenetic tree.Methods Pharyngeal swab samples from patients were collected by Centre for Disease Control and Prevention and sentinel hospitals distributed in Henan province.Influenza A (H1N1) virus strains were isolated from throat swab samples.Twenty of the virusiso latio nswere chosen to extractRN A.Prmiers were designed for RT PCR to amplify the genes encoding HA prote in.Gene and prote in sequence mutations were analyzed by sequencing.Results To tally 51 influenza(H 1N1) virus were isolated and 18 of 20 HA gene was amplified.The two gene fragm entswere 1024 bp and 654 bp, consistent with the expected size.Basic local a lingnment search tool(BLA ST) analysis showed that in fluenza A(H1N1) virus HA gene 433 T/C(N145 S/P) mutant distributed in many parts of China.Evolutionary tree analysis revealed that the poin tmutation may be come from pig people cross infection.Conclusion The individual amino acid of influenza A(H1N1) HA mutatied during the swine flu season in China, but did not change in an tigenicity.

Keywords: influenza A(H1N1) virus virus isolation gene sequencing HA gene mutation

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