Characterization of rifampicin-resistant Mycobacterium tuberculosis in Taiwan

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INTRODUCTION

Among infectious diseases, tuberculosis (TB) is one of the most frequent causes of death in the world, with more than 2 million TB-related deaths reported each year (Dye et al., 1999). In 1997, an estimated 8 million new cases were reported and approximately 2 billion people, one third of the world’s population, were infected with Mycobacterium tuberculosis (Dye et al., 1999). TB is one of the most important communicable diseases in Taiwan. It was the twelfth most common cause of death in 1998. The rates of incidence and mortality of TB per 100 000 population were respectively 64·89 and 6·93 in the same year (Kan, 2000). In recent years, the control of TB has been impeded by the emergence of drug-resistant M. tuberculosis strains (Kan, 2000).

Rifampicin has proven to be an effective antituberculosis agent and its use has greatly shortened the duration of chemotherapy for the treatment of TB. Rifampicin resistance heralds higher rates of treatment failure and death for the patient and a poor outcome if the isolate is also resistant to isoniazid (Goble et al., 1993). The action of rifampicin is believed to interfere with transcription in bacteria by binding to the β subunit of RNA polymerase (the product of the rpoB gene) (Jin & Gross, 1988). Mutations in certain highly conserved codons encoded by the rpoB gene) (Jin & Gross, 1988). Mutations in certain highly conserved codons encoded by the rpoB gene) (Jin & Gross, 1988). Mutations in certain highly conserved codons encoded by the rpoB gene) (Jin & Gross, 1988). In rifampicin-resistant strains, the β subunit of RNA polymerase is incapable of being functional. Since Rif r strains are a matter of great concern in Taiwan (Chiang et al., 1998; Wang & Lin, 2001), it is of interest to study the molecular basis of rifampicin resistance in these local resistant isolates. One recent report concerned with the genotype of rpoB of Rif r M. tuberculosis isolates from northern Taiwan reported four substitutions and one insertion (Qian et al., 2002). The mutation patterns among large...
numbers of isolates from Kaohsiung, in southern Taiwan, acquired in this work should allow a better understanding of any hot-spot regions on this gene for suitable rapid diagnosis and proper control of TB in Taiwan.

The correlation between the level of resistance to rifampicin and different mutational sites in the 69-bp core region of rpoB seemed to vary in different regions (Mani et al., 2001; Williams et al., 1998; Ohno et al., 1997). Thus, the MICS of rifampicin for Rifr strains of M. tuberculosis with known alterations in rpoB were determined.

Resistance to rifampicin has previously been associated with mutations in the early region of rpoB in addition to mutations in the middle or end regions of this gene in *Helicobacter pylori* (Lee et al., 1995), detection of laboratory contamination (Ramos et al., 1994). The rifampicin concentration was 1·0 mg l−1 to determine the MIC of rifampicin of each isolate, serial twofold dilutions of rifampicin were incorporated in 7H10 agar at concentrations that ranged from 0 to 256 mg ml−1. Sets of quadrant Petri dishes (one quadrant in each plate contained drug-free medium) were inoculated with each isolate. Plates tested in duplicate, were incubated at 37 °C in the presence of 5 % CO2. Each plate was checked weekly and results were recorded after weeks 3 and 4. The MIC was defined as the lowest concentration of drug that inhibited growth of the bacterial population by more than 99 %.

DNA extraction. Genomic DNA was extracted as described by van Soolingen et al. (1994) with modifications. Bacteria were harvested from the Lowerstein–Jensen slopes, heat-killed and incubated with lysosome (1 h, 37 °C) followed by digestion with 50 μg proteinase K in 10 % SDS for 30 min at 65 °C. A further incubation with CTAB/NaCl for 10 min at 65 °C was followed by precipitation using chloroform/isoamyl alcohol (24:1, v/v). Genomic DNA was extracted with phenol/chloroform and precipitated with 100 % ethanol.

PCR amplification of mycobacterial strains. Aliquots of purified mycobacterial DNA (10–20 μg) were added to PCR reagents. The 157-bp rpoB fragment (nt 1846–2002) was amplified by using the primers Tr8 (5′-TGAGACCGCGCGAACCTC-TCA-3′) and Tr9 (5′-CCGCCGGCCGATCAAGGAGT-3′) as described previously (Telenti et al., 1993). To target a 365-bp fragment (early part) of rpoB in *M. tuberculosis*, primers Th176F (5′-CTTCTCCGGGTCGATGGTCT-TG-3′) and Th176R (5′-GGCCGTTCCTGACGCTAAACTG-3′) were used (Heep et al., 2000).

Purification of PCR products and DNA sequencing. Template DNA was purified from the PCR products by using QIAquick PCR purification kit (Qiagen). Nucleotide sequencing was performed with the ABI PRISM Dye terminator cycle sequencing ready reaction kit (Perkin Elmer) and the reactions were analysed on an ABI PRISM 373A DNA sequencer.

Restriction fragment length polymorphism (RFLP). Fifty-five Rifr *M. tuberculosis* isolates were available for RFLP analysis. DNA fingerprinting was performed as described previously (van Embden et al., 1993; van Soolingen et al., 1994). Briefly, genomic DNA was digested with PvuII for 4–6 h before being separated electrophoretically in a 1 % agarose gel in 1 × TBE running buffer at a constant voltage of 32 V for 16 h. Next, the separated DNA fragments were transferred onto Hybond nylon membrane (Amersham). Hybridization was then performed using a digoxigenin-labelled 245-bp fragment of IS6110 (25 ng ml−1) as the DNA probe. Membranes were hybridized overnight under stringent conditions at 65 °C. Hybridized digoxigenin-labelled probe was detected with the DIG luminescent detection kit (Boehringer Mannheim) following the manufacturer’s instructions.

As recommended previously (van Embden et al., 1993), PvuII-digested genomic DNA of *M. tuberculosis* reference strain MT.14323 served as an external control of the hybridization conditions and a mixture of PvuII-digested supercoiled DNA ladder and Haelll-digested φX174 DNA served as an internal marker.

Cluster analysis. DNA fingerprints were analysed by the GelCompar software (version 4.0; Applied Maths). A cluster was defined as two or more isolates with identical RFLP patterns when five or more copies of IS6100 were present. Autoradiograms were digitized by using a scanner with an optical resolution of 300 d.p.i. The sizes of IS6110 RFLP fragments were calculated by comparison of their mobilities with those of a set of internal markers of known molecular sizes (van Soolingen et al., 1994). The accuracy of the normalization procedure was controlled by comparing the IS6110 fingerprint patterns of reference strain *M. tuberculosis* MT.14323. The fingerprint patterns were analysed for similarity by using the Dice coefficient and a dendrogram was
calculated with the unweighted-pair group method using average linkage (UPGMA) according to the supplier’s instructions. Band positions were determined by using the peak-find function of the GelCompar software and were controlled manually by comparison with the original IS6110 autoradiogram.

**Statistical analysis.** The Mann–Whitney test was used for comparing mean MICs with the software package SPSS (SPSS Institute); \( P < 0.05 \) was considered significant.

**RESULTS**

In this study, 63 Rif\( ^{r} \) isolates and 12 rifampicin-sensitive (Rifs) clinical isolates were first examined for mutations in a 157-bp fragment of \( rpoB \). Of 63 Rif\( ^{r} \) isolates, 84\% (53/63) of the isolates showed mutations in this region. When compared with the published sequence, 15·9\% (10/63) of the Rif\( ^{r} \) isolates and 12 Rifs strains exhibited no mutations in this region. The most prevalent mutation sites were in codons 531 (41·5\%), 526 (18·9\%), 516 (15·1\%) and 533 (7·5\%) (Table 1). The mutations found within the 69-bp core region of \( rpoB \) in 53 of the resistant isolates are shown in Fig. 1.

A total of 16 different mutations and five novel alleles were identified within a 157-bp region of \( rpoB \) of 53 Rif\( ^{r} \) clinical isolates (Table 1; Fig. 1). Of the five novel alleles, one allele revealed changes of two bases in codon 516 (GAC\( \rightarrow \)Asp) and the other four alleles showed point mutations in two separate codons: codons 511 (CTG\( \rightarrow \)CCG; Leu\( \rightarrow \)Pro) and 516 (GAC\( \rightarrow \)GCG; Asp\( \rightarrow \)Gly); codons 526 (CAC\( \rightarrow \)TAC; His\( \rightarrow \)Tyr) and 521 (CTG\( \rightarrow \)CTA; Leu\( \rightarrow \)Leu); codons 526 (CAC\( \rightarrow \)CGG; His\( \rightarrow \)Arg) and 529 (CGA\( \rightarrow \)CAA; Arg\( \rightarrow \)Gln); and codons 516 (GAC\( \rightarrow \)AAC; Asp\( \rightarrow \)Asn) and 533 (CTG\( \rightarrow \)CGG; Leu\( \rightarrow \)Pro) (Table 1).

The agar proportion method was used to understand the relationship between the degree of resistance to rifampicin and the mutation site. Growth of the 12 sensitive strains was inhibited at rifampicin concentrations \( \leq 0.25 \mu \text{g ml}^{-1} \), indicating the susceptibility of these strains. Isolates with mutations in the 69-bp core region of \( rpoB \) were highly resistant to rifampicin, with MICs ranging from 8 to 256 \( \mu \text{g ml}^{-1} \), and the mean MIC was 92·38 \( \mu \text{g ml}^{-1} \) (Table 1). The MICs for the remaining 10 resistant isolates were between 2 and 128 \( \mu \text{g ml}^{-1} \) and the mean MIC was 24·8 \( \mu \text{g ml}^{-1} \). Our results revealed that strains with mutations in the 69-bp core region had significantly higher MICs than those without mutations in this region (\( P < 0.05 \)).

For the 10 Rif\( ^{r} \) isolates without mutations in the 157-bp fragment, the possibility of mutations occurring in the early region (365-bp fragment) of \( rpoB \) was then examined. PCR-single-strand conformation polymorphism analysis and DNA sequencing exhibited patterns the same as that of \( M. tuberculosis \) isolates and their levels of rifampicin susceptibility

<table>
<thead>
<tr>
<th>Mutated codon(s)</th>
<th>Specific mutation(s)</th>
<th>( n (%)^{*} )</th>
<th>MIC (( \mu \text{g ml}^{-1} ))( ^{†} )</th>
</tr>
</thead>
<tbody>
<tr>
<td>531</td>
<td>TCG(Ser)( \rightarrow )TTG(Leu)</td>
<td>22 (41·5)</td>
<td>32 (1), 64 (9), 128 (11), 256 (1)</td>
</tr>
<tr>
<td>526</td>
<td>CAC(His)( \rightarrow )GAC(Asp)</td>
<td>3 (5·7)</td>
<td>128</td>
</tr>
<tr>
<td></td>
<td>CAC(His)( \rightarrow )CGC(Arg)</td>
<td>2 (3·8)</td>
<td>32</td>
</tr>
<tr>
<td></td>
<td>CAC(His)( \rightarrow )TAC(Tyr)</td>
<td>5 (9·4)</td>
<td>32 (1), 128 (3), 256 (1)</td>
</tr>
<tr>
<td>516</td>
<td>GAC(Asp)( \rightarrow )GTC(Val)</td>
<td>3 (5·7)</td>
<td>32 (1), 64 (2)</td>
</tr>
<tr>
<td></td>
<td>GAC(Asp)( \rightarrow )TAC(Tyr)</td>
<td>3 (5·7)</td>
<td>16 (1), 64 (2)</td>
</tr>
<tr>
<td>533</td>
<td>CTG(Leu)( \rightarrow )CGG(Pro)</td>
<td>2 (3·8)</td>
<td>128</td>
</tr>
<tr>
<td>511</td>
<td>CTG(Leu)( \rightarrow )CGG(Pro)</td>
<td>4 (7·5)</td>
<td>8 (1), 64 (2), 128 (1)</td>
</tr>
<tr>
<td>522</td>
<td>TCG(Ser)( \rightarrow )TTG(Leu)</td>
<td>1 (1·9)</td>
<td>32</td>
</tr>
<tr>
<td>511, 516</td>
<td>CTG(Leu)( \rightarrow )CGG(Pro), GAC(Asp)( \rightarrow )GCC(Gly)( ^{†} )</td>
<td>2 (3·8)</td>
<td>64</td>
</tr>
<tr>
<td></td>
<td>CTG(Leu)( \rightarrow )CGG(Pro), GAC(Asp)( \rightarrow )TAC(Tyr)</td>
<td>1 (1·9)</td>
<td>128</td>
</tr>
<tr>
<td>526, 521</td>
<td>CAC(His)( \rightarrow )TAC(Tyr), CTG(Leu)( \rightarrow )CTA(Leu)( ^{†} )</td>
<td>1 (1·9)</td>
<td>128</td>
</tr>
<tr>
<td>526, 529</td>
<td>CAC(His)( \rightarrow )CGC(Arg), CGA(Arg)( \rightarrow )GAC(Gln)( ^{†} )</td>
<td>1 (1·9)</td>
<td>64</td>
</tr>
<tr>
<td>516, 526</td>
<td>GAC(Asp)( \rightarrow )GCC(Ala), CAC(His)( \rightarrow )GAC(Asp)( ^{†} )</td>
<td>1 (1·9)</td>
<td>128</td>
</tr>
<tr>
<td>516, 533</td>
<td>GAC(Asp)( \rightarrow )AAC(Asn), CTG(Leu)( \rightarrow )CGG(Pro)( ^{†} )</td>
<td>1 (1·9)</td>
<td>64</td>
</tr>
<tr>
<td>None</td>
<td>None</td>
<td>10</td>
<td>2 (2), 4 (1), 8 (2), 16 (2), 32 (2), 128 (1)</td>
</tr>
</tbody>
</table>

\( ^{*} \)Percentages of isolates carrying mutations in the core region are given in parentheses.

\( ^{†} \)Where strains with the same mutation(s) gave different MIC values, the number of strains exhibiting each MIC is given in parentheses.

\( ^{‡} \)Novel pattern of substitution.
tuberculosis Mt.14323 (data not shown). These results demonstrated that these 10 rifr isolates did not show mutations in the 157-bp or 365-bp fragment of \(rpoB\).

In this study, 55 Rifr \textit{M. tuberculosis} isolates were analysed by the standardized DNA fingerprinting method with IS\(6110\) as a genetic marker. The IS\(6110\) fingerprint patterns generated were highly variable (Fig. 2). The number of copies of IS\(6110\) per isolate varied from two to 19, with sizes ranging from 600 to 16,000 bp. The majority of the 55 isolates (85\%), contained six to 16 copies, with a median of 10 bands (Fig. 3). No isolates lacking IS\(6110\) were found.

The similarities of all 55 IS\(6110\) fingerprint patterns were then analysed. A total of 54 of 55 RFLP types were defined at the 90\% similarity level (Fig. 4). Two (C14 and C389) of 17 isolates with mutations in codon 531 had 95.5\% similarity, with different drug-resistance patterns. Isolate C14 was susceptible to kanamycin and ethambutol, while C389 was resistant to both of these drugs. Close relatedness was not observed between other resistant isolates carrying mutations in either of the two other highly mutated sites, codons 526 and 516 (data not shown).

**DISCUSSION**

It was observed that the majority (75.5\%) of Rifr \textit{M. tuberculosis} isolates contained missense mutations that led to substitutions of amino acids at Ser-531 (41.5\%), His-526 (18.9\%) or Asp-516 (15.1\%) in the core region of \(rpoB\). While codon 531 is the most common site of nucleotide substitutions worldwide, mutations at the other two prevalent sites (codons 526 and 516) in our strains occur at different frequencies in strains from other geographical regions (Qian et al., 2002; Pozzi et al., 1999; Taniguchi et al., 1996). Distinctly, about 8\% of Rifr \textit{M. tuberculosis} isolates displayed point mutations in codon 533 in this study. However, this missense mutation in codon 533 only occurred at low frequency (<3.3\%) or no mutations at all were reported in other geographical regions (Mani et al., 2001; Pozzi et al., 1999; Bartfai et al., 2001; Valim et al., 2000). These differences may be attributed to geographical genetic differences in Rifr \textit{M. tuberculosis} strains and the transmission of these strains among patients in different countries. Unexpectedly, 10 (15.9\%) of the 63 Rifr clinical isolates in this study showed no mutations in the sequenced 157-bp region of \(rpoB\), despite the fact that these isolates were resistant to rifampicin. A comparable high frequency (20\%; 4/20) of Rifr isolates with no mutations in this core region was also reported recently from northern Taiwan (Qian et al.,...
2002). The frequency is comparatively higher than those that have been reported for Rif\(^R\) isolates from other geographical areas. More than 90% of Rif\(^R\) strains from other regions had mutations located in the 69-bp core region (Telenti et al., 1993; Mani et al., 2001; Masiota-Bernard et al., 1998; Ohno et al., 1996; Williams et al., 1994). DNA sequencing of the early part of rpoB in these 10 Rif\(^R\) isolates showed no mutations in a 365-bp region. This indicated the possible occurrence of an alteration outside the two regions of rpoB examined, such as mutations in V176F (Heep et al., 2001) and codon 381 (Taniguchi et al., 1996). Among other explanations, several additional genes may be involved in rifampicin resistance. A change in the antibiotic permeability of a membrane or in metabolism could also give rise to the rifampicin-resistant phenotype (Hui et al., 1977; Konno et al., 1973).

In general, amino acid substitution in the 69-bp core region led to higher levels of resistance to rifampicin than those isolates without mutations in this region ($P < 0.05$, Table 1). Some investigators have even demonstrated that different levels of resistance are associated with different mutational
sites in this region (Ohno et al., 1996, 1997; Taniguchi et al., 1996). Thus, strains with mutations in either codon 531 or 526 were usually highly rifampicin-resistant, as revealed in this report and others (Ohno et al., 1996; Williams et al., 1998; Taniguchi et al., 1996). However, in contrast to previous findings on mutations in codon 533 (Ohno et al., 1996), our four isolates with amino acid substitution in this codon (Leu→Pro) did not show a consistently low level of resistance (MIC < 2 μg ml⁻¹). Likewise, high MICs (＞128 μg ml⁻¹) for isolates with mutations in codon 516 or 533 were also observed in India (Mani et al., 2001). Thus, the association between particular mutational sites on rpoB and the drug susceptibility of multidrug-resistant M. tuberculosis strains is not apparent in some areas, including Taiwan. Noticeably, the same mutation in the same codon in the 69-bp region did not reflect the same level of drug resistance in these resistant isolates (Table 1; Ohno et al., 1996). Some other additional factor(s) might contribute to the variation in drug resistance (Hui et al., 1997; Konno et al., 1973). Thus, sequencing of rpoB is not completely able to replace traditional methods of susceptibility testing to detect the level of rifampicin resistance of M. tuberculosis.

The results showed that RifR M. tuberculosis strains from this area were highly polymorphic. The majority of the TB cases were therefore presumed to be the result of re-activation of previously contracted M. tuberculosis infections. Furthermore, our results showed that most isolates, even with the same mutated codon, did not have similar patterns or locations of IS6110 copies (Fig. 5). This suggests that acquisition of rifampicin resistance followed the infection of a rifampicin-susceptible strain in this work. In contrast to a report from Cape Town, where most drug-resistant TB cultures derived from Hungary by DNA sequencing and the line probe assay. J Clin Microbiol 39, 3736–3739.


Rifampicin-resistant M. tuberculosis


