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论文

# 福建省耐多药结核分枝杆菌MLVA分型分析

陈求扬[1,2], 梁庆福[1,2], 林建[1], 林淑芳[1,2], 赵永[1], 魏淑贞[1], 逄宇[3], 郑金凤[1,2], 王玉锋[3], 赵雁林[3]

1. 福建省疾病预防控制中心 福建省人兽共患病研究重点实验室, 福州 350001;
2. 福建省医科大学公共卫生学院教学基地;
3. 中国疾病预防控制中心结核病预防控制中心国家结核病参比实验室

摘要:

目的 了解福建省耐多药结核分枝杆菌分子流行病学特征,为控制耐多药肺结核提供参考依据。方法 采用多位点数目可变串联重复序列基因分型(MLVA)方法,对30个监测点纳入监测的所有耐多药结核分枝杆菌分离菌株DNA进行检测,使用BioNumerics(Version 4.5)软件进行聚类分析。结果 76株耐多药结核分枝杆菌被分为Ⅰ、Ⅱ、Ⅲ三大基因群,分别包含Ⅰ群5株(6.6%)、Ⅱ群68株(89.5%)、Ⅲ群3株(3.9%);在株水平基因分型上,有19株菌成7簇,各包含2~4株菌,成簇菌株来源于同一县区或不同县区。结论 福建省耐多药结核分枝杆菌菌株主要流行株为Ⅱ群菌株;部分菌株存在县区内,甚至跨县域的近期传播流行。

关键词: 结核分枝杆菌 多位点可变数目串联重复序列 基因分型 耐多药

# Genotyping of multi-drug resistant *Mycobacterium tuberculosis* clinical isolates from Fujian province with multiple loci variable number tandem repeat analysis

**CHEN Qiu-yang, LIANG Qing-fu, LIN Jian, et al**

Fujian Provincial Center for Disease Control and Prevention, Fujian Province Key Laboratory of Zoonosis, Fuzhou, Fujian Province 350001, China

**Abstract**:

**Objective** To explore the characteristics of molecular epidemiology of multi-drug *Mycobacterium tuberculosis* clinical isolates in Fujian province,and to provide reference for multi-drug-resistant tuberculosis(MDR-TB) control.**Methods** All MDR-TB isolates were selected from 30 survey sites,and the bacterial DNA of these strains were detected by PCR to amplify the loci simultaneously with multiple variable number tandem repeat analysis(MLVA),and the clustering of genotypes was analyzed with BioNumerics(Version 4.5).**Results** Through MLVA,76 strains of multi-drug resistant *Mycobacterium tuberculosis* were divided into 3 genogroups,i.e.Ⅰ,Ⅱ,Ⅲ genogroup.The Ⅰ genogroup consists of 5 strains (6.6%),Ⅱ genogroup consists of 68 strains(89.5%),and Ⅲ genogroup consists of 3 strains(3.9%).At the strain level,19 isolates were categorized into 7 clusters,each cluster including 2-4 strains,and the clustering strains were collected from the same county or different county.**Conclusion** The strain of Ⅱ genogroup is the main epidemic strain in Fujian province,and some genotypes of strains spread recently in some county,even spread across counties.We should strengthen the control of drug resistant tuberculosis.

**Keywords**: *Mycobacterium tuberculosis* MLVA genotype multi-drug resistance

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通讯作者：

作者简介：

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