

论著

肺炎克雷伯菌16S rRNA甲基化酶耐药基因研究

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摘要:

目的了解肺炎克雷伯菌对氨基糖苷类抗生素的敏感性及16S rRNA甲基化酶检出情况。方法收集中南大学湘雅医院2009年1—7月非重复肺炎克雷伯菌96株, 采用琼脂稀释法对庆大霉素、阿米卡星、妥布霉素的最低抑菌浓度(MIC)进行检测; 聚合酶链反应(PCR)扩增16S rRNA甲基化酶基因armA、rmtA、rmtB、rmtC、rmtD和npmA。结果肺炎克雷伯菌对阿米卡星、庆大霉素及妥布霉素的MIC₅₀分别为256 μg/mL、512 μg/mL和512 μg/mL; MIC₉₀均为>512 μg/mL; 耐药率分别为21.88%、63.54%、41.67%。68株(70.83%)菌至少对1种药物耐药, 21株(21.88%)菌对3种药物均耐药。22株(22.92%)菌armA基因扩增阳性, 未扩增到rmtA、rmtB、rmtC、rmtD和npmA基因; 22株armA阳性菌株中, 17株(77.27%)对3种氨基糖苷类抗生素均耐药。armA阳性株与armA(FJ410928.1)基因序列同源性为100%。结论携带armA型16S rRNA甲基化酶基因是肺炎克雷伯菌对氨基糖苷类药物高水平耐药的主要机制之一。

关键词: 肺炎克雷伯菌 16S rRNA甲基化酶 聚合酶链反应 抗药性 微生物

Drug resistance genes of 16S rRNA methylase in *Klebsiella pneumoniae*

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Abstract:

Objective To investigate antimicrobial susceptibility of *Klebsiella pneumoniae* (*K. pneumoniae*) to aminoglycosides and detection of 16S rRNA methylase genes in *K. pneumoniae*. Methods Ninety six non-repetitive clinical *K. pneumoniae* isolates were collected from Xiangya hospital of Central South University from January to July 2009, minimal inhibitory concentrations (MICs) of gentamycin, amikacin and tobramycin were determined by agar dilution method; genotype of 16S rRNA methylase genes (armA, rmtA, rmtB, rmtC, rmtD, npmA) were detected by polymerase chain reaction (PCR). Results MIC₅₀ of amikacin, gentamycin and tobramycin was 256 μg/mL, 512 μg/mL and 512 μg/mL respectively; and MIC₉₀ were all > 512 μg/mL; antimicrobial resistance rate was 21.88%, 63.54%, and 41.67% respectively. 68 isolates (70.83%) were resistant to at least one kind of antimicrobial agent, 21 isolates (21.88%) were resistant to three kinds of antimicrobial agents. 22 isolates (22.92%) carried armA, but rmtA, rmtB, rmtC, rmtD and npmA were not detected; of 22 isolates harboring armA 16S rRNA methylase genes, 17 (77.27%) were highly resistant to gentamicin, amikacin and tobramycin, the homology of armA positive isolate and armA (FJ410928.1) was 100%. Conclusion armA 16S rRNA methylase gene harbored in *K. pneumoniae* plays an important role in aminoglycoside resistance.

Keywords: *Klebsiella pneumoniae* 16S rRNA methylase polymerase chain reaction drug resistance, microbial

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