

Abstract

Purpose

The objective of this study is to facilitate a better understanding of the molecular genetic basis of drug-resistant *Mycobacterium tuberculosis* (*M. tuberculosis*) strains in Taiwan. Compilation of data obtained from this study will facilitate the development of a rapid method for the early diagnosis of tuberculosis and identification of resistance to first-line antituberculosis drugs that are essential for efficient treatment and transmission control of the disease.

Material and Methods

A total of 1,245 and 3,038 drug-resistance *M. tuberculosis* strains were collected in 2004 and 2005, respectively from several clinical Mycobacteriology laboratories in different geographic regions of Taiwan. Both spoligotyping and standard IS6110 restriction fragment length polymorphism analysis were applied in this study. Drug susceptibility testing for each isolate was performed using an indirect agar proportion method or MGIT liquid system. multidrug-resistant (MDR) tuberculosis was defined as isolates resistant to at least isoniazid and rifampin. The genotypes were scanned and analyzed using Bionumerics® software, version 2.0 (Applied Maths., Kortrijk, Belgium). A statistical analysis was performed using EpiInfo 6.04 (Center for Disease Control and Prevention, Atlanta, Ga.).

Results

Overall, a RFLP dendrogram of 78 MDR strains revealed 60 unique genotypes and 8 clusters. Among the 2,302 drug-resistant isolates genotyped, 41.3% (950/2,302) were Beijing family genotypes.

Conclusion and Suggestions

Based on the results of IS6110 RFLP fingerprinting, the drug-resistance isolates were highly genetic diverse. The transmission of drug-resistance clones was unlikely. A long-term follow-up laboratory program is suggested for monitoring the accomplishment of the National Tuberculosis Program.

Key Words: Drug resistance, *Mycobacterium tuberculosis*, genomic database