

# 大肠埃希菌氨基糖苷类耐药株 **aac(3) II** 基因保守区分析 Conserved Region Analysis of **aac(3) II** Gene From **E.coli Aminoglycoside Resistance Strain**

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聚合酶链反应; DNA测序; 耐药基因; 氨基糖苷类抗生素; 钝化酶 Key words: PCR; DNA sequencing; Drug resistance gene; Aminoglycoside; Modifying enzyme

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## 摘要

常规方法分离鉴定47株大肠埃希菌,以标准纸片扩散法(K B法)对其进行常用氨基糖苷类药物敏感性测定,耐药株经PCR检测 **aac(3) II** 基因保守区,扩增产物进行DNA测序分析。初步探讨大肠埃希菌氨基糖苷类抗生素耐药株与 **aac(3) II** 基因保守区之间的关系,结果显示本地区大肠埃希菌氨基糖苷类抗生素耐药株的 **aac(3) II** 基因保守区具65位G、84位T和65位A、84位C两种基因型,且高度耐药菌株皆为65位G、84位T基因型。

Abstract:According to standard K B method,bacteriostatic tests were performed to screen out aminoglycoside resistance bacteria from 47 strains of isolated E.coli .To analyze correlations between the degree of E.coli aminoglycoside resistance and **aac(3) II** gene conserved region,PCR amplified **aac(3) II** gene conserved regions and were analyzed by DNA sequencing.The results showed that there were two species of **aac(3) II** gene type including 65G and 84T or 65A and 84C in the samples.Strains with high activity of modifying enzyme to gentamicin all were 65G and 84T **aac(3) II** gene type.

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## Abstract

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