

论文

广东省外环境O1/O139群霍乱弧菌毒力基因分型

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摘要:

目的 分析广东省外环境来源O1/O139群霍乱弧菌毒力基因的携带及基因分型特征,为霍乱防控提供依据。**方法** 选取2008—2009年广东省O1/O139群霍乱弧菌水体分离株69株,水产品分离株16株和同期病例分离株5株,应用多重聚合酶链反应对ctxA、ace、zot、tcpA、tcpI、hlyA、ompU、toxR等8种毒力基因进行检测和分型分析。**结果** 90株O1/O139群霍乱弧菌均携带hlyA和toxR基因;5株病例菌株中有3株携带8种毒力基因,另外2株小川型菌株为非产毒株,基因型为hlyA⁺toxR⁺ompU⁺zot⁺tcpA⁺tcpI⁺型和hlyA⁺toxR⁺tcpA⁺型;水体菌株中,稻叶型菌株以hlyA⁺toxR⁺ompU⁺ace+zot⁺tcpI⁺型(34.15%)为主,小川型(66.67%)和O139群(70%)以hlyA⁺toxR⁺型为主;水产品菌株中,稻叶型菌株以hlyA⁺toxR⁺ompU⁺tcpI⁺型(75.00%)为主,小川型菌株各种基因型别均有分布,无明显优势基因型别。**结论** 广东省外环境来源O1/O139群霍乱弧菌以非产毒株广泛存在,毒力基因型别多样。

关键词: 霍乱弧菌 聚合酶链反应 毒力基因

Genotypes associated with virulence in environmental isolates of O1/O139 *Vibrio cholerae* in Guangdong province

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Abstract:

Objective To analyze the virulence genes and genotyping characteristics of environmental O1/O139 *Vibrio cholerae*(*V.cholerae*)in Guangdong province and to provide the basis for the prevention and control of cholera.**Methods** Eight pairs of primers were designed according to ctxA,ace,zot,tcpA,tcpI,hlyA,ompU,and toxR.The multi-plex PCR(MPCR)was established to detect 90 *V.cholerae* O1/O139 strains isolated between 2008 and 2009(69 aquatic strains,16 sea food strains and 5 clinical strains).Genotypes associated with the virulence were determined then according to the result of the MPCR.**Results** The hlyA and toxR genes were positive in all the isolates.Three of five clinical isolates were detected for eight virulence genes and the other two isolates displayed the genotype of virulence with toxR⁺,ompU⁺,zot⁺,tcpA⁺,tcpI⁺,hlyA⁺,toxR⁺,and tcpA⁺.For the aquatic isolates,14 Inaba strains (34.15%,14/41)were hlyA⁺,toxR⁺,ompU⁺,ace⁺,zot⁺,tcpI⁺,while 12 Ogawa strains(66.67%,12/18)and 7 O139 strains(70%,7/10)were hlyA⁺and toxR⁺.For sea-food isolates,3 Inaba strains(75%,3/4)were hlyA⁺,toxR⁺,ompU⁺,and tcpI⁺; while the Ogawa strains presented different genotypes.**Conclusion** The environmental O1/O139 *Vibrio cholerae* in Guangdong province display widespread non-toxigenic strains with virulence genotype diversity.

Keywords: *Vibrio cholerae* polymerase chain reaction virulence gene

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