DETECTION OF DISCORDANT ISOLATES OF DRUG RESISTANT MYCOBACTERIUM TUBERCULOSIS

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CHAPTER 1

INTRODUCTION

Tuberculosis is a highly prevalent and widespread disease caused by the acid fast bacteria, *Mycobacterium tuberculosis*. The World Health Organization (WHO) estimates that approximately one-third of the world's population is currently infected with the bacteria and a global plan has been made to control the disease and even eliminate it as a public health problem by 2050 (1). A portion of the strategy utilized by this plan includes directly observed treatment, short-course (DOTS) which involves directly observing patients taking their medication. Through the use of DOTS, the proper dosage and correct regimen of drugs can be ensured, which when abused, can lead to the development of multi-drug resistant tuberculosis (MDR-TB). A second portion of the strategy is addressing the problem of MDR-TB by improving tuberculosis control programs and implementing a MDR-TB response. Early diagnosis and the use of effective and affordable alternative drugs used to treat MDR-TB are key elements in the MDR-TB response. A considerable amount of effort must be made to prevent and reduce the amount of MDR-TB cases, which continues to threaten the global control of tuberculosis.

The spread of tuberculosis occurs when bacteria become aerosolized through a cough or sneeze by an infected person and is inhaled by a new host. In most cases, the immune system is able to suppress the reproduction of the bacteria in the body and the disease becomes latent. This latent infection is unnoticed by the host as no symptoms of tuberculosis appear. However, when the immune system is unable to control the bacteria, an active form of the disease develops and can be transmitted, which may include resistant bacilli.

In 2010, the incidence of tuberculosis was estimated to be 8.8 million cases globally, which is roughly equal to 128 cases per 100,000 (2). The top five countries with the highest amount of cases were

India (2-2.5 million), China (0.9-1.2 million), South Africa (0.4-0.59 million), Indonesia (0.37-0.54), and Pakistan (0.33 million-0.48 million) (2).

The prevalence of tuberculosis has been slowly declining. The global prevalence of tuberculosis was roughly 12 million cases or 178 cases per 100,000 with a majority in the South East Asia region and the African region (2). Of the 12 million prevalent cases of tuberculosis in 2010, 650,000 (5.4%) were estimated to be MDR-TB (2).

The mortality of tuberculosis has dramatically decreased since 1990. WHO has set up a benchmark to halve the 1990 mortality rate of tuberculosis by 2015. In 2010, the mortality rate was about a third lower compared to 1990 (2). An estimated 1.1 million deaths from tuberculosis occurred in HIV-negative cases and .35 million deaths in HIV-positive cases, totaling about 1.4 million deaths or 20 deaths per 100,000 (2). All of the regions monitored by WHO have already met the mortality benchmark, with the exception of the South East Asia region, which is on track to meet it by 2015, and the African region, which is not expected to meet this goal.

Tuberculosis treatment is performed through a regimen of various antibiotics which include rifampin, isoniazid, ethambutol, and pyrazinamide, with the first two drugs being the most used (3). These antibiotics are known as first line drugs and are extremely effective in killing *M. tuberculosis*; rifampin and isoniazid kill 99% of the bacilli within the first two months of therapy (4). The formal definition of MDR-TB requires the resistance to both rifampin and isoniazid.

While less effective than first line drugs, second line drugs such as aminoglycosides, fluoroquinolones, ethionamide, and para-aminosalicyclic acid are critical in the treatment of tuberculosis resistant to first line drugs like MDR-TB. A more extreme form of resistant tuberculosis known as extensively drug resistant tuberculosis (XDR-TB) develops when resistance to these second line drugs occurs, specifically, fluoroquinolones and aminoglycosides.

1.1 Statement of the Problem and Its Significance

Early diagnosis of MDR-TB is critical for proper treatment. With a regimen of rifampin and isoniazid, a patient with active tuberculosis can become non-infectious within 2 weeks (5). However, as resistance to these two drugs develops, second line antibiotic treatment must be used which lasts an extra 6 to 18 months and patients remain infectious for a longer period of time, which can further propagate the spread of MDR-TB (6).

Testing for antibiotic resistance in *M. tuberculosis* is a lengthy process due to its long generation time. The WHO standard guideline for the drug susceptibility test of *M. tuberculosis* is inoculating the bacteria through dilution on Löwenstein Jensen agar with a set concentration of test antibiotic and incubating it at 37 degrees Celsius. Colonies are then counted on the 28^{th} day and a proportion is calculated by comparing the colony count of the test medium to a control. If the proportion exceeds a critical proportion or if no colonies appear in the lowest drug concentration medium with the highest inoculum, the isolate is determined to be resistant or sensitive, respectively. However, if neither criteria are matched, the incubation must continue until the 40^{th} day where the final results are read through the same process (7).

Drug susceptibility testing of clinical isolates is also rare. In 2010, only 1.8% of new global cases of tuberculosis have been tested for resistance (8). The highest amount of testing has been in the European region with 30% of new cases tested and the lowest have been in the two regions with the highest prevalence of tuberculosis—the African region (0.2%) and the South East Asia region (0.1%) (8). More testing has been performed for previously treated cases of tuberculosis than new cases. 6.4% of the global existing cases have been tested, with the European region leading at 50.7% of cases tested and the Western Pacific region (1.6%) and the South East Asia region (0.3%) at the lowest (8).

Alternative diagnostic techniques are necessary to bolster the proportion of tuberculosis cases tested for resistance. One such method is sequence based, where genes associated with resistance to a particular antibiotic are sequenced and analyzed for mutations known to cause resistance. This technique

is advantageous to drug susceptibility testing in that it is rapid and data can be readily compared between laboratories (9). However, since this technique relies on the detection of specific mutations, all mutations that cause resistance must be known beforehand. Although antibiotic resistance in *M. tuberculosis* is extensively studied, not all causative mutations have been recorded, as proven by the existence of isolates that are phenotypically resistant but genotypically sensitive. These isolates are known as discordant isolates, which are prime candidates for the study of novel mutations.

One weakness of sequence based techniques is that different mutations have variable effects on the gene or protein depending on the type of mutation and the location of it. As a result, different levels of resistance can occur. For example, mutations in codon 522 and 533 of the gene *rpoB* have been linked to low level rifampin resistance compared to mutations in neighboring codons (10). Thus, it is important not only to detect a mutation, but to determine the type as well. Different proportions of mutations between resistant isolates can also provide useful data to determine high confidence mutations. This would allow laboratories to analyze specific areas in a gene for common mutations, further increasing the efficiency of the sequence diagnostic test.

1.2 Hypothesis

The development of drug resistance strains in *M. tuberculosis* ultimately relies on exposure to the resistant drug because the presence of drug resistance mutations does not confer any selective advantage over strains lacking those mutations until exposure occurs (15). Within each geographical region, strains of *M. tuberculosis* may be under unique and various selective pressures to develop specific types of polymorphisms. Therefore, it can be hypothesized that there are genetic differences in the drug resistant strains of *M. tuberculosis* found in different regions and that the proportion of polymorphisms in genes associated with drug resistance will be different between geographic locations.

1.3 Study Objectives

1. To sequence the "hot spot" regions of nine genes (*rpoB, inhA* promoter, *katG, ahpC* promoter, *gyrA, gyrB, rrs, eis* promoter, and *tlyA*).
2. To identify discordant isolates through the comparison of drug susceptibility data and sequence data.
3. To further define the resistance patterns found in *M. tuberculosis* within and between different geographical regions represented by the widely dispersed study sites

CHAPTER 2

LITERATURE REVIEW

Resistance in *M. tuberculosis* usually develops through single nucleotide polymorphisms (SNPs) within specific genes. Since *M. tuberculosis* has been known to rarely exchange DNA with its surrounding environment, resistance associated mutations are confined to the bacterial chromosome (11). *Mycobacterium* species do contain an 18 kb plasmid; however, this plasmid is not known to contribute to drug resistance (46). Mutations can cause resistance by altering the drug target (12), titrating the drug through overexpression of the drug target (13), or inactivating an enzyme required in the pathway of the drug (14). Conveniently, SNPs often occur within a particular region of a gene, which is known as a "hot spot" for mutations. Analyses of these "hot spots" can provide a quick and effective method to screen a particular isolate for resistance.

Drug resistant mutations do not provide the bacterium with a selective advantage over sensitive strains unless exposed to the resistant drug (15). However, when exposure does occur, the sensitive strains are killed and the residual drug resistant bacteria that survive continue to multiply. This process is the pre-dominant method of the development of MDR-TB (15). Since rifampin and isoniazid are often used in conjunction (3), bacteria resistant to both drugs (MDR-TB) are selected for when these two drugs are misused. When a patient fails to comply with a treatment or when a physician incorrectly adjusts treatment, such as adding a single drug to a failing regimen, sensitive strains can become MDR-TB (16). To counteract this event, DOTS has been implemented to prevent the development of MDR-TB through patient adherence and confirmation of correct antibiotic therapy.

2.1 Rifampin

Rifampin is one of the first line drugs used in treating tuberculosis. Resistance to this drug is extensively studied and well-characterized. Rifampin interferes with transcription by targeting the RNA polymerase and preventing the elongation of full-length transcripts (17). A previous study using

rifampin on *Escherichia coli* has demonstrated that rifampin specifically interacts with the beta subunit and mutations in the gene which encode it, *rpoB*, created a conformational change that weakens the binding of the antibiotic (18). Mutations which confer resistance to rifampin are found almost exclusively in the *rpoB* gene. Furthermore, these mutations are mostly confined to a small 81 base pair region, known as the core region or the rifampin resistance determining region, that spans from codon 507 to codon 533 (19, 20, 44, 45). Mutations in codon 533 have been disputed to have a varying effect on resistance to rifampin. However, a recent study of rifampin resistant isolates has determined that mutations in codon 533 were not associated with resistance (47). In a study where the rifampin resistance determining region was sequenced from 242 MDR-TB isolates, 61.2% had a mutation in codon 531, 19.4% in codon 526, and 7.4% in codon 516 (21). 9 isolates (3.7%) had no mutations within the rifampin resistance determining region (21). Rifampin discordant isolates are hypothesized to have mutations in the other subunits of the RNA polymerase enzyme or in genes that affect the permeability of rifampin (19).

2.2 Isoniazid

Isoniazid is commonly used with rifampin in tuberculosis treatment. Unlike rifampin, the isoniazid pathway contains many enzymes that affect its ability to kill *M. tuberculosis*. When isoniazid enters the bacteria, it must first be converted into an active form by the catalase-peroxidase enzyme, KatG (22). Since KatG is the only enzyme capable of activating isoniazid, a loss of function could provide resistance by preventing the activation. When a functional KatG was transformed into isoniazid resistant strains of *Mycobacterium smegmatis*, it was noted that susceptibility to the antibiotic was restored (23). Although mutations can occur throughout *katG*, mutations in codon 315 are the most common. In one study, the authors analyzed the *katG* gene of 85 isoniazid resistant isolates and found that 49 (58%) of the isolates had mutations within codon 315 (24). Additionally, a second study reported 68% of isoniazid resistant isolates from Africa had mutations in the same codon (25). Aslan et. al has also reported mutations in codon 279, which was found in 4 of 30 isoniazid resistant strains (48). The loss of function

of the bacterial catalase-peroxidase enzyme is a trade off—the bacterium becomes resistant to isoniazid, but is unable to detoxify peroxides. Thus, complete loss of function is rare and mutations which create a balance between resistance and detoxification are selected for. It is thought that mutations within codon 315 are common because the resulting inhibition of the enzyme provides sufficient resistance and detoxification at the same time (26).

AhpC is an enzyme that when overexpressed, is able to replace KatG loss of function. Insertion of a multi copy plasmid containing *ahpC* into *M. tuberculosis* resulted in an increased resistance to cumene hydroperoxide (27). However, the selective pressure for developing *ahpC* mutations ultimately depends on the residual activity of KatG (28). Mutations which upregulate the expression of this enzyme occur in the promoter region. Two transitions, a C/T and a G/A at nucleotide positions -39 and -46 respectively, are the most observed mutations (9).

InhA, an enoyl-ACP reductase involved in the synthesis of fatty acids, is the target for activated isoniazid. When isoniazid becomes activated, isonicotinic acyl-NADH is formed, which the enzyme has a higher affinity for than its cofactor, NADH (29). Musser et al. analyzed the *inhA* gene of isoniazid resistant isolates and found that 11 out of 51 isolates contained a C/T transition at nucleotide position -15 (24). Because the mutations were located in the promoter region of the gene, it was hypothesized that *inhA* could be overexpressed, which would elevate drug target levels and cause resistance through a drug titration mechanism (26). Mduli et al. inserted a single copy integrating vector containing the promoter region of *inhA* with mutations in nucleotide positions -8 and -15 into *M. tuberculosis* and found a slight increase to isoniazid resistance (30).

2.3 Fluoroquinolones

Fluoroquinolones are considered second line drugs and are crucial for the treatment of MDR-TB. The mechanism of action for fluoroquinolones is that it inhibits the supercoiling and relaxation performed by the enzyme DNA gyrase. This enzyme is comprised of two types of subunits, A and B, which are

encoded by *gyrA* and *gyrB* respectively. Mutations within these two genes are thought to interfere with radical interaction between the enzyme and the antibiotic (31). Similar to *rpoB*, *gyrA* contains a "hot spot" for resistance conferring mutations known as the Quinolone Resistance Determining Region (QRDR), with the most common occurring in codons 88 to 95 (32). Although mutations were frequently found in codon 95, no relationship was found between those mutations and fluoroquinolone resistance (33). Instead, the presence or absence of mutations in codon 95 is used as genetic marker to divide the *M. tuberculosis* complex into three different lineage groups (34). Resistance conferring mutations are primarily found in the *gyrA* gene; 42-85% of fluoroquinolone resistant clinical isolates contained mutations within *gyrA* (26). Sequencing of the *gyrA* gene from 95 clinical isolates showed a mutation distribution of 56.8% in codon 94, 25.3% in codon 90, and 6.3% in codon 91 (35).

While most mutations that confer fluoroquinolone resistance occur in *gyrA*, the proportion of clinical isolates which contain *gyrB* mutations has been increasing. Many mutations have been documented through the sequencing of *gyrB*. However, only two codons have been proven to confer resistance to fluoroquinolones: Codons 510 and 512 (36, 37). Mutations in codon 510 provided a 4-fold increase in resistance (36). Additionally, mutations in codon 512 had a 2.5 to 36-fold increase in the concentration of fluoroquinolone needed to inhibit the enzymatic activity of DNA gyrase by half. (37).

2.4 Aminoglycosides

The aminoglycosides are a group of second line antibiotics that include kanamycin, amikacin, and capreomycin. These antibiotics inhibit the synthesis of protein in the bacteria. Mutations which confer resistance to the aminoglycosides are mostly found in the *rrs* gene, which encodes for the 16s rRNA. Mutations in three nucleotide positions within the *rrs* gene have been associated with resistance: 1401, 1402, and 1484. Depending on the location, a mutation within these nucleotide positions provides a unique resistance profile in terms of which of the aminoglycosides it confers resistance to. Mutations in 1401 have been associated with amikacin and kanamycin resistance (38, 39). In addition, 1402 mutations

are associated with kanamycin resistance and mutations in position 1484 confer resistance to kanamycin and capreomycin (39).

Using transposon mutagenesis, Maus et. al has found a new gene linked to capreomycin resistance, *tlyA*, which encodes for a rRNA methyl transferase (40). Susceptibility to capreomycin was restored in transposon mutants when complemented with *tlyA* (40). Spontaneous mutations within *tlyA* found in capreomycin resistant strains of *M. tuberculosis* consisted mostly of SNPs that were found in various nucleotide positions across the structural gene (40). It is hypothesized that loss of *tlyA* function would create un-methylated ribosomes, which capreomycin would be unable to interact with (40).

The gene *eis* encodes for an aminoglycoside acetyltransferase and has several important properties. When the *M. tuberculosis eis* gene was introduced to *Mycobacterium smegmatis*, which lacks *eis*, a 5-10 fold increase in intracellular survival was observed when phagocytosed by the human macrophage cell line U-937 (41). Secondly, mutations within the promoter region of the gene have been linked to kanamycin resistance (42). Overexpression of this enzyme allows for the acetylation of kanamycin, which in turn, inactivates the antibiotic (42). Sequence analysis of 42 kanamycin resistant clinical isolates revealed mutations in 4 nucleotide positions of the *eis* promoter: -10, -12, -14, and -37 (42).

CHAPTER 3

MATERIALS AND METHODS

3.1 Isolate Selection

A total of 407 isolates were collected from four different study sites and were provided by the University of California at San Diego: 123 isolates from the Philippines, 100 isolates from South Africa, 96 isolates from India, and 88 isolates from Moldova. Isolates were chosen based on convenience sampling. Drug susceptibility test data from a bank of clinical isolates were examined and isolates for this study were selected to maximize the diversity of drug resistance patterns. The sample contained a small selection of isolates that were determined to be pan-susceptible to rifampin, isoniazid, fluoroquinolones, and aminoglycosides through drug susceptibility testing for the purposes of reference and control.

3.2 DNA Extraction

DNA extraction of *M. tuberculosis* was performed by a method developed by van Sooligen et. al with minor modifications (43).

Isolates were grown on Löwenstein Jensen medium. Several loopfuls of bacteria were collected on wooden applicator sticks and transferred to a micro-centrifuge tube. The bacteria were then killed through exposure of ethanol and heat. Samples were centrifuged for 5 minutes at 12,000g and lysozyme (50 µl of 10 mg/ml) was added to each sample and incubated at 37° C overnight. The samples were collected and sodium dodecyl sulfate (75 µl; 10%) and proteinase K (5 µl; 10 mg/ml) was added and incubated for 10 minutes at 65°C. After incubation, 5M NaCl (100µl) and CTAB/NaCL solution (100 µl; 0.7M NaCl, 274mM CTAB) was added and incubated for another 10 minutes at 65°C. A volume of chloroform/isoamyl alcohol (750 µl; 24:1) was added to the samples and centrifuged for 5 minutes at 12,000g. The supernatant was collected and isopropanol (450 µl) was used to precipitate the nucleic

acids. Each sample was then incubated at -20°C for 30 minutes and centrifuged for 15 minutes at 12,000g. The supernatant above the pellet of DNA was discarded and 70% ethanol was added (750 µl). The samples were then centrifuged for 5 minutes at 12,000g and the supernatant was again discarded, with a slight volume above the pellet remaining. After a final centrifugation of 1 minute at 12,000g, the last of the supernatant was removed and the samples were allowed to air dry for 30 minutes. The DNA was then dissolved into sterile distilled water.

3.3 Polymerase Chain Reaction (PCR)

All genes were amplified using real-time PCR, with the exception of *tlyA*, which was amplified using conventional PCR because of the large amplicon size.

3.3.1 Real-time PCR

PCRs were performed with 2x LightCycler 480 SYBR Green I Master (Roche), .4 µM each of forward and reverse primers (Table 3.1), and 10 ng of *M. tuberculosis* genomic DNA. The reactions began with an initial denaturation at 95°C for 5 min and were followed by 45 cycles of amplification consisting of denaturation at 95°C for 10 sec, an annealing temperature based on the primer set (Table 3.1) for 10 sec, and extension at 72°C for 10 sec. These reactions were conducted in a Roche Lightcycler 480 II Real-Time PCR Instrument. For each run, a positive control (H37rV) and a negative control (reaction mixture lacking genomic DNA) was included. Positive reactions resulted in a sigmoid curve of fluorescence signal and negative reactions showed no increase in fluorescence. Fluorescence curves were analyzed using the second derivative maximum method to determine the crossing point.

3.3.2 Conventional PCR

Conventional PCR for amplification of the *tlyA* gene was performed using 2x TopTaq Master Mix (Qiagen), 4 µM each of forward and reverse primers (Table 3.1), and 10 ng of *M. tuberculosis* genomic DNA. The reactions began with an initial denaturation for 95°C for 5 min and were followed by

45 cycles of amplification consisting of denaturation at 95°C for 60 sec, an annealing temperature at 55° for 60 sec, and extension at 72°C for 90 sec. Reactions were conducted in a Perkin Elmer Cetus DNA Thermal Cycler. For each run, a positive control (H37rV) and a negative control (reaction mixture lacking genomic DNA) was included.

3.4 Gel Electrophoresis

Gel electrophoresis of PCR products amplified through conventional PCR was performed on a 2% agarose gel with ethidium bromide (500 ng/ml). 8 µl of PCR products were mixed with 2 µl of 5x nucleic acid sample loading buffer (Bio-Rad) before loading. Positive reactions contained a fluorescent band after exposure to ultraviolet light while negative reactions lacked the presence of a band.

3.5 Purification of PCR Products

3.5.1 Purification of Real-Time PCR Products

Real-time PCR products were purified using the MinElute 96 UF PCR purification kit (Qiagen). 20 µl of distilled water was used to elute the products.

3.5.2 Purification of Conventional PCR Products

Reactions amplified through conventional PCR were purified using silica membrane spin columns from the QIAquick PCR purification kit (Qiagen). 30 µl of distilled water was used to elute the products.

3.6 DNA Sequencing

DNA sequencing was performed by the Advanced Studies of Genomics, Proteomics, and Bioinformatics at the University of Hawaii at Manoa using an Applied Biosystems 3730 XL Analyzer in conjunction with BigDye Terminator v3.1 Cycle Sequencing Kit. Forward primers were used for sense sequencing of the product, with the exception of *tlyA*, which was assembled via primer walking. The

chromatograms were scored by the ABI base caller with the sensitivity set at Q20. Any bases scored as "N" were visually read and a base letter was assigned or if the chromatogram was unclear, the sequencing was repeated as necessary.

3.7 Drug Susceptibility Testing

Antibiotic resistance testing for each isolate was performed at the respective study site and resistance was determined using the proportion method (7). Two serial dilutions of standard suspension are made (10^{-3} mg/ml and 10^{-5} mg/ml) and 0.2 ml of each dilution is used to inoculate Löwenstein Jensen agar with variable antibiotic concentrations depending on the drug. The inoculated media are then incubated at 37° C for 28-40 days. After incubation, colonies are counted and a proportion is calculated by comparing resistant colonies to the colonies grown on media lacking the antibiotic. If the proportion exceeds a critical proportion, the isolate is classified as resistant. Likewise, if the proportion is lower than the critical proportion, the isolate is classified as sensitive.

Table 3.1 – Primers used for amplification of gene targets

Target	Primer Sequences (5'-3')	Annealing Temp. (°C)	Product Size (bp)
rpoB	CGTGGAGGCGATCACACCGCAGTT AGTGCGACGGGTGCACGTCGCGGACCT	60	215
gyrA	GGTGCTCTATGAAATGTTCG GCTTCGGTGTACCTCATCG	60	234
gyrB	CGATGTTCCAGGCGATACTT ATCTTGTGGTAGCGCAGCTT	60	163
rrs	GTAATCGCAGATCAGCAACG TTTTCGTGGTGCTCCTTAGAA	60	216
tlyA	GTCTCTGGCCGAACTCGAAG ATTGTCGCCCAATACTTTTTCTAC	60	1000
eis promoter	AAATTCGTCGCTGATTCTCG CGCGACGAAACTGAGACC	54	387
katG	CATGAACGACGTCGAAACAG CTCTTCGTCAGCTCCCACTC	55	270
inhA promoter	AGAAAGGGATCCGTCATGGT GTCACATTCGACGCCAAAC	55	340
ahpC promoter	CACTGCTGAACCACTGCTTT CAGTGGCATGACTCTCCTCA	55	196

3.8 Statistical Analyses

The data were analyzed using a chi-square test for differences. Chi-square values and p-values were calculated using EpiInfo v. 3.5.1. (CDC, Atlanta GA). All tests were two-tailed and p-values less than or equal to 0.05 were considered statistically significant.

For the calculation of chi-square values and p-values for differences in polymorphisms between study groups, only isolates that contained a resistance conferring mutation for the antibiotic of interest were counted towards the total, such that any isolates that lacked a mutation were excluded.

For the calculation of chi-square values and p-values for the differences in discordance between study groups, only isolates that displayed resistance to drug susceptibility testing for the antibiotic of interest were counted towards the total, such that any isolates that were sensitive to the drug were excluded.

CHAPTER 4

RESULTS

4.1 Distribution of Resistance Conferring Mutations

4.1.1 Pan-susceptible Isolates

Drug susceptibility testing (DST) data indicated that thirty one isolates were pan-susceptible to the four antibiotics groups. Sequencing of nine genes associated with drug resistance determined that twenty six of these isolates lacked any resistance conferring mutations, which is in agreement with the DST data. However, five of the isolates did contain at least one known resistance conferring mutation despite being classified as sensitive. These isolates were classified as reverse discordant isolates on the basis of being sensitive on exposure to a particular antibiotic but still containing a known resistance conferring polymorphism. The twenty six pan-susceptible isolates were excluded from the calculation of any proportions or percentages, reducing the total sample size to 381 (India: 96, Moldova: 82, Philippines: 110, South Africa: 93).

4.1.2 Rifampin Resistance

The 81 base pair region contained in the gene *rpoB* known as the rifampin resistance determining region was sequenced for all isolates (Table 4.1). The most prevalent mutation found within this region was TCG531TTG. This mutation appeared to divide the four study groups into two groups: A group with a large proportion of isolates containing the mutation; India and Moldova (79.2% and 78.0% respectively), and another group with a moderate proportion of isolates containing the mutation; the Philippines and South Africa (47.3%, 43.0%). Differences between study sites in the same group were not significant. However, the differences in the proportions of isolates containing the TCG531TTG mutation were significant when the India and Moldova group were combined and compared to the isolates of both the Philippines and South Africa group ($p < 0.001$). The Philippines isolates were also

found to have a large diversity of mutations in codon 526 with 7 different types of polymorphisms. Compared to the other study sites, South African isolates had a significantly higher proportion ($p < 0.001$) of isolates having mutations found in codon 516, which mostly consisted of GAC516GGC. All isolates from South Africa that contained this type of mutation had an additional mutation, CTG533CGG.

Table 4.1 – Distribution of mutations found in the rifampin resistance determining region

		IN		**MD**		**PH**		**ZA**	
Polymorphism	Codon	n	%	n	%	n	%	n	%
CTG/CCG	511	-	-	-	-	1	0.9	-	-
AGC/ACC	512	-	-	-	-	1	0.9	-	-
CAA/AAA	513	2	2.1	-	-	2	1.8	1	1.1
CAA/CCA	513	1	1.0	-	-	-	-	-	-
ATG/ATA	515	1	1.0	-	-	-	-	-	-
GAC/GGC	516	-	-	-	-	1	0.9	33	35.5
GAC/GTC	516	4	4.2	11	13.4	2	1.8	8	8.6
GAC/TAC	516	-	-	2	2.4	2	1.8	-	-
TCG/TTG	522	-	-	-	-	2	1.8	-	-
CAC/TAC	526	3	3.1	-	-	10	9.1	7	7.5
CAC/TGC	526	1	1.0	-	-	3	2.7	-	-
CAC/AAC	526	1	1.0	-	-	-	-	-	-
CAC/CTC	526	-	-	1	1.2	3	2.7	-	-
CAC/GAC	526	-	-	-	-	4	3.6	-	-
CAC/GGC	526	-	-	-	-	1	0.9	-	-
CAC/CGC	526	-	-	-	-	8	7.3	-	-
CAC/CCC	526	-	-	-	-	1	0.9	-	-
TCG/TTG	531	76	79.2	64	78.0	52	47.3	40	43.0
TCG/TGG	531	-	-	1	1.2	5	4.5	-	-
CTG/CCG	533	-	-	-	-	1	0.9	34	36.6
No mutation	-	8	8.3	3	3.7	14	12.7	4	4.3

IN, India; MD, Moldova; PH, Philippines, ZA, South Africa

4.1.3 Isoniazid Resistance

A large portion of isolates from all four study groups had AGC315ACC mutations in the gene *katG* (Table 4.2). This mutation was the most prevalent in isolates from Moldova with all isolates containing the mutation. The Moldova study group was found to have a significantly higher proportion of isolates containing the AGC315ACC mutations compared to the rest of the study groups ($p \leq 0.05$). A second type of mutation that has been linked to isoniazid resistance (49), GGC279GAC, was not observed in any isolates.

T-8A, T-8C, and C-15T mutations were found in the promoter of *inhA* (Table 4.3). Although T-8A mutations were rarely found in isolates from India and not found in Moldova and the Philippines, 35 isolates (37.6%) from South Africa had the mutation. Additionally, the T-8C mutation was rarely found in India and Moldova, but not found in the Philippines or South Africa. The most common mutation was C-15T, which was found in all four study groups. The differences in the proportions of isolates containing C-15T mutations in the four study groups were found to be significant ($p = 0.001$).

ahpC promoter mutations were only found in isolates from India (Table 4.4). 18 out of 96 Indian isolates (18.8%) had a G-48A mutation.

Table 4.2 – Distribution of mutations found in *katG*

		IN		**MD**		**PH**		**ZA**	
Polymorphism	Codon	n	%	n	%	n	%	n	%
AGC/ACC	315	75	78.1	82	100.0	64	58.2	84	90.3
No mutation	-	21	21.9	-	-	46	41.8	9	9.7

Table 4.3 – Distribution of mutations found in the promoter of *inhA*

		IN		**MD**		**PH**		**ZA**	
Polymorphism	Nucleotide	n	%	n	%	n	%	n	%
T/A	-8	2	2.1	-	-	-	-	35	37.6
T/C	-8	5	5.2	2	2.4	-	-	-	-
C/T	-15	17	17.7	40	48.8	34	31.0	32	34.4
No mutation	-	72	75.0	40	48.8	76	69.0	26	28.0

Table 4.4 – Distribution of mutations found in the promoter of *ahpC*

		IN		**MD**		**PH**		**ZA**	
Polymorphism	Nucleotide	n	%	n	%	n	%	n	%
G/A	-46	18	18.8	-	-	-	-	-	-
No mutation	-	78	81.3	82	100.0	110	100.0	93	100.0

4.1.4 Fluoroquinolone Resistance

The quinolone resistance determining region of the gene *gyrA* was sequenced for all isolates (Table 4.5). GCG90GTG mutations were found in all study groups. South Africa was significantly different to India ($p = 0.041$) and Moldova ($p < 0.001$), but not to the Philippines. Likewise, India was significantly different to Moldova ($p < 0.001$), but not to the Philippines. TCG91CCG mutations were rare and only found in isolates from India and Moldova. Codon 94 mutations were the most commonly found, with India having the highest proportion (67.6%), Moldova and South Africa having medial values (42.7%, 44.1%, respectively), and the Philippines having the lowest amount (17.3%). The differences in proportions of codon 94 were significantly different when India was compared to Moldova ($p = 0.049$) and South Africa ($p < 0.001$), but not to the Philippines.

gyrB mutations were extremely rare; only 3 Indian isolates (3.1%) and 1 Moldova isolate (1.1%) had a mutation in *gyrB* (Table 4.6). The two types of mutations found were AAC510ACC and GCG515GTG.

Table 4.5 – Distribution of mutations found in the quinolone resistance determining region of *gyrA*

		IN		**MD**		**PH**		**ZA**	
Polymorphism	Codon	n	%	n	%	n	%	n	%
GCG/GTG	90	16	16.7	18	22.0	14	12.7	41	44.1
TCG/CCG	91	1	1.0	3	3.7	-	-	-	-
GAC/AAC	94	10	10.4	3	3.7	1	0.9	8	8.6
GAC/CAC	94	2	2.1	2	2.4	-	-	-	-
GAC/TAC	94	3	3.1	8	9.8	4	3.6	1	1.1
GAC/GCC	94	13	13.5	7	8.5	1	0.9	3	3.2
GAC/GGC	94	37	38.5	15	18.3	13	11.8	30	32.3
AGC/ACC	95	89	92.7	82	100.0	108	98.2	92	98.9
No mutation	-	14	14.6	26	31.7	78	70.9	10	10.8

Table 4.6 – Distribution of mutations found in *gyrB*

		IN		**MD**		**PH**		**ZA**	
Polymorphism	Codon	n	%	n	%	n	%	n	%
AAC/ACC	510	1	1.0	1	1.2	-	-	-	-
GCG/GTG	515	2	2.1	-	-	-	-	-	-
No mutation	-	93	96.9	81	98.8	110	100.0	93	100.0

4.1.5 Aminoglycoside Resistance

A1401G mutations in the gene *rrs* were highly prevalent in isolates from South Africa and India and were less observed in isolates from Moldova and the Philippines (Table 4.7). Moldova was significantly different from all other study groups ($p < 0.001$). Additionally, India was significantly different from South Africa ($p = 0.041$), but not to the Philippines. No mutations were found in

nucleotide position 1402 and G1484T mutations were rarely found in isolates from India and Moldova only.

Most of the isolates within the study sites contained no mutations in the promoter of *eis*, with the exception of Moldova, in which a large proportion of isolates (48.8%) had a C-12T mutation that was unique to the Moldova isolates (Table 4.8). Furthermore, two rare types of mutations were observed and were specific to one or two study sites: G-10A (Moldova and Philippines) and G-37T (India and Philippines). C-14T mutations were found at a higher proportion than the previous two among isolates from India, Moldova, and South Africa.

The entire structural gene of *tlyA* was sequenced, but no known resistance associated mutations were observed.

Table 4.7 – Distribution of mutations found in *rrs*

		IN		**MD**		**PH**		**ZA**	
Polymorphism	Nucleotide	n	%	n	%	n	%	n	%
A/G	1401	66	68.8	21	25.6	18	16.4	84	90.3
G/T	1484	2	2.1	1	1.2	-	-	-	-
No mutation	-	28	29.2	60	73.2	92	83.6	9	9.7

Table 4.8 – Distribution of mutations found in the promoter of *eis*

		IN		**MD**		**PH**		**ZA**	
Polymorphism	Nucleotide	n	%	n	%	n	%	n	%
G/A	-10	-	-	3	3.7	1	0.9	-	-
C/T	-12	-	-	40	48.8	-	-	-	-
C/T	-14	5	5.2	6	7.3	-	-	1	1.1
G/T	-37	1	1.0	-	-	1	0.9	-	-
No mutation	-	90	93.8	33	40.2	108	98.2	92	98.9

4.2 Identification and Distribution of Discordant and Reverse Discordant Isolates

Sequence data and DST data was compared and each isolate was classified into four different groups (Table 4.9). When an isolate had agreement between sequence data and DST, it was classified as either susceptible or resistant based on whether it contained a known marker for resistance and showed resistance upon exposure to a particular antibiotic. Alternatively, if an isolate did not contain a marker for resistance but still displayed growth on exposure, it was classified as discordant. Similarly, if an isolate contained a marker for resistance but was susceptible, it was classified as reverse discordant.

The average discordant rate for rifampin was the lowest among on the four antibiotic groups. Differences in the discordance proportions for rifampin between study groups were not significant. The total isoniazid and aminoglycoside discordance frequencies were comparable. However, these frequencies differ between study groups. Moldova had discordance proportions for isoniazid that were significantly different from India ($p = 0.011$) and the Philippines ($p < 0.001$), but not South Africa. The Philippines also had isonizaid discordance frequencies that were significantly different from South Africa ($p = 0.004$), but not to India. Similar to rifampin, no significant differences in aminoglycoside discordance were found between the four study groups. Discordant frequencies were found to be the highest in the fluoroquinolones. India was significantly different from Moldova ($p = 0.01$) and the Philippines ($p < 0.001$), but not to South Africa. South Africa was also significantly different from Moldova ($p = 0.002$) and the Philippines ($p < 0.001$). Fluoroquinolone resistance DST data were not available for 28 isolates from the Philippines. Therefore, these isolates could not be identified as discordant or reverse discordant and discordant percentages for fluoroquinolone resistance in the Philippines may be misrepresentative.

45 out of the 381 isolates (11.8%) contained at least one reverse discordance (Table 4.11). Of this 45, 5 isolates were determined to be pan-susceptible through DST, but still contained a mutation known to confer resistance. Reverse discordances were the lowest among rifampin and stable between

isoniazid and the fluoroquinolones. The frequency of reverse discordances was the highest in the aminoglycosides due to Moldova isolates having a large proportion of non-agreement between aminoglycoside markers and drug testing. Between study sites, Moldova accounted for the majority of reverse discordant isolates with 32 of the 48 (66.7%) reverse originating from Moldova. Interestingly, no reverse discordant isolates were found in South Africa.

Table 4.9 – Distribution and classification of isolates into four groups

	IN		**MD**		**PH**		**ZA**		**Total**	
Drug	n	%	n	%	n	%	n	%	n	%
Rifampin										
Susceptible	4	4.2	-	-	9	8.2	1	1.1	14	3.7
Resistant	88	91.7	78	95.1	91	82.7	89	95.7	346	90.8
Discordant	4	4.2	3	3.7	6	5.5	3	3.2	16	4.2
Reverse	-	-	1	1.2	4	3.6	-	-	5	1.3
Isoniazid										
Susceptible	-	-	-	-	5	4.5	-	-	5	1.3
Resistant	83	86.5	81	98.8	85	77.3	90	96.8	339	89.0
Discordant	9	9.4	-	-	17	15.5	3	3.2	29	7.6
Reverse	4	4.2	1	1.2	3	2.7	-	-	8	2.1
Fluoroquinolones										
Susceptible	4	4.2	7	8.5	35	31.8	5	5.4	51	13.4
Resistant	82	85.4	48	58.5	26	23.6	83	89.2	239	62.7
Discordant	10	10.4	19	23.2	19	17.3	5	5.4	53	13.9
Reverse	-	-	8	9.8	2	1.8	-	-	10	2.6
No Data	-	-	-	-	28	25.5	-	-	28	7.3
Aminoglycosides										
Susceptible	4	4.2	11	13.4	85	77.3	-	-	100	26.2
Resistant	73	76.0	41	50.0	19	17.3	85	91.4	218	57.2
Discordant	19	19.8	5	6.1	5	4.5	8	8.6	37	9.7
Reverse	-	-	25	30.5	1	0.9	-	-	26	6.8

4.3 Identification and Distribution of Multidrug Discordant and Reverse Discordant Isolates

After determining the resistance profile for rifampin, isoniazid, fluoroquinolones, and aminoglycosides, each isolate was further classified as multidrug discordant and multidrug reverse discordant if it contained more than one discordances across antibiotic groups (Table 4.10 and Table 4.11). The number of isolates with discordances for the four antibiotic groups was stable across study sites with the exception of South Africa, which showed a high level of agreement between sequence data and DST data. Multidrug reverse discordances were found to be rare with only 3 out of the 381 isolates containing more than 1 discordance.

Table 4.10 – Multidrug discordance frequencies

	IN		**MD**		**PH**		**ZA**	
No. of Discordances	n	%	n	%	n	%	n	%
0	64	66.7	58	70.7	73	66.4	81	87.1
1	25	26.0	22	26.8	32	29.1	7	7.5
2	5	5.2	1	1.2	2	1.8	4	4.3
3	1	1.0	1	1.2	2	1.8	-	-
4	1	1.0	-	-	1	0.9	1	1.1

Table 4.11 – Reverse discordance frequencies by resistance profile and study site

	IN		MD		PI		ZA		Total (by Drug)	
Reverse Discordance	n	%	n	%	n	%	n	%	n	%
RIF	-	-	-	-	2	4.4	-	-	2	4.4
FQL	-	-	7	15.6	1	2.2	-	-	8	17.8
AMI	-	-	24	53.3	1	2.2	-	-	25	55.6
INH	4	8.9	-	-	3	6.7	-	-	7	15.6
RIF + FQL	-	-	-	-	1	2.2	-	-	1	2.2
RIF + INH	-	-	-	-	1	2.2	-	-	1	2.2
RIF + FQL + AMI + INH	-	-	1	2.2	-	-	-	-	1	2.2
Total (by Study Site)	4	8.9	32	71.1	9	20.0	-	-	45	100.0

4.4 Identification of Shared Types Between Isolates

To determine the diversity of drug resistance and polymorphisms found in the four study groups, isolates were typed using a constructed profile that was based on antibiotic resistance (susceptible, resistant, discordant, or reverse discordant) and the polymorphisms found within the nine genes. Each profile was then compared to other isolates and the amount of isolates that shared the exact same profile were counted (Table 4.12, 4.13, 4.14 and 4.15).

Table 4.12 – Shared types between isolates from India

	Resistance Pattern				Sequence Pattern							
n	RIF	FQL	AMI	INH	rpoB	gyrA	gyrB	Rrs	eis	katG	inhA	ahpC
14	R	R	R	R	531TTG	94GGC		1401G		315ACC		
8	R	R	R	R	531TTG	90GTG		1401G		315ACC		
4	R	D	R	R	531TTG			1401G		315ACC		
4	R	R	R	R	531TTG	94GGC		1401G		315ACC	-15T	
4	S	S	S	RD								-46A
3	R	R	D	R	531TTG	94GGC				315ACC		
3	R	R	R	D	531TTG	94AAC		1401G				
3	R	R	R	R	531TTG	94AAC		1401G		315ACC		
3	R	R	R	R	531TTG	94GGC		1401G		315ACC	-8C	
3	R	R	R	R	531TTG	94GCC		1401G		315ACC		
2	R	R	D	R	531TTG	94GGC				315ACC	-15T	
2	R	R	R	R	531TTG	94GGC			-14T	315ACC	-15T	
2	R	R	R	R	531TTG	94GGC		1401G		315ACC	-8A	

S, Susceptible; R, Resistant; D, Discordant; RD, Reverse discordant

Table 4.13 – Shared types between isolates from Moldova

	Resistance Pattern				Sequence Pattern							
n	RIF	FQL	AMI	INH	rpoB	gyrA	gyrB	Rrs	Eis	katG	inhA	ahpC
6	R	D	RD	R	531TTG				-12T	315ACC	-15T	
3	R	R	RD	R	531TTG	94TAC			-12T	315ACC	-15T	
3	R	R	RD	R	531TTG	94GGC			-12T	315ACC	-15T	
3	R	R	RD	R	531TTG	94GCC			-12T	315ACC	-15T	
3	R	S	R	R	531TTG				-12T	315ACC	-15T	
2	R	D	R	R	531TTG			1401G		315ACC		
2	R	D	S	R	531TTG					315ACC		
2	R	D	S	R	516GTC					315ACC		
2	R	R	R	R	531TTG	94TAC		1401G	-12T	315ACC	-15T	
2	R	R	R	R	531TTG	94GGC			-12T	315ACC	-15T	
2	R	R	R	R	531TTG	94GCC		1401G		315ACC		
2	R	R	R	R	531TTG	90GTG		1401G		315ACC		
2	R	R	RD	R	531TTG	90GTG			-12T	315ACC	-15T	
2	R	R	RD	R	531TTG	94AAC			-12T	315ACC	-15T	
2	R	R	S	R	516GTC	91CCG				315ACC		
2	R	RD	R	R	531TTG	94GGC		1401G		315ACC		
2	R	RD	R	R	531TTG	90GTG		1401G		315ACC		

Table 4.14 – Shared types between isolates from the Philippines

	Resistance Pattern				Sequence Pattern							
n	RIF	FQL	AMI	INH	rpoB	gyrA	gyrB	rrs	eis	katG	inhA	ahpC
8	R	S	S	R	531TTG					315ACC		
5	R	ND	R	R	531TTG			1401G		315ACC		
5	R	ND	S	R	531TTG					315ACC		
4	R	D	S	R	531TTG					315ACC		
4	R	R	S	R	531TGG	94GGC				315ACC		
3	R	S	R	R	531TTG			1401G		315ACC		
3	R	S	S	D	531TTG							
2	R	R	R	D	526CGC	90GTG		1401G				
2	R	R	S	R	531TTG	90GTG					-15T	
2	R	S	S	R	531TTG						-15T	
2	R	ND	R	R	526CGC			1401G			-15T	
2	R	ND	S	D	531TTG							
2	R	ND	S	R	526TAC						-15T	
2	R	ND	S	R	531TTG						-15T	
2	S	D	S	S								
2	S	S	S	R							-15T	

Table 4.15 – Shared types between isolates from South Africa

	Resistance Pattern				Sequence Pattern							
n	RIF	FQL	AMI	INH	rpoB	gyrA	gyrB	Rrs	eis	katG	inhA	ahpC
33	R	R	R	R	516GGC/533CCG	90GTG		1401G		315ACC	-8A	
11	R	R	R	R	531TTG	94GGC		1401G		315ACC	-15T	
9	R	R	R	R	531TTG	94GGC		1401G		315ACC		
5	R	R	R	R	526TAC	94GGC		1401G		315ACC	-15T	
3	R	R	R	R	516GTC	94AAC		1401G		315ACC		
3	R	R	R	R	531TTG	94GCC		1401G			-15T	
2	R	D	R	R	531TTG			1401G		315ACC	-15T	
2	R	R	R	R	516GTC	94GGC		1401G		315ACC		
2	R	R	R	R	531TTG	90GTG		1401G		315ACC	-15T	
2	R	R	R	R	531TTG	94AAC		1401G		315ACC	-15T	
2	R	S	R	R	516GTC			1401G		315ACC		

Table 4.16 – Unique type total by study groups

Study Group	Unique Types	%
India	54	56.3
Moldova	57	69.5
Philippines	77	70.0
South Africa	30	32.3
All	198	52.0

CHAPTER 5

DISCUSSION

Current drug susceptibility testing for *M. tuberculosis* is a lengthy and rarely performed process that is necessary for the proper treatment and detection of drug resistant tuberculosis (8). Novel alternative diagnostic techniques such as the sequencing of genes associated with resistance can be used to efficiently determine the resistance profile of a particular isolate. However, before this technique can be used, resistance associated mutations must be known. The distribution of the different types of mutations, as well as the locations within the drug target of clinical isolates is important to establish a base of expected results when using sequences for diagnostic tests. By observing the frequency of the type and location of a particular mutation or group of mutations, rapid laboratory procedures such as real-time PCR and line test, such as the Hain test, can be used to quickly assess several resistances.

One drawback on relying on mutations for the determination of phenotypic resistance is that mutations that confer resistance can occur in many different genes and not all mutations have been documented. Therefore, some isolates may be classified as susceptible when in fact a mutation that confers resistance is present. Isolates may also utilize different resistance methods such as efflux pumps or drug permeation, instead of the alteration of drug targets. Discordant isolates which show resistance upon drug exposure but contain no known resistance conferring mutation can provide an estimate of the sensitivity of a sequence based diagnostic test using the nine genes.

Another drawback is that mutations often have differential impacts on the minimum inhibitory concentration. Thus, despite having a mutation, isolates can still be falsely classified as resistant if the mutation had only a slight effect on the minimum inhibitory concentration. Similar to discordant isolates, reverse discordant isolates which contain a known resistance conferring mutation but is susceptible to the drug can provide an estimate of the specificity.

5.1 Polymorphism, Discordant, and Reverse Discordant Frequencies to Four Antibiotic Groups

5.1.1 Rifampin

The distribution of resistance conferring mutations within the rifampin resistance determining region was consistent with a similar study performed by Luo et al., who found that most mutations occurred in codon 531 (61.2%) (21). The most prevalent mutation, TCG531TTG, divided the four study sites into two significantly different groups. The India and Moldova group had a significantly higher proportion of this mutation compared to the Philippines and South Africa group. Interestingly, a distinct resistance pattern consisting of GAC516GGC and CTG533CGG mutations occurred in a large proportion of South African isolates (36.6%). This pattern was unusual since almost all other isolates contained only a single mutation within the region. Because mutations are selected for under evolutionary pressure, the South African isolates may be under a unique pressure to develop these double mutations. However, the effect of CTG533CGG has been inconsistent across several studies and may not confer resistance or is thought to confer a low level of resistance (47).

Despite having only one gene tested for resistance to rifampin, discordant frequencies was the lowest among this antibiotic suggesting that rifampin resistance is highly associated with *rpoB*, especially within the rifampin resistance determining region. Rifampin reverse discordant frequencies was also the lowest of the antibiotic groups indicating that sequence based tests for rifampin has the highest sensitivity and specificity of the four antibiotic groups. Discordance rates for rifampin were not found to be significantly different between all study groups, indicating that rifampin discordance was stable between geographic locations.

5.1.2 Isoniazid

Isoniazid resistance was largely due to the presence of AGC315ACC mutations within *katG*. This mutation was found in a significantly higher proportion of isolates from Moldova compared to the rest of the study sites. Although the AGC315ACC mutation is strongly associated with isoniazid

resistance, this mutation contributed to a large proportion of isoniazid reverse discordant isolates (37.5%). Despite the large proportion of *katG* AGC315ACC mutations, 31 out of the 339 isolates resistant to isoniazid (9.1%) contained a wild-type *katG* but a mutation in the *inhA* promoter. Thus, inclusion of the *inhA* promoter increased the sensitivity of determining isoniazid resistance by 8.4%. *ahpC* promoter mutations were only found 18 isolates, all originating from India (18.8%), which may be a regional anomaly. This data is in agreement with the findings of Sreevatsan et al. that *ahpC* promoters are rarely found in clinical isolates (28). Of the isoniazid resistant isolates from India, 3 (3.6%) had a wild type *katG* and *inhA* promoter which indicates that inclusion of the *ahpC* promoter would only slightly increase the sensitivity by 3.2%. However, four isolates also had *ahpC* promoter mutations without mutations in *katG* and *inhA*, but still displayed susceptibility to isoniazid. Sequencing of the *ahpC* promoter may not be necessary for isolates originating in South Africa, Philippines, and Moldova, since no *ahpC* promoter mutations were found in those study sites.

Discordance for isoniazid was the second lowest of the four antibiotic groups with 7.6% of all isolates being discordant. However, reverse discordance for isoniazid was only the third lowest with 2.1% being reverse discordant, which may be due to errors in drug susceptibility testing as indicated by the strong relationship between *katG* AGC315ACC mutations and isoniazid resistance. Moldova had the lowest isoniazid discordance frequency of the four study groups; no isolates from Moldova were found to be discordant. This low frequency was found to be significantly different to India and the Philippines, but not to South Africa. The Philippines had the highest discordance frequency compared to the rest of the study groups and was significantly different compared to the South Africa study group but not to India.

5.1.3 Fluoroquinolones

All 237 isolates classified as fluoroquinolone resistant had a mutation within *gyrA* indicating a strong association between fluoroquinolone resistance and *gyrA*. *gyrB* mutations were rarely found (1.0%) and were always in conjunction with a mutation in *gyrA*. Mutations in *gyrB* were not observed for

isolates originating from the Philippines and South Africa. The distribution of mutations within the quinolone resistance determining region of *gyrA* was comparable to other similar studies with a majority of the mutations occurring in codon 94 (35). Codon 94 mutations were found in a significantly higher proportion of isolates originating from India when compared to the South Africa and Moldova study group, but not to the Philippines. Although the evolutionary marker AGC95ACC mutation does not confer resistance to fluoroquinolones, only 14 isolates (3.6%) lacked this mutation. Thus, a great majority of the isolates in this study belong to either group 1 or group 2 of the *M. tuberculosis* evolutionary complex (34). Reverse discordances were found in only two types of mutations, GCG90GTG and GAC94GGC. However, these mutations were also found in isolates classified as resistant. An unknown mechanism or clerical error could be responsible for the differentiation of resistances between these two mutations and drug susceptibility testing should be re-done for these isolates.

The fluoroquinolones had the highest discordance frequency of the four antibiotics (14.3%), but the second lowest reverse discordance frequency (2.6%). Discordance rates were significantly higher in Moldova when compared to South Africa and India, but not to the Philppines. Similarly, the Philippines were also significantly different to South Africa and India. Thus, fluoroqunilone discordance split the four study sites into two groups, a group with a higher frequency (Moldova and the Philippines) and a group with a lower frequency (South Africa and India).

5.1.3 Aminoglycosides

Mutations within the gene *rrs* accounted for a large portion of aminoglycoside resistance. The A1401G mutation was found to be the dominant mutation in *rrs* with only three isolates of all *rrs* mutation containing isolates having a G1484T mutation (1.6%). Moldova had a significantly lower proportion of A1401G mutations in aminoglycoside resistant isolates. Mutations in *eis* were rare for all study sites except Moldova, which commonly contained the unique mutation C-12T. However,

association between this mutation and aminoglycoside resistance is questionable since all 25 Moldova isoniazid reverse discordant isolates contained this mutation, which consisted of 96.2% of all aminoglycoside reverse discordant isolates in this study. Of the 218 aminoglycoside resistant isolates, 32 isolates (14.7%) had an *eis* promoter mutation but lacked a *rrs* mutation. Therefore, similar to the promoter of *inhA*, inclusion of the *eis* promoter can increase the sensitivity of detecting isolates resistant to aminoglycosides by 12.5%. Furthermore, no resistance associated mutations were found in *tlyA* for all isolates. The absence of *tlyA* mutations was not entirely unexpected since another study compared *tlyA* mutations between clinical isolates and *in vitro* selected isolates and found that *tlyA* mutations were found almost exclusively in the *in vitro* selected isolates (50).

Discordant frequencies for the aminoglycosides were the second highest of the four antibiotic groups. Similar to rifampin, no significant differences were found in aminoglycoside discordance between the four study groups. The aminoglycosides had the highest reverse discordant frequency, which was largely due to the questionable C-12T mutation found in the *eis* promoter of the isolates from Moldova.

5.2 Differences in Polymorphism Frequencies between Study Sites

Genetic differences in the genes associated with drug resistance were found between the four study sites, with some isolates from a single geographical location having a propensity to develop a particular polymorphism compared to other study sites. The exact cause of these differences, however, is difficult to determine because of the various mechanisms that could cause a particular pattern to develop.

Selective pressure for the development of drug resistant strains ultimately depends on exposure to the antibiotic. Although the WHO have made recommendations for some aspects of treatment regimens, such as which antibiotics to use, dosage, and length of treatment (55), variations in regimens still occur between countries, especially within the private sector (56). Differences in the type of antibiotic prescribed could apply an uneven selective pressure on isolates to develop a drug resistant mutation. One

study examining tuberculosis regimens in India found that 100 doctors prescribed 80 different regimens (57). Another study revealed that private providers in the Philippines prescribed inappropriate regimens 89% of the time (58). Additionally, differences in dosage of the antibiotic could select strains that have mutations that confer a high level of minimum inhibitory concentration resistance compared to a low one. Variations in dosage of sold antibiotic have been observed between countries. The average sold dose for rifampin was about 390 mg in India, 420 mg in the Philippines, and 290 mg in South Africa (56). Patient adherence also plays a key role in the development of drug resistance. Failure to comply with a regimen allows residual bacteria to survive and multiply, leading to the development of drug resistance. Studies examining the differences in antibiotic regimens and patient adherence between countries are rare and could provide some insight to the type and degree of antibiotic resistances.

Another possible explanation for higher frequencies of a particular polymorphism in a specific study site is clonal transmission of an antibiotic resistant strain. Previous outbreaks of MDR-TB have been demonstrated to be clonally transmitted, such as the MDR-TB outbreak in the 1990-1993 era of New York and the 2002 era of Japan (59, 60) and an XDR-TB outbreak in the 2006 era of South Africa (61). However, there is some evidence that clonal transmission of MDR-TB may be a rare event. Drug resistance mutations often occur with a loss in fitness to the bacteria, such as the deactivation of the catalase-peroxidase enzyme KatG to prevent isoniazid activation. This loss in fitness could allow susceptible strains to predominantly spread over resistant strains. One example was in a 12 year period in Cape Town, South Africa, where the Beijing strain, a strain of *M. tuberculosis* that is commonly found to be drug resistant, was observed to grow exponentially over other strains. However, the amount of drug resistant Beijing cases remained constant, indicating that the spread of this strain was largely in part due to drug susceptible isolates (62).

Selection bias could have also impacted the results due to the nature of convenience sampling. Each study site contained a bank of known drug resistant isolates and isolates were chosen based on their resistance profile. However, one study site may have had low diversity among the banked isolates,

allowing disproportionate selection. Random sampling for isolates resistant to a particular drug could control for possible selection bias.

5.3 Multidrug Discordance

Multidrug discordance was observed in 19 of the 381 isolates (5.0%). Interestingly, three isolates were discordant for all four antibiotic groups. Multidrug discordance can be caused through a number of methods which includes mutations occurring in unknown genes, decreased permeability to drugs, and efflux pumps. Drug permeability is not well studied in *M. tuberculosis*; however, few studies suggest that some strains might employ this technique. Other mycobacteria like *Mycobacterium intracellulare* and *Mycobacterium smegmatis* have been shown to have rifampin susceptible RNA polymerases yet still have resistance due to a permeability barrier (51). Furthermore, when *M. tuberculosis* isolates resistant to rifampin, isoniazid, and streptomycin were exposed to sub-minimum inhibitory concentrations of compounds which alter the permeability of the cell wall such as ethambutol, a 4 to 64 fold increase in susceptibility was observed (52).

M. tuberculosis has been known to contain several efflux pumps, some of which provide resistance to one or more antibiotics. For example, overexpression of the drug efflux gene *jefA* conferred resistance to isonizaid and ethambutol (53). Louw et al. also demonstrated that when rifampin resistant isolates were exposed to rifampin, resistance to the fluoroquinolone ofloxacin also occurred. However, when efflux pump inhibitors were added, no fluoroquinolone resistance was observed (54). Any of these alternative mechanisms could provide a plausible explanation for multidrug discordances. The further study of multidrug discordant isolates is a field of research which could provide useful and new information on resistance mechanisms of *M. tuberculosis*.

Additionally, the three isolates make up a small minority of the total isolates in this study (0.8%) and the multidrug discordance could be due to clerical error or drug susceptibility testing error.

5.4 Multidrug Reverse Discordance

Three out of the 381 isolates (0.8%) contained more than one reverse discordance. Of the three, two isolates had two reverse discordances and one isolate was reverse discordant to all four antibiotic groups. These multi drug reverse discordances were most likely a result of clerical error as it is highly unlikely that differential minimum inhibitory concentrations affected these isolates since they do contain mutations highly associated with high level drug resistance such as the TCG531TTG mutation in *rpoB*.

5.5 Drug Resistance Profiles of Isolates

Comparison between drug susceptibility data and sequencing data identified 199 (51.8%) unique resistance profiles out of the 384 isolates containing at least one drug resistance conferring mutation. The two study groups with most diversity were Moldova and the Philippines, where 69.5% and 70.0% of the isolates contained a unique resistance profile, respectively. However, the diversity of the South African study group was remarkably low, where only 32.3% of the isolates contained a unique profile. This low diversity was due to a large proportion of isolates sharing a single type. 33 out of the 93 South African isolates contained the exact same profile, noted by the unusual GAC516GGC and CTG533CGG double mutations found in the *rpoB* gene. Selection bias for the isolates from South Africa could have accounted for the low diversity within that region.

5.6 Concluding Remarks and Future Work

Because of the rapidness of the delivery of results, utilization of sequence based diagnostic tests can be a viable and efficient alternative to the standard drug susceptibility tests currently used to test for resistance in *M. tuberculosis*. While drug susceptibility testing requires the slow growth of the mycobacteria that can take up to 28-40 days, the DNA of the bacteria can be quickly amplified using polymerase chain reaction and scanned for mutations within several days. Nine genes were screened for mutations in 407 clinical isolates which showed that some genes like *rpoB* or *gyrA* are heavily associated with resistance while others, namely the promoter of *ahpC, tlyA,* and *gyrB,* contribute little to no

resistance in clinical isolates. Four study sites were examined and showed some differences in the resistance patterns found in the nine genes, which could possibly provide an estimation of the generalizability of the sequence based test. However, no distinctive resistance pattern between the four antibiotic groups was observed for one particular study group. The exact cause of the different proportions for a particular mutation within a gene is still unknown, and additional research analyzing the different possible mechanisms for the development of a particular mutation could complement a sequence based diagnostic test. Through these nine genes, a high level of specificity and a slightly lower sensitivity have been demonstrated by identifying discordant and reverse discordant isolates. The sensitivity of the test could perhaps be increased by the inclusion of more genes, though the test would still not account for additional resistance mechanisms such as efflux and drug permeability. The proportion of clinical isolates that employ those mechanisms and whether known markers for it exist would greatly benefit this alternative diagnostic test. Further research should be also be done to determine the underlying cause of discordance in the select few isolates, which could lead to the identification of novel resistance genes or polymorphisms.

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CHAPTER 6

SUPPLEMENTAL

Table 6.1 – rpoB sequences of isolates from India by codon

Isolate ID	507	508	509	510	511	512	513	514	515	516	517	518	519	520
H37Rv	GGC	ACC	AGC	CAG	CTG	AGC	CAA	TTC	ATG	GAC	CAG	AAC	AAC	CCG
1-1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-4	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
1-5	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-6	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-7	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-8	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-9	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-10	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-11	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-12	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-13	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-14	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-15	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-16	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-17	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-18	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-19	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-20	-	-	-	-	-	-	CCA	-	-	-	-	-	-	-
1-21	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-22	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-23	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-24	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-25	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-26	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-27	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
1-28	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-29	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-30	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-31	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-32	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-33	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Table 6.1 – rpoB sequences of isolates from India by codon (continued)

Isolate ID	521	522	523	524	525	526	527	528	529	530	531	532	533
H37Rv	CTG	TCG	GGG	TTG	ACC	CAC	AAG	CGC	CGA	CTG	TCG	GCG	CTG
1-1	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-2	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-3	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-4	-	-	-	-	-	-	-	-	-	-	-	-	-
1-5	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-6	-	-	-	-	-	-	-	-	-	-	-	-	-
1-7	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-8	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-9	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-10	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-11	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-12	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-13	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-14	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-15	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-16	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-17	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-18	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-19	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-20	-	-	-	-	-	-	-	-	-	-	-	-	-
1-21	-	-	-	-	-	-	-	-	-	-	-	-	-
1-22	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-23	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-24	-	-	-	-	-	-	-	-	-	-	-	-	-
1-25	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-26	-	-	-	-	-	TGC	-	-	-	-	-	-	-
1-27	-	-	-	-	-	-	-	-	-	-	-	-	-
1-28	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-29	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-30	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-31	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-32	-	-	-	-	-	TAC	-	-	-	-	-	-	-
1-33	-	-	-	-	-	-	-	-	-	-	TTG	-	-

Table 6.1 – rpoB sequences of isolates from India by codon (continued)

Isolate ID	507	508	509	510	511	512	513	514	515	516	517	518	519	520
H37Rv	GGC	ACC	AGC	CAG	CTG	AGC	CAA	TTC	ATG	GAC	CAG	AAC	AAC	CCG
1-34	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-35	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-36	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-37	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-38	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-39	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-40	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-41	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-42	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-43	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-44	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-45	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-46	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-47	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-48	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-49	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-50	-	-	CGC	-	-	-	-	-	-	-	-	-	-	-
1-51	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-52	-	-	-	-	-	-	AAA	-	-	-	-	-	-	-
1-53	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-54	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-55	-	-	-	-	-	-	-	-	ATA	-	-	-	-	-
1-56	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-57	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-58	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-59	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
1-60	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-61	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-62	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-63	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-64	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-65	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-66	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Table 6.1 – rpoB sequences of isolates from India by codon (continued)

Isolate ID	521	522	523	524	525	526	527	528	529	530	531	532	533
H37Rv	CTG	TCG	GGG	TTG	ACC	CAC	AAG	CGC	CGA	CTG	TCG	GCG	CTG
1-34	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-35	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-36	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-37	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-38	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-39	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-40	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-41	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-42	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-43	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-44	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-45	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-46	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-47	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-48	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-49	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-50	-	-	-	-	-	TAC	-	-	-	-	-	-	-
1-51	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-52	-	-	-	-	-	-	-	-	-	-	-	-	-
1-53	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-54	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-55	-	-	-	-	-	AAC	-	-	-	-	-	-	-
1-56	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-57	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-58	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-59	-	-	-	-	-	-	-	-	-	-	-	-	-
1-60	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-61	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-62	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-63	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-64	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-65	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-66	-	-	-	-	-	-	-	-	-	-	TTG	-	-

Table 6.1 – rpoB sequences of isolates from India by codon (continued)

Isolate ID	507	508	509	510	511	512	513	514	515	516	517	518	519	520
H37RV	GGC	ACC	AGC	CAG	CTG	AGC	CAA	TTC	ATG	GAC	CAG	AAC	AAC	CCG
1-67	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-68	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-69	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-70	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-71	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-72	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-73	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-74	-	-	-	-	-	-	AAA	-	-	-	-	-	-	-
1-75	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-76	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-77	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-78	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-79	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-80	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-81	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-82	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-83	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-84	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-85	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-86	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
1-87	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-88	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-89	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-90	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-91	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-92	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-93	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-94	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-95	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1-96	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Table 6.1 – rpoB sequences of isolates from India by codon (continued)

Isolate ID	521	522	523	524	525	526	527	528	529	530	531	532	533
H37RV	CTG	TCG	GGG	TTG	ACC	CAC	AAG	CGC	CGA	CTG	TCG	GCG	CTG
1-67	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-68	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-69	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-70	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-71	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-72	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-73	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-74	-	-	-	-	-	-	-	-	-	-	-	-	-
1-75	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-76	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-77	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-78	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-79	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-80	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-81	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-82	-	-	-	-	-	TAC	-	-	-	-	-	-	-
1-83	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-84	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-85	-	-	-	-	-	-	-	-	-	-	-	-	-
1-86	-	-	-	-	-	-	-	-	-	-	-	-	-
1-87	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-88	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-89	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-90	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-91	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-92	-	-	-	-	-	-	-	-	-	-	TTG	-	-
1-93	-	-	-	-	-	-	-	-	-	-	-	-	-
1-94	-	-	-	-	-	-	-	-	-	-	-	-	-
1-95	-	-	-	-	-	-	-	-	-	-	-	-	-
1-96	-	-	-	-	-	-	-	-	-	-	-	-	-

Table 6.2 – rpoB sequences of isolates from Moldova by codon

Isolate ID	507	508	509	510	511	512	513	514	515	516	517	518	519	520
H37Rv	GGC	ACC	AGC	CAG	CTG	AGC	CAA	TTC	ATG	GAC	CAG	AAC	AAC	CCG
2-1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-4	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-5	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-6	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
2-7	-	-	-	-	-	-	-	-	-	TAC	-	-	-	-
2-8	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
2-9	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-10	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
2-11	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-12	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-13	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
2-14	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
2-15	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-16	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-17	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-18	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-19	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-20	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-21	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-22	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-23	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-24	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-25	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-26	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-27	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-28	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-29	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
2-30	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-31	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-32	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-33	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Table 6.2 – rpoB sequences of isolates from Moldova by codon (continued)

Isolate ID	521	522	523	524	525	526	527	528	529	530	531	532	533
H37Rv	CTG	TCG	GGG	TTG	ACC	CAC	AAG	CGC	CGA	CTG	TCG	GCG	CTG
2-1	-	-	-	-	-	-	-	-	-	-	-	-	-
2-2	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-3	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-4	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-5	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-6	-	-	-	-	-	-	-	-	-	-	-	-	-
2-7	-	-	-	-	-	-	-	-	-	-	-	-	-
2-8	-	-	-	-	-	-	-	-	-	-	-	-	-
2-9	-	-	-	-	-	-	-	-	-	-	-	-	-
2-10	-	-	-	-	-	-	-	-	-	-	-	-	-
2-11	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-12	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-13	-	-	-	-	-	-	-	-	-	-	-	-	-
2-14	-	-	-	-	-	-	-	-	-	-	-	-	-
2-15	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-16	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-17	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-18	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-19	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-20	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-21	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-22	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-23	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-24	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-25	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-26	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-27	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-28	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-29	-	-	-	-	-	-	-	-	-	-	-	-	-
2-30	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-31	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-32	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-33	-	-	-	-	-	-	-	-	-	-	TTG	-	-

Table 6.2 – rpoB sequences of isolates from Moldova by codon (continued)

Isolate ID	507	508	509	510	511	512	513	514	515	516	517	518	519	520
H37Rv	GGC	ACC	AGC	CAG	CTG	AGC	CAA	TTC	ATG	GAC	CAG	AAC	AAC	CCG
2-34	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-35	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-36	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-37	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-38	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-39	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-40	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-41	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-42	-	-	-	-	-	-	-	-	-	TAC	-	-	-	-
2-43	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-44	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-45	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-46	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-47	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-48	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
2-49	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-50	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-51	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-52	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-53	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-54	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-55	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-56	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-57	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
2-58	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-59	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-60	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-61	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-62	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-63	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-64	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
2-65	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-66	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Table 6.2 – rpoB sequences of isolates from Moldova by codon (continued)

Isolate ID	521	522	523	524	525	526	527	528	529	530	531	532	533
H37Rv	CTG	TCG	GGG	TTG	ACC	CAC	AAG	CGC	CGA	CTG	TCG	GCG	CTG
2-34	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-35	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-36	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-37	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-38	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-39	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-40	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-41	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-42	-	-	-	-	-	-	-	-	-	-	-	-	-
2-43	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-44	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-45	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-46	-	-	-	-	-	CTC	-	-	-	-	-	-	-
2-47	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-48	-	-	-	-	-	-	-	-	-	-	-	-	-
2-49	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-50	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-51	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-52	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-53	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-54	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-55	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-56	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-57	-	-	-	-	-	-	-	-	-	-	-	-	-
2-58	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-59	-	-	-	-	-	-	-	-	-	-	TGG	-	-
2-60	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-61	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-62	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-63	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-64	-	-	-	-	-	-	-	-	-	-	-	-	-
2-65	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-66	-	-	-	-	-	-	-	-	-	-	TTG	-	-

Table 6.2 – rpoB sequences of isolates from Moldova by codon (continued)

Isolate ID	507	508	509	510	511	512	513	514	515	516	517	518	519	520
H37Rv	GGC	ACC	AGC	CAG	CTG	AGC	CAA	TTC	ATG	GAC	CAG	AAC	AAC	CCG
2-67	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-68	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-69	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-70	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-71	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
2-72	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-73	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-74	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-75	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-76	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-77	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-78	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-79	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
2-80	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-81	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-82	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-83	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-84	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-85	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-86	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-87	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2-88	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Table 6.2 – rpoB sequences of isolates from Moldova by codon (continued)

Isolate ID	521	522	523	524	525	526	527	528	529	530	531	532	533
H37Rv	CTG	TCG	GGG	TTG	ACC	CAC	AAG	CGC	CGA	CTG	TCG	GCG	CTG
2-67	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-68	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-69	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-70	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-71	-	-	-	-	-	-	-	-	-	-	-	-	-
2-72	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-73	-	-	-	-	-	-	-	-	-	-	-	-	-
2-74	-	-	-	-	-	-	-	-	-	-	-	-	-
2-75	-	-	-	-	-	-	-	-	-	-	-	-	-
2-76	-	-	-	-	-	-	-	-	-	-	-	-	-
2-77	-	-	-	-	-	-	-	-	-	-	-	-	-
2-78	-	-	-	-	-	-	-	-	-	-	-	-	-
2-79	-	-	-	-	-	-	-	-	-	-	-	-	-
2-80	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-81	-	-	-	-	-	-	-	-	-	-	-	-	-
2-82	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-83	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-84	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-85	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-86	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-87	-	-	-	-	-	-	-	-	-	-	TTG	-	-
2-88	-	-	-	-	-	-	-	-	-	-	TTG	-	-

Table 6.3 – rpoB sequences of isolates from the Philippines by codon

Isolate ID	507	508	509	510	511	512	513	514	515	516	517	518	519	520
H37Rv	GGC	ACC	AGC	CAG	CTG	AGC	CAA	TTC	ATG	GAC	CAG	AAC	AAC	CCG
3-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-4	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-5	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-6	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-7	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-8	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-9	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-10	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-11	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-12	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-13	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
3-14	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-15	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-16	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-17	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-18	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-19	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-20	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-21	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-22	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-23	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-24	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-25	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-26	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-27	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-28	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-29	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-30	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-31	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-32	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-33	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Table 6.3 – rpoB sequences of isolates from the Philippines by codon (continued)

Isolate ID	521	522	523	524	525	526	527	528	529	530	531	532	533
H37Rv	CTG	TCG	GGG	TTG	ACC	CAC	AAG	CGC	CGA	CTG	TCG	GCG	CTG
3-2	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-3	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-4	-	-	-	-	-	TGC	-	-	-	-	-	-	-
3-5	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-6	-	-	-	-	-	-	-	-	-	-	-	-	-
3-7	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-8	-	-	-	-	-	CGC	-	-	-	-	-	-	-
3-9	-	-	-	-	-	-	-	-	-	-	TGG	-	-
3-10	-	-	-	-	-	CGC	-	-	-	-	-	-	-
3-11	-	-	-	-	-	TAC	-	-	-	-	-	-	-
3-12	-	-	-	-	-	-	-	-	-	-	-	-	-
3-13	-	-	-	-	-	-	-	-	-	-	-	-	-
3-14	-	-	-	-	-	TAC	-	-	-	-	-	-	-
3-15	-	-	-	-	-	-	-	-	-	-	-	-	-
3-16	-	-	-	-	-	-	-	-	-	-	-	-	-
3-17	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-18	-	-	-	-	-	-	-	-	-	-	TGG	-	-
3-19	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-20	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-21	-	-	-	-	-	GAC	-	-	-	-	-	-	-
3-22	-	-	-	-	-	-	-	-	-	-	TGG	-	-
3-23	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-24	-	-	-	-	-	-	-	-	-	-	-	-	-
3-25	-	-	-	-	-	-	-	-	-	-	-	-	-
3-26	-	-	-	-	-	-	-	-	-	-	-	-	-
3-27	-	-	-	-	-	-	-	-	-	-	-	-	-
3-28	-	-	-	-	-	CGC	-	-	-	-	-	-	-
3-29	-	-	-	-	-	CCC	-	-	-	-	-	-	-
3-30	-	-	-	-	-	-	-	-	-	-	TGG	-	-
3-31	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-32	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-33	-	-	-	-	-	TAC	-	-	-	-	-	-	-

Table 6.3 – rpoB sequences of isolates from the Philippines by codon (continued)

Isolate ID	507	508	509	510	511	512	513	514	515	516	517	518	519	520
H37Rv	GGC	ACC	AGC	CAG	CTG	AGC	CAA	TTC	ATG	GAC	CAG	AAC	AAC	CCG
3-34	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-35	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-36	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-37	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-38	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-39	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-40	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-41	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-42	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-43	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-44	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-45	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-46	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-47	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-48	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-49	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-50	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-51	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-52	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-53	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-54	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-55	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-56	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-57	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-58	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-59	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-60	-	-	-	-	-	-	-	-	-	TAC	-	-	-	-
3-61	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-62	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-63	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-64	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-65	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-66	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Table 6.3 – rpoB sequences of isolates from the Philippines by codon (continued)

Isolate ID	521	522	523	524	525	526	527	528	529	530	531	532	533
H37Rv	CTG	TCG	GGG	TTG	ACC	CAC	AAG	CGC	CGA	CTG	TCG	GCG	CTG
3-34	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-35	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-36	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-37	-	-	-	-	-	-	-	-	-	-	-	-	-
3-38	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-39	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-40	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-41	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-42	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-43	-	-	-	-	-	TAC	-	-	-	-	-	-	-
3-44	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-45	-	-	-	-	-	-	-	-	-	-	-	-	-
3-46	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-47	-	-	-	-	-	GAC	-	-	-	-	-	-	-
3-48	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-49	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-50	-	-	-	-	-	-	-	-	-	-	-	-	-
3-51	-	-	-	-	-	-	-	-	-	-	-	-	-
3-52	-	-	-	-	-	-	-	-	-	-	-	-	-
3-53	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-54	-	-	-	-	-	-	-	-	-	-	-	-	-
3-55	-	-	-	-	-	-	-	-	-	-	-	-	-
3-56	-	-	-	-	-	CTC	-	-	-	-	-	-	-
3-57	-	-	-	-	-	-	-	-	-	-	-	-	-
3-58	-	-	-	-	-	-	-	-	-	-	-	-	-
3-59	-	-	-	-	-	-	-	-	-	-	-	-	-
3-60	-	-	-	-	-	-	-	-	-	-	-	-	-
3-61	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-62	-	-	-	-	-	CGC	-	-	-	-	-	-	-
3-63	-	-	-	-	-	-	-	-	-	-	-	-	-
3-64	-	-	-	-	-	CGC	-	-	-	-	-	-	-
3-65	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-66	-	-	-	-	-	-	-	-	-	-	TTG	-	-

Table 6.3 – rpoB sequences of isolates from the Philippines by codon (continued)

Isolate ID	507	508	509	510	511	512	513	514	515	516	517	518	519	520
H37Rv	GGC	ACC	AGC	CAG	CTG	AGC	CAA	TTC	ATG	GAC	CAG	AAC	AAC	CCG
3-67	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-68	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-69	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-70	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-71	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-72	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-73	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-74	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-76	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-77	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-78	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-79	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-80	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-81	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-82	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-83	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-84	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-85	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-86	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-87	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-88	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-89	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-90	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-91	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-92	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-93	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-94	-	-	-	-	CCG	ACC	-	-	-	TAC	-	-	-	-
3-95	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-96	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-97	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-98	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-99	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Table 6.3 – rpoB sequences of isolates from the Philippines by codon (continued)

Isolate ID	521	522	523	524	525	526	527	528	529	530	531	532	533
H37Rv	CTG	TCG	GGG	TTG	ACC	CAC	AAG	CGC	CGA	CTG	TCG	GCG	CTG
3-67	-	-	-	-	-	TAC	-	-	-	-	-	-	-
3-68	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-69	-	-	-	-	-	CGC	-	-	-	-	-	-	-
3-70	-	-	-	-	-	CGC	-	-	-	-	-	-	-
3-71	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-72	-	-	-	-	-	GGC	-	-	-	-	-	-	-
3-73	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-74	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-76	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-77	-	-	-	-	-	TAC	-	-	-	-	-	-	-
3-78	-	-	-	-	-	GAC	-	-	-	-	-	-	-
3-79	-	-	-	-	-	TGC	-	-	-	-	-	-	-
3-80	-	-	-	-	-	-	-	-	-	-	-	-	CCG
3-81	-	-	-	-	-	-	-	-	-	-	-	-	-
3-82	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-83	-	TTG	-	-	-	-	-	-	-	-	-	-	-
3-84	-	-	-	-	-	TGC	-	-	-	-	-	-	-
3-85	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-86	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-87	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-88	-	-	-	-	-	CTC	-	-	-	-	-	-	-
3-89	-	-	-	-	-	-	-	-	-	-	TGG	-	-
3-90	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-91	-	-	-	-	-	CTC	-	-	-	-	-	-	-
3-92	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-93	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-94	-	-	-	-	-	-	-	-	-	-	-	-	-
3-95	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-96	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-97	-	-	-	-	-	-	-	-	-	-	-	-	-
3-98	-	-	-	-	-	-	-	-	-	-	-	-	-
3-99	-	-	-	-	-	-	-	-	-	-	-	-	-

Table 6.3 – rpoB sequences of isolates from the Philippines by codon (continued)

Isolate ID	507	508	509	510	511	512	513	514	515	516	517	518	519	520
H37Rv	GGC	ACC	AGC	CAG	CTG	AGC	CAA	TTC	ATG	GAC	CAG	AAC	AAC	CCG
3-100	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-101	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-102	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-103	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-104	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-105	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-106	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-107	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-108	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-109	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-110	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-111	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-112	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-113	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-114	-	-	-	-	-	-	AAA	-	-	-	-	-	-	-
3-115	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-116	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-117	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-118	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-119	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-120	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-121	-	-	-	-	-	-	AAA	-	-	-	-	-	-	-
3-122	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-123	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3-124	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
3-125	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Table 6.3 – rpoB sequences of isolates from the Philippines by codon (continued)

Isolate ID	521	522	523	524	525	526	527	528	529	530	531	532	533
H37Rv	CTG	TCG	GGG	TTG	ACC	CAC	AAG	CGC	CGA	CTG	TCG	GCG	CTG
3-100	-	-	-	-	-	AGC	-	-	-	-	-	-	-
3-101	-	TTG	-	-	-	-	-	-	-	-	-	-	-
3-102	-	-	-	-	-	TAC	-	-	-	-	-	-	-
3-103	-	-	-	-	-	-	-	-	-	-	-	-	-
3-104	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-105	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-106	-	-	-	-	-	TAC	-	-	-	-	-	-	-
3-107	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-108	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-109	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-110	-	-	-	-	-	-	-	-	-	-	-	-	-
3-111	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-112	-	-	-	-	-	-	-	-	-	-	-	-	-
3-113	-	-	-	-	-	CGC	-	-	-	-	-	-	-
3-114	-	-	-	-	-	-	-	-	-	-	-	-	-
3-115	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-116	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-117	-	-	-	-	-	-	-	-	-	-	-	-	-
3-118	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-119	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-120	-	-	-	-	-	TAC	-	-	-	-	-	-	-
3-121	-	-	-	-	-	GAC	-	-	-	-	-	-	-
3-122	-	-	-	-	-	TAC	-	-	-	-	-	-	-
3-123	-	-	-	-	-	-	-	-	-	-	TTG	-	-
3-124	-	-	-	-	-	-	-	-	-	-	-	-	-
3-125	-	-	-	-	-	-	-	-	-	-	TTG	-	-

Table 6.4 – rpoB sequences of isolates from South Africa by codon

Isolate ID	507	508	509	510	511	512	513	514	515	516	517	518	519	520
H37RV	GGC	ACC	AGC	CAG	CTG	AGC	CAA	TTC	ATG	GAC	CAG	AAC	AAC	CCG
4-1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-4	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-5	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-6	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-7	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-8	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-9	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-10	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-11	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-12	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-13	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-14	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-15	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-16	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-17	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-18	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-19	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-20	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-21	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-22	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-23	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-24	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-25	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-26	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-27	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-28	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-29	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-30	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-31	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-32	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-33	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-

Table 6.4 – rpoB sequences of isolates from South Africa by codon (continued)

Isolate ID	521	522	523	524	525	526	527	528	529	530	531	532	533
H37RV	CTG	TCG	GGG	TTG	ACC	CAC	AAG	CGC	CGA	CTG	TCG	GCG	CTG
4-1	-	-	-	-	-	TAC	-	-	-	-	-	-	-
4-2	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-3	-	-	-	-	-	TAC	-	-	-	-	-	-	-
4-4	-	-	-	-	-	TAC	-	-	-	-	-	-	-
4-5	-	-	-	-	-	TAC	-	-	-	-	-	-	-
4-6	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-7	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-8	-	-	-	-	-	TAC	-	-	-	-	-	-	-
4-9	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-10	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-11	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-12	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-13	-	-	-	-	-	TAC	-	-	-	-	TNG	-	-
4-14	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-15	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-16	-	-	-	-	-	TAC	-	-	-	-	-	-	-
4-17	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-18	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-19	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-20	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-21	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-22	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-23	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-24	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-25	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-26	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-27	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-28	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-29	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-30	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-31	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-32	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-33	-	-	-	-	-	-	-	-	-	-	-	-	CCG

Table 6.4 – rpoB sequences of isolates from South Africa by codon (continued)

Isolate ID	507	508	509	510	511	512	513	514	515	516	517	518	519	520
H37RV	GGC	ACC	AGC	CAG	CTG	AGC	CAA	TTC	ATG	GAC	CAG	AAC	AAC	CCG
4-34	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-35	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-36	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-37	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-38	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-39	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-40	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-41	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-42	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-43	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-44	-	-	-	-	-	-	-	-	-	GNC	-	-	-	-
4-45	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-46	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-47	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-48	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-49	-	-	-	-	-	-	-	-	-	GGC	-	-	-	-
4-50	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-51	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-52	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
4-53	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
4-54	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-55	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-56	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-57	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-58	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-59	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-60	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-61	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-62	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-63	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-64	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-65	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-66	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-

Table 6.4 – rpoB sequences of isolates from South Africa by codon (continued)

Isolate ID	521	522	523	524	525	526	527	528	529	530	531	532	533
H37RV	CTG	TCG	GGG	TTG	ACC	CAC	AAG	CGC	CGA	CTG	TCG	GCG	CTG
4-34	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-35	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-36	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-37	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-38	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-39	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-40	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-41	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-42	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-43	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-44	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-45	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-46	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-47	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-48	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-49	-	-	-	-	-	-	-	-	-	-	-	-	CCG
4-50	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-51	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-52	-	-	-	-	-	-	-	-	-	-	-	-	-
4-53	-	-	-	-	-	-	-	-	-	-	-	-	-
4-54	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-55	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-56	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-57	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-58	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-59	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-60	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-61	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-62	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-63	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-64	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-65	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-66	-	-	-	-	-	-	-	-	-	-	-	-	-

Table 6.4 – rpoB sequences of isolates from South Africa by codon (continued)

Isolate ID	507	508	509	510	511	512	513	514	515	516	517	518	519	520
H37RV	GGC	ACC	AGC	CAG	CTG	AGC	CAA	TTC	ATG	GAC	CAG	AAC	AAC	CCG
4-67	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-68	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-69	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-70	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
4-71	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-72	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-73	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-74	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-75	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
4-76	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
4-77	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-78	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-79	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-80	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-81	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-82	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-83	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-84	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-85	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-86	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-87	-	-	-	-	-	-	AAA	-	-	-	-	-	-	-
4-88	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
4-89	-	-	-	-	-	-	-	-	-	GTC	-	-	-	-
4-90	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-91	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-92	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-93	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-94	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-95	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-96	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-97	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-98	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-99	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-100	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Table 6.4 – rpoB sequences of isolates from South Africa by codon (continued)

Isolate ID	521	522	523	524	525	526	527	528	529	530	531	532	533
H37RV	CTG	TCG	GGG	TTG	ACC	CAC	AAG	CGC	CGA	CTG	TCG	GCG	CTG
4-67	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-68	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-69	-	-	-	-	-	-	-	-	-	-	-	-	-
4-70	-	-	-	-	-	-	-	-	-	-	-	-	-
4-71	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-72	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-73	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-74	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-75	-	-	-	-	-	-	-	-	-	-	-	-	-
4-76	-	-	-	-	-	-	-	-	-	-	-	-	-
4-77	-	-	-	-	-	-	-	-	-	-	-	-	-
4-78	-	-	-	-	-	-	-	-	-	-	-	-	-
4-79	-	-	-	-	-	-	-	-	-	-	-	-	-
4-80	-	-	-	-	-	-	-	-	-	-	-	-	-
4-81	-	-	-	-	-	-	-	-	-	-	-	-	-
4-82	-	-	-	-	-	-	-	-	-	-	-	-	-
4-83	-	-	-	-	-	-	-	-	-	-	-	-	-
4-84	-	-	-	-	-	-	-	-	-	-	-	-	-
4-85	-	-	-	-	-	-	-	-	-	-	-	-	-
4-86	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-87	-	-	-	-	-	-	-	-	-	-	-	-	-
4-88	-	-	-	-	-	-	-	-	-	-	-	-	-
4-89	-	-	-	-	-	-	-	-	-	-	-	-	-
4-90	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-91	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-92	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-93	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-94	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-95	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-96	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-97	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-98	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-99	-	-	-	-	-	-	-	-	-	-	TTG	-	-
4-100	-	-	-	-	-	-	-	-	-	-	TTG	-	-

Table 6.5 – katG sequences of isolates from India by codon

Isolate ID	279	315
H37Rv	GGC	AGC
1-1	-	-
1-2	-	ACC
1-3	-	ACC
1-4	-	ACC
1-5	-	ACC
1-6	-	-
1-7	-	-
1-8	-	-
1-9	-	ACC
1-10	-	ACC
1-11	-	ACC
1-12	-	-
1-13	-	ACC
1-14	-	ACC
1-15	-	ACC
1-16	-	-
1-17	-	ACC
1-18	-	ACC
1-19	-	ACC
1-20	-	ACC
1-21	-	-
1-22	-	ACC
1-23	-	ACC
1-24	-	-
1-25	-	-
1-26	-	-
1-27	-	-
1-28	-	-
1-29	-	-
1-30	-	ACC
1-31	-	ACC
1-32	-	-
1-33	-	ACC

Isolate ID	279	315
H37Rv	GGC	AGC
1-34	-	ACC
1-35	-	ACC
1-36	-	ACC
1-37	-	ACC
1-38	-	ACC
1-39	-	ACC
1-40	-	ACC
1-41	-	ACC
1-42	-	ACC
1-43	-	ACC
1-44	-	ACC
1-45	-	ACC
1-46	-	ACC
1-47	-	ACC
1-48	-	ACC
1-49	-	ACC
1-50	-	ACC
1-51	-	ACC
1-52	-	ACC
1-53	-	-
1-54	-	ACC
1-55	-	ACC
1-56	-	ACC
1-57	-	ACC
1-58	-	ACC
1-59	-	ACC
1-60	-	ACC
1-61	-	ACC
1-62	-	ACC
1-63	-	ACC
1-64	-	ACC
1-65	-	ACC
1-66	-	ACC

Isolate ID	279	315
H37Rv	GGC	AGC
1-67	-	ACC
1-68	-	ACC
1-69	-	ACC
1-70	-	ACC
1-71	-	ACC
1-72	-	ACC
1-73	-	ACC
1-74	-	ACC
1-75	-	ACC
1-76	-	ACC
1-77	-	ACC
1-78	-	ACC
1-79	-	ACC
1-80	-	ACC
1-81	-	-
1-82	-	ACC
1-83	-	ACC
1-84	-	ACC
1-85	-	-
1-86	-	ACC
1-87	-	ACC
1-88	-	ACC
1-89	-	ACC
1-90	-	ACC
1-91	-	ACC
1-92	-	ACC
1-93	-	-
1-94	-	-
1-95	-	-
1-96	-	-

Table 6.6 – katG sequences of isolates from Moldova by codon

Isolate ID	279	315
H37Rv	GGC	AGC
2-1	-	ACC
2-2	-	ACC
2-3	-	ACC
2-4	-	ACC
2-5	-	ACC
2-6	-	ACC
2-7	-	ACC
2-8	-	ACC
2-9	-	ACC
2-10	-	ACC
2-11	-	ACC
2-12	-	ACC
2-13	-	ACC
2-14	-	ACC
2-15	-	ACC
2-16	-	ACC
2-17	-	ACC
2-18	-	ACC
2-19	-	ACC
2-20	-	ACC
2-21	-	ACC
2-22	-	ACC
2-23	-	ACC
2-24	-	ACC
2-25	-	ACC
2-26	-	ACC
2-27	-	ACC
2-28	-	ACC
2-29	-	ACC
2-30	-	ACC
2-31	-	ACC
2-32	-	ACC
2-33	-	ACC

Isolate ID	279	315
H37Rv	GGC	AGC
2-34	-	ACC
2-35	-	ACC
2-36	-	ACC
2-37	-	ACC
2-38	-	ACC
2-39	-	ACC
2-40	-	ACC
2-41	-	ACC
2-42	-	ACC
2-43	-	ACC
2-44	-	ACC
2-45	-	ACC
2-46	-	ACC
2-47	-	ACC
2-48	-	ACC
2-49	-	ACC
2-50	-	ACC
2-51	-	ACC
2-52	-	ACC
2-53	-	ACC
2-54	-	ACC
2-55	-	ACC
2-56	-	ACC
2-57	-	ACC
2-58	-	ACC
2-59	-	ACC
2-60	-	ACC
2-61	-	ACC
2-62	-	ACC
2-63	-	ACC
2-64	-	ACC
2-65	-	ACC
2-66	-	ACC

Isolate ID	279	315
H37Rv	GGC	AGC
2-67	-	ACC
2-68	-	ACC
2-69	-	ACC
2-70	-	ACC
2-71	-	ACC
2-72	-	ACC
2-73	-	-
2-74	-	-
2-75	-	-
2-76	-	-
2-77	-	-
2-78	-	-
2-79	-	ACC
2-80	-	ACC
2-81	-	ACC
2-82	-	ACC
2-83	-	ACC
2-84	-	ACC
2-85	-	ACC
2-86	-	ACC
2-87	-	ACC
2-88	-	ACC

Table 6.7 – katG sequences of isolates from the Philippines by codon

Isolate ID	279	315
H37Rv	GGC	AGC
3-2	-	ACC
3-3	-	ACC
3-4	-	ACC
3-5	-	ACC
3-6	-	-
3-7	-	-
3-8	-	-
3-9	-	ACC
3-10	-	ACC
3-11	-	ACC
3-12	-	-
3-13	-	ACC
3-14	-	ACC
3-15	-	-
3-16	-	-
3-17	-	ACC
3-18	-	ACC
3-19	-	ACC
3-20	-	ACC
3-21	-	-
3-22	-	ACC
3-23	-	ACC
3-24	-	-
3-25	-	-
3-26	-	-
3-27	-	-
3-28	-	-
3-29	-	-
3-30	-	ACC
3-31	-	ACC
3-32	-	ACC
3-33	-	ACC
3-34	-	ACC

Isolate ID	279	315
H37Rv	GGC	AGC
3-35	-	ACC
3-36	-	ACC
3-37	-	ACC
3-38	-	ACC
3-39	-	-
3-40	-	ACC
3-41	-	-
3-42	-	-
3-43	-	-
3-44	-	ACC
3-45	-	-
3-46	-	ACC
3-47	-	ACC
3-48	-	ACC
3-49	-	ACC
3-50	-	-
3-51	-	-
3-52	-	-
3-53	-	ACC
3-54	-	-
3-55	-	-
3-56	-	-
3-57	-	-
3-58	-	-
3-59	-	-
3-60	-	ACC
3-61	-	ACC
3-62	-	-
3-63	-	-
3-64	-	-
3-65	-	-
3-66	-	-
3-67	-	ACC

Isolate ID	279	315
H37Rv	GGC	AGC
3-68	-	ACC
3-69	-	-
3-70	-	ACC
3-71	-	ACC
3-72	-	ACC
3-73	-	-
3-74	-	ACC
3-76	-	-
3-77	-	ACC
3-78	-	ACC
3-79	-	-
3-80	-	-
3-81	-	-
3-82	-	ACC
3-83	-	ACC
3-84	-	-
3-85	-	-
3-86	-	-
3-87	-	ACC
3-88	-	-
3-89	-	ACC
3-90	-	ACC
3-91	-	ACC
3-92	-	ACC
3-93	-	ACC
3-94	-	ACC
3-95	-	ACC
3-96	-	ACC
3-97	-	ACC
3-98	-	ACC
3-99	-	ACC
3-100	-	ACC
3-101	-	ACC

Table 6.7 – katG sequences of isolates from the Philippines by codon (continued)

Isolate ID	279	315
H37Rv	GGC	AGC
3-102	-	ACC
3-103	-	-
3-104	-	ACC
3-105	-	-
3-106	-	-
3-107	-	-
3-108	-	ACC
3-109	-	-
3-110	-	ACC
3-111	-	ACC
3-112	-	ACC
3-113	-	ACC
3-114	-	-
3-115	-	-
3-116	-	-
3-117	-	-
3-118	-	ACC
3-119	-	-
3-120	-	-
3-121	-	-
3-122	-	-
3-123	-	-
3-124	-	ACC
3-125	-	ACC

Table 6.8 – katG sequences of isolates from South Africa by codon

Isolate ID	279	315
H37Rv	GGC	AGC
4-1	-	ACC
4-2	-	ACC
4-3	-	ACC
4-4	-	ACC
4-5	-	ACC
4-6	-	ACC
4-7	-	ACC
4-8	-	ACC
4-9	-	ACC
4-10	-	ACC
4-11	-	ACC
4-12	-	ACC
4-13	-	ACC
4-14	-	-
4-15	-	ACC
4-16	-	ACC
4-17	-	ACC
4-18	-	ACC
4-19	-	ACC
4-20	-	ACC
4-21	-	ACC
4-22	-	ACC
4-23	-	ACC
4-24	-	ACC
4-25	-	ACC
4-26	-	ACC
4-27	-	ACC
4-28	-	ACC
4-29	-	ACC
4-30	-	ACC
4-31	-	ACC
4-32	-	ACC
4-33	-	ACC

Isolate ID	279	315
H37Rv	GGC	AGC
4-34	-	ACC
4-35	-	ACC
4-36	-	ACC
4-37	-	ACC
4-38	-	ACC
4-39	-	ACC
4-40	-	ACC
4-41	-	ACC
4-42	-	ACC
4-43	-	ACC
4-44	-	ACC
4-45	-	ACC
4-46	-	ACC
4-47	-	ACC
4-48	-	ACC
4-49	-	ACC
4-50	-	ACC
4-51	-	ACC
4-52	-	ACC
4-53	-	ACC
4-54	-	ACC
4-55	-	ACC
4-56	-	ACC
4-57	-	ACC
4-58	-	ACC
4-59	-	ACC
4-60	-	ACC
4-61	-	ACC
4-62	-	ACC
4-63	-	ACC
4-64	-	ACC
4-65	-	ACC
4-66	-	ACC

Isolate ID	279	315
H37Rv	GGC	AGC
4-67	-	ACC
4-68	-	ACC
4-69	-	-
4-70	-	ACC
4-71	-	ACC
4-72	-	ACC
4-73	-	-
4-74	-	-
4-75	-	ACC
4-76	-	ACC
4-77	-	ACC
4-78	-	-
4-79	-	ACC
4-80	-	-
4-81	-	-
4-82	-	-
4-83	-	-
4-84	-	-
4-85	-	-
4-86	-	ACC
4-87	-	ACC
4-88	-	ACC
4-89	-	ACC
4-90	-	-
4-91	-	ACC
4-92	-	ACC
4-93	-	-
4-94	-	ACC
4-95	-	-
4-96	-	ACC
4-97	-	ACC
4-98	-	-
4-99	-	-
4-100	-	ACC

Table 6.9 – inhA promoter sequences of isolates from India by nucleotide position

Isolate ID	-8	-15
H37Rv	T	C
1-1	-	-
1-2	-	-
1-3	-	-
1-4	-	-
1-5	-	-
1-6	-	-
1-7	-	-
1-8	-	-
1-9	-	-
1-10	C	-
1-11	-	-
1-12	-	T
1-13	-	T
1-14	-	T
1-15	-	-
1-16	-	T
1-17	-	-
1-18	-	-
1-19	-	-
1-20	-	-
1-21	-	-
1-22	-	-
1-23	-	-
1-24	-	T
1-25	-	-
1-26	-	-
1-27	-	-
1-28	-	T
1-29	-	-
1-30	-	-
1-31	-	-
1-32	-	-
1-33	-	-

Isolate ID	-8	-15
H37Rv	T	C
1-34	-	-
1-35	-	T
1-36	-	-
1-37	-	T
1-38	C	-
1-39	-	-
1-40	-	-
1-41	-	T
1-42	-	T
1-43	-	-
1-44	A	-
1-45	C	-
1-46	-	T
1-47	-	-
1-48	-	-
1-49	-	-
1-50	-	-
1-51	A	-
1-52	-	-
1-53	-	-
1-54	-	T
1-55	-	-
1-56	-	-
1-57	-	-
1-58	-	-
1-59	-	-
1-60	-	-
1-61	-	-
1-62	-	-
1-63	-	-
1-64	-	-
1-65	-	-
1-66	-	-

Isolate ID	-8	-15
H37Rv	T	C
1-67	-	-
1-68	-	-
1-69	-	T
1-70	-	T
1-71	C	-
1-72	-	-
1-73	-	-
1-74	-	-
1-75	C	-
1-76	-	-
1-77	-	-
1-78	-	-
1-79	-	-
1-80	-	-
1-81	-	T
1-82	-	-
1-83	-	-
1-84	-	-
1-85	-	-
1-86	-	T
1-87	-	-
1-88	-	-
1-89	-	T
1-90	-	-
1-91	-	-
1-92	-	-
1-93	-	-
1-94	-	-
1-95	-	-
1-96	-	-

Table 6.10 – inhA promoter sequences of isolates from Moldova by nucleotide position

Isolate ID	-8	-15
H37Rv	T	C
2-1	-	-
2-2	-	-
2-3	-	-
2-4	-	-
2-5	-	T
2-6	-	-
2-7	-	-
2-8	-	-
2-9	-	-
2-10	-	-
2-11	-	T
2-12	-	T
2-13	-	-
2-14	-	-
2-15	-	T
2-16	-	T
2-17	-	T
2-18	-	-
2-19	-	T
2-20	-	T
2-21	-	T
2-22	-	T
2-23	-	-
2-24	-	-
2-25	-	-
2-26	C	-
2-27	-	-
2-28	-	T
2-29	-	-
2-30	C	-
2-31	-	T
2-32	-	-
2-33	-	-

Isolate ID	-8	-15
H37Rv	T	C
2-34	-	-
2-35	-	T
2-36	-	T
2-37	-	T
2-38	-	-
2-39	-	-
2-40	-	T
2-41	-	-
2-42	-	-
2-43	G	-
2-44	-	T
2-45	-	T
2-46	-	-
2-47	-	-
2-48	-	T
2-49	-	T
2-50	-	T
2-51	-	T
2-52	-	T
2-53	-	T
2-54	-	T
2-55	-	T
2-56	-	T
2-57	-	T
2-58	-	T
2-59	-	T
2-60	-	-
2-61	-	T
2-62	-	-
2-63	-	T
2-64	-	-
2-65	-	-
2-66	-	T

Isolate ID	-8	-15
H37Rv	T	C
2-67	-	T
2-68	-	T
2-69	-	-
2-70	-	T
2-71	-	-
2-72	-	T
2-73	-	-
2-74	-	-
2-75	-	-
2-76	-	-
2-77	-	-
2-78	-	-
2-79	-	-
2-80	-	-
2-81	-	-
2-82	-	-
2-83	-	T
2-84	-	-
2-85	-	T
2-86	-	-
2-87	-	-
2-88	-	T

Table 6.11 – inhA promoter sequences of isolates from the Philippines by nucleotide position

Isolate ID	-8	-15
H37Rv	T	C
3-2	-	-
3-3	-	-
3-4	-	-
3-5	-	-
3-6	-	-
3-7	-	T
3-8	-	-
3-9	-	-
3-10	-	-
3-11	G	-
3-12	-	-
3-13	-	-
3-14	-	-
3-15	-	-
3-16	-	-
3-17	-	-
3-18	-	-
3-19	-	-
3-20	-	-
3-21	-	T
3-22	-	-
3-23	-	-
3-24	-	-
3-25	-	-
3-26	-	-
3-27	-	-
3-28	-	-
3-29	-	-
3-30	-	-
3-31	-	-
3-32	-	-
3-33	-	-
3-34	-	-

Isolate ID	-8	-15
H37Rv	T	C
3-35	-	-
3-36	-	-
3-37	-	-
3-38	-	-
3-39	-	-
3-40	-	-
3-41	-	T
3-42	-	-
3-43	-	T
3-44	-	-
3-45	-	T
3-46	-	-
3-47	-	-
3-48	-	-
3-49	-	-
3-50	-	-
3-51	-	-
3-52	-	-
3-53	-	T
3-54	-	-
3-55	-	T
3-56	-	-
3-57	-	-
3-58	-	T
3-59	-	-
3-60	-	T
3-61	-	-
3-62	-	-
3-63	-	T
3-64	-	T
3-65	-	T
3-66	-	T
3-67	-	-

Isolate ID	-8	-15
H37Rv	T	C
3-68	-	-
3-69	-	T
3-70	-	-
3-71	-	-
3-72	-	-
3-73	-	-
3-74	-	-
3-76	-	-
3-77	-	T
3-78	-	-
3-79	-	-
3-80	-	T
3-81	-	-
3-82	-	-
3-83	-	T
3-84	-	T
3-85	-	T
3-86	-	-
3-87	-	-
3-88	-	T
3-89	-	-
3-90	-	-
3-91	-	-
3-92	-	-
3-93	-	-
3-94	-	-
3-95	-	-
3-96	-	-
3-97	-	-
3-98	-	-
3-99	-	-
3-100	-	-
3-101	-	T

Table 6.11 – inhA promoter sequences of isolates from the Philippines by nucleotide position (continued)

Isolate ID	-8	-15
H37Rv	T	C
3-102	-	-
3-103	-	-
3-104	-	T
3-105	-	-
3-106	-	T
3-107	-	T
3-108	-	T
3-109	-	T
3-110	-	-
3-111	-	-
3-112	-	-
3-113	-	T
3-114	-	-
3-115	-	-
3-116	-	T
3-117	-	T
3-118	-	-
3-119	-	T
3-120	-	T
3-121	-	T
3-122	-	T
3-123	-	-
3-124	-	-
3-125	-	-

Table 6.12 – inhA promoter sequences of isolates from South Africa by nucleotide position

Isolate ID	-8	-15
H37Rv	T	C
4-1	-	T
4-2	A	-
4-3	-	T
4-4	-	T
4-5	-	T
4-6	-	-
4-7	-	-
4-8	-	T
4-9	A	-
4-10	A	-
4-11	-	T
4-12	-	-
4-13	-	T
4-14	-	-
4-15	-	-
4-16	-	T
4-17	A	-
4-18	-	-
4-19	A	-
4-20	A	-
4-21	A	-
4-22	A	-
4-23	A	-
4-24	A	-
4-25	A	-
4-26	A	-
4-27	A	-
4-28	A	-
4-29	A	-
4-30	A	-
4-31	A	-
4-32	A	-
4-33	A	-

Isolate ID	-8	-15
H37Rv	T	C
4-34	A	-
4-35	A	-
4-36	A	-
4-37	A	-
4-38	A	-
4-39	A	-
4-40	A	-
4-41	A	-
4-42	A	-
4-43	A	-
4-44	A	-
4-45	A	-
4-46	A	-
4-47	A	-
4-48	A	-
4-49	A	-
4-50	-	T
4-51	-	-
4-52	-	-
4-53	-	-
4-54	-	T
4-55	-	T
4-56	-	T
4-57	-	-
4-58	-	T
4-59	-	T
4-60	-	T
4-61	-	T
4-62	-	T
4-63	-	T
4-64	-	T
4-65	-	T
4-66	-	-

Isolate ID	-8	-15
H37Rv	T	C
4-67	-	T
4-68	-	-
4-69	-	-
4-70	-	-
4-71	-	-
4-72	-	T
4-73	-	T
4-74	-	T
4-75	-	-
4-76	-	-
4-77	-	-
4-78	-	-
4-79	-	-
4-80	-	-
4-81	-	-
4-82	-	-
4-83	-	-
4-84	-	-
4-85	-	-
4-86	-	T
4-87	-	-
4-88	-	-
4-89	-	-
4-90	-	-
4-91	-	T
4-92	-	T
4-93	-	T
4-94	-	-
4-95	-	T
4-96	-	-
4-97	-	T
4-98	-	T
4-99	-	T
4-100	-	-

Table 6.13 – ahpC promoter sequences of isolates from India by nucleotide position

Isolate ID	-39	-46
H37Rv	C	G
1-1	-	-
1-2	-	-
1-3	-	A
1-4	-	-
1-5	-	A
1-6	-	-
1-7	-	-
1-8	-	-
1-9	-	-
1-10	-	-
1-11	-	-
1-12	-	-
1-13	-	-
1-14	-	-
1-15	-	-
1-16	-	A
1-17	-	-
1-18	-	-
1-19	-	-
1-20	-	A
1-21	-	A
1-22	-	-
1-23	-	-
1-24	-	-
1-25	-	-
1-26	-	-
1-27	-	-
1-28	-	-
1-29	-	-
1-30	-	A
1-31	-	-
1-32	-	-
1-33	-	-

Isolate ID	-39	-46
H37Rv	C	G
1-34	-	-
1-35	-	-
1-36	-	-
1-37	-	-
1-38	-	A
1-39	-	-
1-40	-	-
1-41	-	-
1-42	-	-
1-43	-	-
1-44	-	-
1-45	-	-
1-46	-	-
1-47	-	-
1-48	-	-
1-49	-	-
1-50	-	A
1-51	-	-
1-52	-	-
1-53	-	A
1-54	-	-
1-55	-	A
1-56	-	-
1-57	-	-
1-58	-	-
1-59	-	-
1-60	-	-
1-61	-	-
1-62	-	-
1-63	-	-
1-64	-	-
1-65	-	-
1-66	-	-

Isolate ID	-39	-46
H37Rv	C	G
1-67	-	-
1-68	-	-
1-69	-	-
1-70	-	-
1-71	-	-
1-72	-	-
1-73	-	-
1-74	-	-
1-75	-	-
1-76	-	-
1-77	-	-
1-78	-	A
1-79	-	-
1-80	-	-
1-81	-	-
1-82	-	A
1-83	-	-
1-84	-	-
1-85	-	A
1-86	-	-
1-87	-	-
1-88	-	-
1-89	-	-
1-90	-	-
1-91	-	A
1-92	-	-
1-93	-	A
1-94	-	A
1-95	-	A
1-96	-	A

Table 6.14 – gyrA sequences of isolates from India by codon

Isolate ID	74	88	89	90	91	92	93	94	95
H37Rv	GCC	GGC	GAC	GCG	TCG	ATC	TAC	GAC	AGC
1-1	-	-	-	-	-	-	-	AAC	ACC
1-2	-	-	-	-	-	-	-	-	-
1-3	-	-	-	-	-	-	-	GGC	ACC
1-4	-	-	-	-	-	-	-	TAC	-
1-5	-	-	-	GTG	-	-	-	-	ACC
1-6	-	-	-	-	-	-	-	-	ACC
1-7	-	-	-	GTG	-	-	-	-	ACC
1-8	-	-	-	-	-	-	-	AAC	ACC
1-9	-	-	-	-	-	-	-	GCC	ACC
1-10	-	-	-	-	-	-	-	AAC	ACC
1-11	-	-	-	-	-	-	-	GCC	ACC
1-12	-	-	-	-	-	-	-	GGC	ACC
1-13	-	-	-	-	-	-	-	GGC	ACC
1-14	-	-	-	-	-	-	-	GGC	ACC
1-15	-	-	-	-	-	-	-	-	-
1-16	-	-	-	-	-	-	-	GGC	ACC
1-17	-	-	-	-	-	-	-	GGC	ACC
1-18	-	-	-	-	-	-	-	GCC	-
1-19	-	-	-	-	-	-	-	GGC	ACC
1-20	-	-	-	-	-	-	-	GGC	ACC
1-21	-	-	-	-	-	-	-	GGC	ACC
1-22	-	-	-	-	-	-	-	GGC	ACC
1-23	-	-	-	-	-	-	-	GCC	ACC
1-24	-	-	-	-	-	-	-	GGC	ACC
1-25	-	-	-	-	-	-	-	AAC	ACC
1-26	-	-	-	-	-	-	-	GCC	ACC
1-27	-	-	-	-	-	-	-	CAC	ACC
1-28	-	-	-	-	-	-	-	GGC	ACC
1-29	-	-	-	-	-	-	-	GGC	ACC
1-30	-	-	-	-	-	-	-	AAC	ACC
1-31	-	-	-	-	-	-	-	GGC	ACC
1-32	-	-	-	-	-	-	-	-	ACC
1-33	-	-	-	-	-	-	-	GCC	ACC

Table 6.14 – gyrA sequences of isolates from India by codon (continued)

Isolate ID	74	88	89	90	91	92	93	94	95
H37Rv	GCC	GGC	GAC	GCG	TCG	ATC	TAC	GAC	AGC
1-34	-	-	-	-	-	-	-	GCC	ACC
1-35	-	-	-	-	-	-	-	GGC	ACC
1-36	-	-	-	-	-	-	-	GGC	ACC
1-37	-	-	-	-	-	-	-	GGC	ACC
1-38	-	-	-	-	-	-	-	AAC	ACC
1-39	-	-	-	-	-	-	-	GGC	ACC
1-40	-	-	-	-	-	-	-	GGC	ACC
1-41	-	-	-	-	-	-	-	GGC	ACC
1-42	-	-	-	-	-	-	-	GGC	ACC
1-43	-	-	-	-	-	-	-	-	-
1-44	-	-	-	-	-	-	-	GGC	ACC
1-45	-	-	-	-	-	-	-	GGC	ACC
1-46	-	-	-	-	-	-	-	GGC	ACC
1-47	-	-	-	-	-	-	-	GGC	ACC
1-48	-	-	-	-	-	-	-	GGC	ACC
1-49	-	-	-	-	-	-	-	GCC	ACC
1-50	-	-	-	-	-	-	-	TAC	ACC
1-51	-	-	-	-	-	-	-	GGC	ACC
1-52	-	-	-	-	-	-	-	GCC	ACC
1-53	-	-	-	-	-	-	-	GCC	ACC
1-54	-	-	-	-	-	-	-	GGC	ACC
1-55	-	-	-	GTG	-	-	-	-	ACC
1-56	-	-	-	-	-	-	-	GGC	ACC
1-57	-	-	-	-	-	-	-	GCC	ACC
1-58	-	-	-	-	-	-	-	GCC	ACC
1-59	-	-	-	-	-	-	-	CAC	ACC
1-60	-	-	-	-	-	-	-	GGC	ACC
1-61	-	-	-	-	-	-	-	GGC	ACC
1-62	-	-	-	-	-	-	-	GGC	ACC
1-63	-	-	-	-	-	-	-	-	ACC
1-64	-	-	-	-	-	-	-	GGC	ACC
1-65	-	-	-	-	-	-	-	AAC	ACC
1-66	-	-	-	-	-	-	-	GGC	ACC

Table 6.14 – gyrA sequences of isolates from India by codon (continued)

Isolate ID	74	88	89	90	91	92	93	94	95
H37Rv	GCC	GGC	GAC	GCG	TCG	ATC	TAC	GAC	AGC
1-67	-	-	-	-	-	-	-	AAC	ACC
1-68	-	-	-	-	-	-	-	GGC	ACC
1-69	-	-	-	-	-	-	-	AAC	ACC
1-70	-	-	-	-	-	-	-	-	ACC
1-71	-	-	-	-	-	-	-	GGC	ACC
1-72	-	-	-	GTG	-	-	-	-	ACC
1-73	-	-	-	-	-	-	-	-	ACC
1-74	-	-	-	GTG	-	-	-	-	ACC
1-75	-	-	-	-	-	-	-	GGC	ACC
1-76	-	TGC	-	-	-	-	-	-	-
1-77	-	-	-	GTG	-	-	-	-	ACC
1-78	-	-	-	GTG	-	-	-	-	ACC
1-79	-	-	-	-	-	-	-	TAC	ACC
1-80	-	-	-	GTG	-	-	-	-	ACC
1-81	-	-	-	GTG	-	-	-	-	ACC
1-82	-	-	-	-	-	-	-	-	ACC
1-83	-	-	-	GTG	-	-	-	-	-
1-84	-	-	-	GTG	-	-	-	-	ACC
1-85	-	-	-	-	-	-	-	-	ACC
1-86	-	-	-	-	-	-	-	AAC	ACC
1-87	-	-	-	GTG	-	-	-	-	ACC
1-88	-	-	-	-	-	-	-	GCC	ACC
1-89	-	-	-	GTG	-	-	-	-	ACC
1-90	-	-	-	GTG	-	-	-	-	ACC
1-91	-	-	-	GTG	-	-	-	-	ACC
1-92	-	-	-	GTG	-	-	-	-	ACC
1-93	-	-	-	-	-	-	-	-	ACC
1-94	-	-	-	-	-	-	-	-	ACC
1-95	-	-	-	-	-	-	-	-	ACC
1-96	-	-	-	-	-	-	-	-	ACC

Table 6.15 – gyrA sequences of isolates from Moldova by codon

Isolate ID	74	88	89	90	91	92	93	94	95
H37Rv	GCC	GGC	GAC	GCG	TCG	ATC	TAC	GAC	AGC
2-1	-	-	-	-	-	-	-	TAC	ACC
2-2	-	-	-	-	-	-	-	-	ACC
2-3	-	-	-	-	-	-	-	GGC	ACC
2-4	-	-	-	-	-	-	-	-	ACC
2-5	-	-	-	-	-	-	-	TAC	ACC
2-6	-	-	-	-	-	-	-	-	ACC
2-7	-	-	-	-	-	-	-	GGC	ACC
2-8	-	-	-	-	-	-	-	-	ACC
2-9	-	-	-	-	-	-	-	GGC	ACC
2-10	-	-	-	-	-	-	-	-	ACC
2-11	-	-	-	-	-	-	-	-	ACC
2-12	-	-	-	-	-	-	-	GNC	ACC
2-13	-	-	-	-	CCG	-	-	-	ACC
2-14	-	-	-	-	CCG	-	-	-	ACC
2-15	-	-	-	GTG	-	-	-	-	ACC
2-16	-	-	-	-	-	-	-	GGC	ACC
2-17	-	-	-	-	-	-	-	AAC	ACC
2-18	-	-	-	GTG	-	-	-	-	ACC
2-19	-	-	-	-	-	-	-	-	ACC
2-20	-	TGC	-	-	-	-	-	-	ACC
2-21	-	-	-	-	-	-	-	TAC	ACC
2-22	-	-	-	-	-	-	-	GGC	ACC
2-23	-	-	-	-	-	-	-	GGC	ACC
2-24	-	-	-	-	-	-	-	TAC	ACC
2-25	-	-	-	-	-	-	-	-	ACC
2-26	-	-	-	GTG	-	-	-	-	ACC
2-27	-	-	-	-	-	-	-	-	ACC
2-28	-	-	-	-	-	-	-	-	ACC
2-29	-	-	-	GTG	-	-	-	-	ACC
2-30	-	-	-	GTG	-	-	-	-	ACC
2-31	-	-	-	-	-	-	-	GCC	ACC
2-32	-	-	-	-	-	-	-	GCC	ACC
2-33	-	-	-	GTG	-	-	-	-	ACC

Table 6.15 – gyrA sequences of isolates from Moldova by codon (continued)

Isolate ID	74	88	89	90	91	92	93	94	95
H37Rv	GCC	GGC	GAC	GCG	TCG	ATC	TAC	GAC	AGC
2-34	-	-	-	GTG	-	-	-	-	ACC
2-35	-	-	-	-	-	-	-	AAC	ACC
2-36	-	-	-	-	-	-	-	GCC	ACC
2-37	-	-	-	GTG	-	-	-	-	ACC
2-38	-	-	-	GTG	-	-	-	-	ACC
2-39	-	-	-	-	-	-	-	-	ACC
2-40	-	-	-	-	-	-	-	GGC	ACC
2-41	-	-	-	-	-	-	-	GGC	ACC
2-42	-	-	-	GTG	-	-	-	-	ACC
2-43	-	-	-	-	-	-	-	GCC	ACC
2-44	-	-	-	-	-	-	-	CAC	ACC
2-45	-	-	-	-	-	-	-	GGC	ACC
2-46	-	-	-	-	-	-	-	-	ACC
2-47	-	-	-	-	-	-	-	-	ACC
2-48	-	-	-	-	-	-	-	-	ACC
2-49	-	-	-	-	-	-	-	GGC	ACC
2-50	-	-	-	GTG	-	-	-	-	ACC
2-51	-	-	-	-	-	-	-	AAC	ACC
2-52	-	-	-	-	-	-	-	GCC	ACC
2-53	-	-	-	-	-	-	-	-	ACC
2-54	-	-	-	-	-	-	-	GCC	ACC
2-55	-	-	-	-	-	-	-	TAC	ACC
2-56	-	-	-	-	-	-	-	-	ACC
2-57	-	-	-	-	-	-	-	TAC	ACC
2-58	-	-	-	-	-	-	-	GGC	ACC
2-59	-	-	-	-	-	-	-	-	ACC
2-60	-	-	-	GTG	-	-	-	-	ACC
2-61	-	-	-	-	-	-	-	-	ACC
2-62	-	-	-	-	-	-	-	GGC	ACC
2-63	-	-	-	GTG	-	-	-	-	ACC
2-64	-	-	-	-	-	-	-	-	ACC
2-65	-	-	-	-	-	-	-	GGC	ACC
2-66	-	-	-	GTG	-	-	-	NAC	ACC

Table 6.15 – gyrA sequences of isolates from Moldova by codon (continued)

Isolate ID	74	88	89	90	91	92	93	94	95
H37Rv	GCC	GGC	GAC	GCG	TCG	ATC	TAC	GAC	AGC
2-67	-	-	-	-	-	-	-	TAC	ACC
2-68	-	-	-	-	-	-	-	TAC	ACC
2-69	-	-	-	-	-	-	-	GCC	ACC
2-70	-	-	-	-	-	-	-	GGC	ACC
2-71	-	-	-	GTG	-	-	-	-	ACC
2-72	-	-	-	-	-	-	-	CAC	ACC
2-73	-	-	-	-	-	-	-	-	ACC
2-74	-	-	-	-	-	-	-	-	ACC
2-75	-	-	-	-	-	-	-	-	-
2-76	-	-	-	-	-	-	-	-	-
2-77	-	-	-	-	-	-	-	-	ACC
2-78	-	-	-	-	-	-	-	-	-
2-79	-	-	-	GTG	-	-	-	-	ACC
2-80	-	-	-	-	-	-	-	-	ACC
2-81	-	-	-	-	-	-	-	-	ACC
2-82	-	-	-	-	-	-	-	-	ACC
2-83	-	-	-	-	-	-	-	GNC	ACC
2-84	-	-	-	-	CCG	-	-	-	ACC
2-85	-	-	-	-	-	-	-	-	ACC
2-86	-	-	-	GTG	-	-	-	-	ACC
2-87	-	-	-	-	-	-	-	GGC	ACC
2-88	-	-	-	GTG	-	-	-	-	ACC

Table 6.16 – gyrA sequences of isolates from the Philippines by codon

Isolate ID	74	88	89	90	91	92	93	94	95
H37Rv	GCC	GGC	GAC	GCG	TCG	ATC	TAC	GAC	AGC
3-2	-	-	-	-	-	-	-	-	ACC
3-3	-	-	-	-	-	-	-	-	ACC
3-4	-	-	-	-	-	-	-	GGC	ACC
3-5	-	-	-	-	-	-	-	-	ACC
3-6	-	-	-	-	-	-	-	-	ACC
3-7	-	-	-	-	-	-	-	AAC	ACC
3-8	-	-	-	GTG	-	-	-	-	-
3-9	-	-	-	-	-	-	-	-	ACC
3-10	-	-	-	-	-	-	-	-	ACC
3-11	-	-	-	GTG	-	-	-	-	ACC
3-12	-	-	-	-	-	-	-	-	ACC
3-13	-	-	-	-	-	-	-	GGC	ACC
3-14	-	-	-	-	-	-	-	-	ACC
3-15	-	-	-	-	-	-	-	-	ACC
3-16	-	-	-	-	-	-	-	-	ACC
3-17	-	-	-	-	-	-	-	-	ACC
3-18	-	-	-	-	-	-	-	GGC	ACC
3-19	-	-	-	-	-	-	-	GGC	ACC
3-20	-	-	-	GTG	-	-	-	-	ACC
3-21	-	-	-	-	-	-	-	-	ACC
3-22	-	-	-	-	-	-	-	GGC	ACC
3-23	-	-	-	-	-	-	-	-	ACC
3-24	-	-	-	-	-	-	-	-	ACC
3-25	-	-	-	-	-	-	-	-	ACC
3-26	-	-	-	-	-	-	-	-	ACC
3-27	-	-	-	-	-	-	-	-	ACC
3-28	-	-	-	GTG	-	-	-	-	ACC
3-29	-	-	-	GTG	-	-	-	-	ACC
3-30	-	-	-	-	-	-	-	-	ACC
3-31	-	-	-	-	-	-	-	GGC	ACC
3-32	-	-	-	-	-	-	-	TAC	ACC
3-33	-	-	-	-	-	-	-	-	ACC
3-34	-	-	-	-	-	-	-	-	ACC

Table 6.16 – gyrA sequences of isolates from the Philippines by codon (continued)

Isolate ID	74	88	89	90	91	92	93	94	95
H37Rv	GCC	GGC	GAC	GCG	TCG	ATC	TAC	GAC	AGC
3-35	-	-	-	-	-	-	-	-	ACC
3-36	-	-	-	-	-	-	-	-	ACC
3-37	-	-	-	-	-	-	-	-	ACC
3-38	-	-	-	-	-	-	-	-	ACC
3-39	-	-	-	-	-	-	-	-	ACC
3-40	-	-	-	-	-	-	-	-	ACC
3-41	-	-	-	-	-	-	-	-	ACC
3-42	-	-	-	-	-	-	-	-	-
3-43	-	-	-	-	-	-	-	-	ACC
3-44	-	-	-	-	-	-	-	-	ACC
3-45	-	-	-	-	-	-	-	-	ACC
3-46	-	-	-	-	-	-	-	-	ACC
3-47	-	-	-	-	-	-	-	-	ACC
3-48	-	-	-	-	-	-	-	-	ACC
3-49	-	-	-	-	-	-	-	-	ACC
3-50	-	-	-	-	-	-	-	-	ACC
3-51	-	-	-	-	-	-	-	-	ACC
3-52	-	-	-	-	-	-	-	-	ACC
3-53	-	-	-	-	-	-	-	GGC	ACC
3-54	-	-	-	-	-	-	-	-	ACC
3-55	-	-	-	-	-	-	-	-	ACC
3-56	-	-	-	-	-	-	-	-	ACC
3-57	-	-	-	-	-	-	-	-	ACC
3-58	-	-	-	-	-	-	-	-	ACC
3-59	-	-	-	-	-	-	-	-	ACC
3-60	-	-	-	-	-	-	-	GGC	ACC
3-61	-	-	-	-	-	-	-	-	ACC
3-62	-	-	-	GTG	-	-	-	-	ACC
3-63	-	-	-	-	-	-	-	-	ACC
3-64	-	-	-	-	-	-	-	-	ACC
3-65	-	-	-	-	-	-	-	-	ACC
3-66	-	-	-	-	-	-	-	-	ACC
3-67	-	-	-	-	-	-	-	GGC	ACC

Table 6.16 – gyrA sequences of isolates from the Philippines by codon (continued)

Isolate ID	74	88	89	90	91	92	93	94	95
H37Rv	GCC	GGC	GAC	GCG	TCG	ATC	TAC	GAC	AGC
3-68	-	-	-	-	-	-	-	-	ACC
3-69	-	-	-	-	-	-	-	GGC	ACC
3-70	-	-	-	-	-	-	-	-	ACC
3-71	-	-	-	-	-	-	-	-	ACC
3-72	-	-	-	-	-	-	-	GGC	ACC
3-73	-	-	-	GTG	-	-	-	-	ACC
3-74	-	-	-	-	-	-	-	-	ACC
3-76	-	-	-	-	-	-	-	GGC	ACC
3-77	-	-	-	GTG	-	-	-	-	ACC
3-78	-	-	-	-	-	-	-	-	ACC
3-79	-	-	-	-	-	-	-	TAC	ACC
3-80	-	-	-	-	-	-	-	GGC	ACC
3-81	-	-	-	-	-	-	-	-	ACC
3-82	-	-	-	-	-	-	-	-	ACC
3-83	-	-	-	-	-	-	-	-	ACC
3-84	-	-	-	-	-	-	-	-	ACC
3-85	-	-	-	-	-	-	-	-	ACC
3-86	-	-	-	-	-	-	-	-	ACC
3-87	-	-	-	-	-	-	-	-	ACC
3-88	-	-	-	-	-	-	-	-	ACC
3-89	-	-	-	-	-	-	-	-	ACC
3-90	-	-	-	GTG	-	-	-	TAC	ACC
3-91	-	-	-	-	-	-	-	-	ACC
3-92	-	-	-	-	-	-	-	-	ACC
3-93	-	-	-	-	-	-	-	GCC	ACC
3-94	-	-	-	-	-	-	-	-	ACC
3-95	-	-	-	-	-	-	-	-	ACC
3-96	-	-	-	-	-	-	-	-	ACC
3-97	-	-	-	-	-	-	-	-	ACC
3-98	-	-	-	-	-	-	-	-	ACC
3-99	-	-	-	-	-	-	-	-	ACC
3-100	-	-	-	-	-	-	-	-	ACC

Table 6.16 – gyrA sequences of isolates from the Philippines by codon (continued)

Isolate ID	74	88	89	90	91	92	93	94	95
H37Rv	GCC	GGC	GAC	GCG	TCG	ATC	TAC	GAC	AGC
3-101	-	-	-	-	-	-	-	-	ACC
3-102	-	-	-	GTG	-	-	-	-	ACC
3-103	-	-	-	-	-	-	-	-	ACC
3-104	-	-	-	-	-	-	-	TAC	ACC
3-105	-	-	-	GTG	-	-	-	-	ACC
3-106	-	-	-	-	-	-	-	-	ACC
3-107	-	-	-	GTG	-	-	-	-	ACC
3-108	-	-	-	GTG	-	-	-	-	ACC
3-109	-	-	-	GTG	-	-	-	-	ACC
3-110	-	-	-	-	-	-	-	-	ACC
3-111	-	-	-	-	-	-	-	-	ACC
3-112	-	-	-	-	-	-	-	-	ACC
3-113	-	-	-	-	-	-	-	-	ACC
3-114	-	-	-	-	-	-	-	-	ACC
3-115	-	-	-	-	-	-	-	-	ACC
3-116	-	-	-	-	-	-	-	-	ACC
3-117	-	-	-	-	-	-	-	-	ACC
3-118	-	-	-	-	-	-	-	-	ACC
3-119	-	-	-	-	-	-	-	-	ACC
3-120	-	-	-	-	-	-	-	-	ACC
3-121	-	-	-	-	-	-	-	-	ACC
3-122	-	-	-	-	-	-	-	-	ACC
3-123	-	-	-	-	-	-	-	-	ACC
3-124	-	-	-	-	-	-	-	-	ACC
3-125	-	-	-	-	-	-	-	-	ACC

Table 6.17 – gyrA sequences of isolates from South Africa by codon

Isolate ID	74	88	89	90	91	92	93	94	95
H37Rv	GCC	GGC	GAC	GCG	TCG	ATC	TAC	GAC	AGC
4-1	-	-	-	-	-	-	-	GGC	ACC
4-2	-	-	-	-	-	-	-	GGC	ACC
4-3	-	-	-	-	-	-	-	-	ACC
4-4	-	-	-	-	-	-	-	-	ACC
4-5	-	-	-	-	-	-	-	GGC	ACC
4-6	-	-	-	-	-	-	-	GGC	ACC
4-7	-	-	-	-	-	-	-	GGC	ACC
4-8	-	-	-	-	-	-	-	GGC	ACC
4-9	-	-	-	GTG	-	-	-	-	ACC
4-10	-	-	-	GTG	-	-	-	-	ACC
4-11	-	-	-	GTG	-	-	-	-	ACC
4-12	-	-	-	-	-	-	-	GGC	ACC
4-13	-	-	-	-	-	-	-	GGC	ACC
4-14	-	-	-	-	-	-	-	GGC	-
4-15	-	-	-	-	-	-	-	GGC	ACC
4-16	-	-	-	-	-	-	-	GGC	ACC
4-17	-	-	-	GTG	-	-	-	-	ACC
4-18	-	-	-	GTG	-	-	-	-	ACC
4-19	-	-	-	GTG	-	-	-	-	ACC
4-20	-	-	-	GTG	-	-	-	-	ACC
4-21	-	-	-	GTG	-	-	-	-	ACC
4-22	-	-	-	GTG	-	-	-	-	ACC
4-23	-	-	-	GTG	-	-	-	-	ACC
4-24	-	-	-	GTG	-	-	-	-	ACC
4-25	-	-	-	GTG	-	-	-	-	ACC
4-26	-	-	-	GTG	-	-	-	-	ACC
4-27	-	-	-	GTG	-	-	-	-	ACC
4-28	-	-	-	GTG	-	-	-	-	ACC
4-29	-	-	-	GTG	-	-	-	-	ACC
4-30	-	-	-	GTG	-	-	-	-	ACC
4-31	-	-	-	GTG	-	-	-	-	ACC
4-32	-	-	-	GTG	-	-	-	-	ACC
4-33	-	-	-	GTG	-	-	-	-	ACC

Table 6.17 – gyrA sequences of isolates from South Africa by codon (continued)

Isolate ID	74	88	89	90	91	92	93	94	95
H37Rv	GCC	GGC	GAC	GCG	TCG	ATC	TAC	GAC	AGC
4-34	-	-	-	GTG	-	-	-	-	ACC
4-35	-	-	-	GTG	-	-	-	-	ACC
4-36	-	-	-	GTG	-	-	-	-	ACC
4-37	-	-	-	GTG	-	-	-	-	ACC
4-38	-	-	-	GTG	-	-	-	-	ACC
4-39	-	-	-	GTG	-	-	-	-	ACC
4-40	-	-	-	GTG	-	-	-	-	ACC
4-41	-	-	-	GTG	-	-	-	-	ACC
4-42	-	-	-	GTG	-	-	-	-	ACC
4-43	-	-	-	GTG	-	-	-	-	ACC
4-44	-	-	-	-	-	-	-	-	ACC
4-45	-	-	-	GTG	-	-	-	-	ACC
4-46	-	-	-	GTG	-	-	-	-	ACC
4-47	-	-	-	GTG	-	-	-	-	ACC
4-48	-	-	-	GTG	-	-	-	-	ACC
4-49	-	-	-	GTG	-	-	-	-	ACC
4-50	-	-	-	-	-	-	-	TAC	ACC
4-51	-	-	-	-	-	-	-	GGC	ACC
4-52	-	-	-	-	-	-	-	AAC	ACC
4-53	-	-	-	-	-	-	-	GGC	ACC
4-54	-	-	-	-	-	-	-	GGC	ACC
4-55	-	-	-	-	-	-	-	GGC	ACC
4-56	-	-	-	GTG	-	-	-	-	ACC
4-57	-	-	-	-	-	-	-	AAC	ACC
4-58	-	-	-	-	-	-	-	AAC	ACC
4-59	-	-	-	-	-	-	-	-	ACC
4-60	-	-	-	-	-	-	-	GGC	ACC
4-61	-	-	-	GTG	-	-	-	-	ACC
4-62	-	-	-	-	-	-	-	GGC	ACC
4-63	-	-	-	-	-	-	-	GGC	ACC
4-64	-	-	-	-	-	-	-	GGC	ACC
4-65	-	-	-	-	-	-	-	GGC	ACC
4-66	-	-	-	GTG	-	-	-	-	ACC

Table 6.17 – gyrA sequences of isolates from South Africa by codon (continued)

Isolate ID	74	88	89	90	91	92	93	94	95
H37Rv	GCC	GGC	GAC	GCG	TCG	ATC	TAC	GAC	AGC
4-67	-	-	-	-	-	-	-	GGC	ACC
4-68	-	-	-	-	-	-	-	GGC	ACC
4-69	-	-	-	-	-	-	-	-	ACC
4-70	-	-	-	-	-	-	-	GGC	ACC
4-71	-	-	-	-	-	-	-	GGC	ACC
4-72	-	-	-	-	-	-	-	AAC	ACC
4-73	-	-	-	-	-	-	-	GCC	ACC
4-74	-	-	-	-	-	-	-	GCC	ACC
4-75	-	-	-	-	-	-	-	-	ACC
4-76	-	-	-	-	-	-	-	-	ACC
4-77	-	-	-	-	-	-	-	-	ACC
4-78	-	-	-	-	-	-	-	-	ACC
4-79	-	-	-	-	-	-	-	-	ACC
4-80	-	-	-	-	-	-	-	-	ACC
4-81	-	-	-	-	-	-	-	-	ACC
4-82	-	-	-	-	-	-	-	-	ACC
4-83	-	-	-	-	-	-	-	-	ACC
4-84	-	-	-	-	-	-	-	-	-
4-85	-	-	-	-	-	-	-	-	ACC
4-86	-	-	-	-	-	-	-	GGC	ACC
4-87	-	-	-	-	-	-	-	AAC	ACC
4-88	-	-	-	GTG	-	-	-	-	ACC
4-89	-	-	-	-	-	-	-	AAC	ACC
4-90	-	-	-	-	-	-	-	AAC	ACC
4-91	-	-	-	-	-	-	-	GGC	ACC
4-92	-	-	-	-	-	-	-	GGC	ACC
4-93	-	-	-	-	-	-	-	GGC	ACC
4-94	-	-	-	-	-	-	-	GGC	ACC
4-95	-	-	-	-	-	-	-	-	ACC
4-96	-	-	-	GTG	-	-	-	-	ACC
4-97	-	-	-	-	-	-	-	-	ACC
4-98	-	-	-	-	-	-	-	GCC	ACC
4-99	-	-	-	-	-	-	-	-	ACC
4-100	-	-	-	-	-	-	-	GGC	ACC

Table 6.18 – gyrB sequences of select isolates by codon

Isolate ID	Origin	505	510	511	512	514	515
H37Rv	-	GAC	AAC	ACC	GAA	CAG	GCG
1-23	India	-	-	-	-	-	GTG
1-52	India	-	ACC	-	-	-	-
1-58	India	-	AGC	-	-	-	-
1-65	India	-	-	-	GAC	-	-
1-73	India	-	-	-	-	-	GTG
2-51	Moldova	-	-	-	-	-	GTG

Table 6.19 – rrs sequences of isolates from India by nucleotide position

Isolate ID	1401	1402	1484
H37Rv	A	C	G
1-1	G	-	-
1-2	-	-	-
1-3	-	-	-
1-4	G	-	-
1-5	-	-	T
1-6	-	-	-
1-7	-	-	-
1-8	G	-	-
1-9	G	-	-
1-10	G	-	-
1-11	G	-	-
1-12	G	-	-
1-13	G	-	-
1-14	-	-	-
1-15	G	-	-
1-16	G	-	-
1-17	-	-	-
1-18	G	-	-
1-19	G	-	-
1-20	-	-	-
1-21	G	-	-
1-22	G	-	-
1-23	G	-	-
1-24	C	-	-
1-25	G	-	-
1-26	-	-	-
1-27	G	-	-
1-28	-	-	-
1-29	G	-	-
1-30	-	-	T
1-31	G	-	-
1-32	G	-	-
1-33	-	-	-

Isolate ID	1401	1402	1484
H37Rv	A	C	G
1-34	G	-	-
1-35	-	-	-
1-36	G	-	-
1-37	-	-	-
1-38	G	-	-
1-39	G	-	-
1-40	C	-	-
1-41	G	-	-
1-42	G	-	-
1-43	G	-	-
1-44	G	-	-
1-45	G	-	-
1-46	-	-	-
1-47	G	-	-
1-48	G	-	-
1-49	G	-	-
1-50	-	-	-
1-51	G	-	-
1-52	G	-	-
1-53	G	-	-
1-54	G	-	-
1-55	G	-	-
1-56	G	-	-
1-57	G	-	-
1-58	G	-	-
1-59	G	-	-
1-60	-	-	-
1-61	G	-	-
1-62	G	-	-
1-63	G	-	-
1-64	G	-	-
1-65	G	-	-
1-66	G	-	-

Isolate ID	1401	1402	1484
H37Rv	A	C	G
1-67	G	-	-
1-68	-	-	-
1-69	-	-	-
1-70	-	-	-
1-71	G	-	-
1-72	G	-	-
1-73	G	-	-
1-74	G	-	-
1-75	G	-	-
1-76	G	-	-
1-77	G	-	-
1-78	G	-	-
1-79	G	-	-
1-80	G	-	-
1-81	G	-	-
1-82	-	-	-
1-83	-	-	-
1-84	G	-	-
1-85	-	-	-
1-86	G	-	-
1-87	G	-	-
1-88	-	-	-
1-89	G	-	-
1-90	G	-	-
1-91	G	-	-
1-92	G	-	-
1-93	-	-	-
1-94	-	-	-
1-95	-	-	-
1-96	-	-	-

Table 6.20 – rrs sequences of isolates from Moldova by nucleotide position

Isolate ID	1401	1402	1484
H37Rv	A	C	G
2-1	-	-	-
2-2	-	-	-
2-3	G	-	-
2-4	-	-	-
2-5	G	-	-
2-6	-	-	-
2-7	G	-	-
2-8	-	-	-
2-9	-	-	-
2-10	-	-	-
2-11	-	-	-
2-12	-	-	-
2-13	-	-	-
2-14	-	-	-
2-15	-	-	-
2-16	-	-	-
2-17	-	-	-
2-18	-	-	-
2-19	-	-	-
2-20	-	-	-
2-21	-	-	-
2-22	-	-	-
2-23	-	-	-
2-24	-	-	-
2-25	G	-	-
2-26	-	-	-
2-27	-	-	-
2-28	-	-	-
2-29	-	-	-
2-30	G	-	-
2-31	-	-	-
2-32	G	-	-
2-33	G	-	-

Isolate ID	1401	1402	1484
H37Rv	A	C	G
2-34	G	-	-
2-35	-	-	-
2-36	-	-	-
2-37	-	-	-
2-38	-	-	-
2-39	G	-	-
2-40	G	-	-
2-41	-	-	-
2-42	-	-	T
2-43	-	-	-
2-44	-	-	-
2-45	-	-	-
2-46	-	-	-
2-47	-	-	-
2-48	G	-	-
2-49	-	-	-
2-50	-	-	-
2-51	-	-	-
2-52	-	-	-
2-53	-	-	-
2-54	-	-	-
2-55	-	-	-
2-56	-	-	-
2-57	G	-	-
2-58	G	-	-
2-59	-	-	-
2-60	G	-	-
2-61	-	-	-
2-62	G	-	-
2-63	A	-	-
2-64	-	-	-
2-65	-	-	-
2-66	-	-	-

Isolate ID	1401	1402	1484
H37Rv	A	C	G
2-67	G	-	-
2-68	-	-	-
2-69	G	-	-
2-70	-	-	-
2-71	-	-	-
2-72	-	-	-
2-73	-	-	-
2-74	-	-	-
2-75	-	-	-
2-76	-	-	-
2-77	-	-	-
2-78	-	-	-
2-79	-	-	-
2-80	-	-	-
2-81	-	-	-
2-82	G	-	-
2-83	-	-	-
2-84	-	-	-
2-85	-	-	-
2-86	G	-	-
2-87	G	-	-
2-88	-	-	-

Table 6.21 – rrs sequences of isolates from the Philippines by nucleotide position

Isolate ID	1401	1402	1484
H37Rv	A	C	G
3-2	G	-	-
3-3	G	-	-
3-4	G	-	-
3-5	G	-	-
3-6	-	-	-
3-7	G	-	-
3-8	G	-	-
3-9	-	-	-
3-10	-	-	-
3-11	-	-	-
3-12	-	-	-
3-13	-	-	-
3-14	-	-	-
3-15	-	-	-
3-16	-	-	-
3-17	-	-	-
3-18	-	-	-
3-19	-	-	-
3-20	-	-	-
3-21	-	-	-
3-22	-	-	-
3-23	G	-	-
3-24	-	-	-
3-25	-	-	-
3-26	-	-	-
3-27	-	-	-
3-28	-	-	-
3-29	-	-	-
3-30	-	-	-
3-31	-	-	-
3-32	-	-	-
3-33	-	-	-
3-34	-	-	-

Isolate ID	1401	1402	1484
H37Rv	A	C	G
3-35	G	-	-
3-36	G	-	-
3-37	-	-	-
3-38	G	-	-
3-39	-	-	-
3-40	-	-	-
3-41	-	-	-
3-42	-	-	-
3-43	-	-	-
3-44	-	-	-
3-45	-	-	-
3-46	-	-	-
3-47	-	-	-
3-48	-	-	-
3-49	-	-	-
3-50	-	-	-
3-51	-	-	-
3-52	-	-	-
3-53	-	-	-
3-54	-	-	-
3-55	-	-	-
3-56	-	-	-
3-57	-	-	-
3-58	-	-	-
3-59	-	-	-
3-60	-	-	-
3-61	G	-	-
3-62	G	-	-
3-63	-	-	-
3-64	G	-	-
3-65	G	-	-
3-66	-	-	-
3-67	-	-	-

Isolate ID	1401	1402	1484
H37Rv	A	C	G
3-68	G	-	-
3-69	G	-	-
3-70	G	-	-
3-71	-	-	-
3-72	-	-	-
3-73	-	-	-
3-74	-	-	-
3-76	-	-	-
3-77	-	-	-
3-78	-	-	-
3-79	-	-	-
3-80	-	-	-
3-81	-	-	-
3-82	-	-	-
3-83	-	-	-
3-84	-	-	-
3-85	-	-	-
3-86	-	-	-
3-87	-	-	-
3-88	-	-	-
3-89	-	-	-
3-90	-	-	-
3-91	-	-	-
3-92	-	-	-
3-93	-	-	-
3-94	-	-	-
3-95	-	-	-
3-96	-	-	-
3-97	-	-	-
3-98	-	-	-
3-99	-	-	-
3-100	-	-	-
3-101	G	-	-

Table 6.21 – rrs sequences of isolates from the Philippines by nucleotide position (continued)

Isolate ID	1401	1402	1484
H37Rv	A	C	G
3-102	-	-	-
3-103	-	-	-
3-104	-	-	-
3-105	-	-	-
3-106	-	-	-
3-107	-	-	-
3-108	-	-	-
3-109	-	-	-
3-110	-	-	-
3-111	-	-	-
3-112	-	-	-
3-113	-	-	-
3-114	-	-	-
3-115	-	-	-
3-116	-	-	-
3-117	-	-	-
3-118	-	-	-
3-119	-	-	-
3-120	-	-	-
3-121	-	-	-
3-122	-	-	-
3-123	-	-	-
3-124	-	-	-
3-125	-	-	-

Table 6.22 – rrs sequences of isolates from South Africa by nucleotide position

Isolate ID	1401	1402	1484
H37Rv	A	C	G
4-1	G	-	-
4-2	G	-	-
4-3	-	-	-
4-4	G	-	-
4-5	G	-	-
4-6	G	-	-
4-7	G	-	-
4-8	G	-	-
4-9	G	-	-
4-10	G	-	-
4-11	-	-	-
4-12	G	-	-
4-13	G	-	-
4-14	-	-	-
4-15	G	-	-
4-16	G	-	-
4-17	G	-	-
4-18	-	-	-
4-19	G	-	-
4-20	G	-	-
4-21	G	-	-
4-22	G	-	-
4-23	G	-	-
4-24	G	-	-
4-25	G	-	-
4-26	G	-	-
4-27	G	-	-
4-28	G	-	-
4-29	G	-	-
4-30	G	-	-
4-31	G	-	-
4-32	G	-	-
4-33	G	-	-

Isolate ID	1401	1402	1484
H37Rv	A	C	G
4-34	G	-	-
4-35	G	-	-
4-36	G	-	-
4-37	G	-	-
4-38	G	-	-
4-39	G	-	-
4-40	G	-	-
4-41	G	-	-
4-42	G	-	-
4-43	G	-	-
4-44	-	-	-
4-45	G	-	-
4-46	G	-	-
4-47	G	-	-
4-48	G	-	-
4-49	G	-	-
4-50	G	-	-
4-51	G	-	-
4-52	G	-	-
4-53	G	-	-
4-54	G	-	-
4-55	G	-	-
4-56	G	-	-
4-57	-	-	-
4-58	G	-	-
4-59	G	-	-
4-60	G	-	-
4-61	G	-	-
4-62	G	-	-
4-63	G	-	-
4-64	G	-	-
4-65	G	-	-
4-66	G	-	-

Isolate ID	1401	1402	1484
H37Rv	A	C	G
4-67	G	-	-
4-68	G	-	-
4-69	-	-	-
4-70	G	-	-
4-71	G	-	-
4-72	G	-	-
4-73	G	-	-
4-74	G	-	-
4-75	G	-	-
4-76	G	-	-
4-77	G	-	-
4-78	-	-	-
4-79	-	-	-
4-80	-	-	-
4-81	-	-	-
4-82	-	-	-
4-83	-	-	-
4-84	-	-	-
4-85	-	-	-
4-86	G	-	-
4-87	-	-	-
4-88	G	-	-
4-89	G	-	-
4-90	G	-	-
4-91	G	-	-
4-92	G	-	-
4-93	G	-	-
4-94	G	-	-
4-95	G	-	-
4-96	G	-	-
4-97	G	-	-
4-98	G	-	-
4-99	G	-	-
4-100	G	-	-

Table 6.23 – eis promoter sequences of isolates from India by nucleotide position

Isolate ID	-10	-12	-14	-37
H37Rv	G	C	C	G
1-1	-	-	-	-
1-2	-	-	-	-
1-3	-	-	-	-
1-4	-	-	-	-
1-5	-	-	-	-
1-6	-	-	-	-
1-7	-	-	T	-
1-8	-	-	-	-
1-9	-	-	-	-
1-10	-	-	-	-
1-11	-	-	-	-
1-12	-	-	-	-
1-13	-	-	-	-
1-14	-	-	-	-
1-15	-	-	-	-
1-16	-	-	-	T
1-17	-	-	T	-
1-18	-	-	-	-
1-19	-	-	-	-
1-20	-	-	-	-
1-21	-	-	-	-
1-22	-	-	-	-
1-23	-	-	-	-
1-24	-	-	-	-
1-25	-	-	-	-
1-26	-	-	-	-
1-27	-	-	-	-
1-28	-	-	-	-
1-29	-	-	-	-
1-30	-	-	-	-
1-31	-	-	-	-
1-32	-	-	-	-
1-33	-	-	T	-

Isolate ID	-10	-12	-14	-37
H37Rv	G	C	C	G
1-34	-	-	-	-
1-35	-	-	T	-
1-36	-	-	-	-
1-37	-	-	-	-
1-38	-	-	-	-
1-39	-	-	-	-
1-40	-	-	-	-
1-41	-	-	-	-
1-42	-	-	-	-
1-43	-	-	-	-
1-44	-	-	-	-
1-45	-	-	-	-
1-46	-	-	T	-
1-47	-	-	-	-
1-48	-	-	-	-
1-49	-	-	-	-
1-50	-	-	-	-
1-51	-	-	-	-
1-52	-	-	-	-
1-53	-	-	-	-
1-54	-	-	-	-
1-55	-	-	-	-
1-56	-	-	-	-
1-57	-	-	-	-
1-58	-	-	-	-
1-59	-	-	-	-
1-60	-	-	-	-
1-61	-	-	-	-
1-62	-	-	-	-
1-63	-	-	-	-
1-64	-	-	-	-
1-65	-	-	-	-
1-66	-	-	-	-

Isolate ID	-10	-12	-14	-37
H37Rv	G	C	C	G
1-67	-	-	-	-
1-68	-	-	-	-
1-69	-	-	-	-
1-70	-	-	-	-
1-71	-	-	-	-
1-72	-	-	-	-
1-73	-	-	-	-
1-74	-	-	-	-
1-75	-	-	-	-
1-76	-	-	-	-
1-77	-	-	-	-
1-78	-	-	-	-
1-79	-	-	-	-
1-80	-	-	-	-
1-81	-	-	-	-
1-82	-	-	-	-
1-83	-	-	-	-
1-84	-	-	-	-
1-85	-	-	-	-
1-86	-	-	-	-
1-87	-	-	-	-
1-88	-	-	-	-
1-89	-	-	-	-
1-90	-	-	-	-
1-91	-	-	-	-
1-92	-	-	-	-
1-93	-	-	-	-
1-94	-	-	-	-
1-95	-	-	-	-
1-96	-	-	-	-

Table 6.24 – eis promoter sequences of isolates from Moldova by nucleotide position

Isolate ID	-10	-12	-14	-37
H37Rv	G	C	C	G
2-1	-	-	-	-
2-2	-	-	-	-
2-3	-	-	-	-
2-4	-	-	T	-
2-5	-	T	-	-
2-6	-	-	-	-
2-7	-	-	-	-
2-8	-	-	T	-
2-9	-	-	T	-
2-10	-	-	-	-
2-11	-	T	-	-
2-12	-	T	-	-
2-13	-	-	-	-
2-14	-	-	-	-
2-15	-	T	-	-
2-16	-	T	-	-
2-17	-	T	-	-
2-18	-	-	-	-
2-19	-	T	-	-
2-20	-	T	-	-
2-21	-	T	-	-
2-22	-	T	-	-
2-23	-	T	-	-
2-24	-	T	-	-
2-25	-	-	-	-
2-26	-	N	-	-
2-27	A	-	-	-
2-28	-	T	-	-
2-29	-	-	-	-
2-30	-	-	-	-
2-31	-	T	-	-
2-32	-	-	-	-
2-33	-	-	-	-

Isolate ID	-10	-12	-14	-37
H37Rv	G	C	C	G
2-34	-	-	-	-
2-35	-	T	-	-
2-36	-	T	-	-
2-37	-	T	-	-
2-38	A	-	-	-
2-39	-	-	-	-
2-40	-	-	-	-
2-41	-	-	-	-
2-42	-	-	-	-
2-43	-	T	-	-
2-44	-	T	-	-
2-45	-	T	-	-
2-46	-	-	T	-
2-47	A	-	-	-
2-48	-	T	-	-
2-49	-	T	-	-
2-50	-	-	-	-
2-51	-	T	-	-
2-52	-	T	-	-
2-53	-	T	-	-
2-54	-	T	-	-
2-55	-	T	-	-
2-56	-	T	-	-
2-57	-	-	-	-
2-58	-	T	-	-
2-59	-	T	-	-
2-60	-	-	-	-
2-61	-	T	-	-
2-62	-	-	-	-
2-63	-	T	-	-
2-64	-	-	T	-
2-65	-	-	-	-
2-66	-	T	-	-

Isolate ID	-10	-12	-14	-37
H37Rv	G	C	C	G
2-67	-	T	-	-
2-68	-	T	-	-
2-69	-	-	-	-
2-70	-	T	-	-
2-71	-	-	T	-
2-72	-	T	-	-
2-73	-	-	-	-
2-74	-	-	-	-
2-75	-	-	-	-
2-76	-	-	-	-
2-77	-	-	-	-
2-78	-	-	-	-
2-79	-	-	-	-
2-80	-	-	-	-
2-81	-	-	-	-
2-82	-	-	-	-
2-83	-	T	-	-
2-84	-	-	-	-
2-85	-	T	-	-
2-86	-	-	-	-
2-87	-	-	-	-
2-88	-	T	-	-

Table 6.25 – eis promoter sequences of isolates from the Philippines by nucleotide position

Isolate ID	-10	-12	-14	-37
H37Rv	G	C	C	G
3-2	-	-	-	-
3-3	-	-	-	-
3-4	-	-	-	-
3-5	-	-	-	-
3-6	-	-	-	-
3-7	-	-	-	-
3-8	-	-	-	-
3-9	-	-	-	-
3-10	-	-	-	-
3-11	-	-	-	-
3-12	-	-	-	-
3-13	-	-	-	-
3-14	-	-	-	-
3-15	-	-	-	-
3-16	-	-	-	-
3-17	-	-	-	-
3-18	-	-	-	-
3-19	-	-	-	-
3-20	-	-	-	-
3-21	-	-	-	-
3-22	-	-	-	-
3-23	-	-	-	-
3-24	-	-	-	-
3-25	-	-	-	-
3-26	-	-	-	-
3-27	-	-	-	-
3-28	-	-	-	-
3-29	-	-	-	-
3-30	-	-	-	-
3-31	-	-	-	-
3-32	-	-	-	-
3-33	-	-	-	-
3-34	-	-	-	-

Isolate ID	-10	-12	-14	-37
H37Rv	G	C	C	G
3-35	-	-	-	-
3-36	-	-	-	-
3-37	-	-	-	-
3-38	-	-	-	-
3-39	-	-	-	-
3-40	-	-	-	-
3-41	-	-	-	-
3-42	-	-	-	-
3-43	-	-	-	-
3-44	-	-	-	-
3-45	-	-	-	-
3-46	-	-	-	-
3-47	-	-	-	-
3-48	-	-	-	-
3-49	-	-	-	-
3-50	-	-	-	-
3-51	-	-	-	-
3-52	-	-	-	-
3-53	-	-	-	-
3-54	-	-	-	-
3-55	-	-	-	-
3-56	-	-	-	-
3-57	-	-	-	-
3-58	-	-	-	-
3-59	-	-	-	-
3-60	-	-	-	-
3-61	-	-	-	-
3-62	-	-	-	-
3-63	-	-	-	-
3-64	-	-	-	-
3-65	-	-	-	-
3-66	-	-	-	-
3-67	-	-	-	-

Isolate ID	-10	-12	-14	-37
H37Rv	G	C	C	G
3-68	-	-	-	-
3-69	-	-	-	-
3-70	-	-	-	-
3-71	A	-	-	-
3-72	-	-	-	-
3-73	-	-	-	-
3-74	-	-	-	-
3-76	-	-	-	-
3-77	-	-	-	-
3-78	-	-	-	-
3-79	-	-	-	-
3-80	-	-	-	-
3-81	-	-	-	-
3-82	-	-	-	-
3-83	-	-	-	-
3-84	-	-	-	-
3-85	-	-	-	-
3-86	-	-	-	-
3-87	-	-	-	-
3-88	-	-	-	-
3-89	-	-	-	-
3-90	-	-	-	-
3-91	-	-	-	-
3-92	-	-	-	-
3-93	-	-	-	-
3-94	-	-	-	-
3-95	-	-	-	-
3-96	-	-	-	-
3-97	-	-	-	-
3-98	-	-	-	-
3-99	-	-	-	-
3-100	-	-	-	-
3-101	-	-	-	-

Table 6.25 – eis promoter sequences of isolates from the Philippines by nucleotide position (continued)

Isolate ID	-10	-12	-14	-37
H37Rv	G	C	C	G
3-102	-	-	-	-
3-103	-	-	-	-
3-104	-	-	-	-
3-105	-	-	-	-
3-106	-	-	-	-
3-107	-	-	-	-
3-108	-	-	-	-
3-109	-	-	-	-
3-110	-	-	-	-
3-111	-	-	-	-
3-112	-	-	-	-
3-113	-	-	-	-
3-114	-	-	-	-
3-115	-	-	-	-
3-116	-	-	-	-
3-117	-	-	-	-
3-118	-	-	-	-
3-119	-	-	-	-
3-120	-	-	-	-
3-121	-	-	-	-
3-122	-	-	-	T
3-123	-	-	-	-
3-124	-	-	-	-
3-125	-	-	-	-

Table 6.26 – eis promoter sequences of isolates from South Africa by nucleotide position

Isolate ID	-10	-12	-14	-37
H37Rv	G	C	C	G
4-1	-	-	-	-
4-2	-	-	-	-
4-3	-	-	-	-
4-4	-	-	-	-
4-5	-	-	-	-
4-6	-	-	-	-
4-7	-	-	-	-
4-8	-	-	-	-
4-9	-	-	-	-
4-10	-	-	-	-
4-11	-	-	T	-
4-12	-	-	-	-
4-13	-	-	-	-
4-14	-	-	-	-
4-15	-	-	-	-
4-16	-	-	-	-
4-17	-	-	-	-
4-18	-	-	-	-
4-19	-	-	-	-
4-20	-	-	-	-
4-21	-	-	-	-
4-22	-	-	-	-
4-23	-	-	-	-
4-24	-	-	-	-
4-25	-	-	-	-
4-26	-	-	-	-
4-27	-	-	-	-
4-28	-	-	-	-
4-29	-	-	-	-
4-30	-	-	-	-
4-31	-	-	-	-
4-32	-	-	-	-
4-33	-	-	-	-

Isolate ID	-10	-12	-14	-37
H37Rv	G	C	C	G
4-34	-	-	-	-
4-35	-	-	-	-
4-36	-	-	-	-
4-37	-	-	-	-
4-38	-	-	-	-
4-39	-	-	-	-
4-40	-	-	-	-
4-41	-	-	-	-
4-42	-	-	-	-
4-43	-	-	-	-
4-44	-	-	-	-
4-45	-	-	-	-
4-46	-	-	-	-
4-47	-	-	-	-
4-48	-	-	-	-
4-49	-	-	-	-
4-50	-	-	-	-
4-51	-	-	-	-
4-52	-	-	-	-
4-53	-	-	-	-
4-54	-	-	-	-
4-55	-	-	-	-
4-56	-	-	-	-
4-57	-	-	-	-
4-58	-	-	-	-
4-59	-	-	-	-
4-60	-	-	-	-
4-61	-	-	-	-
4-62	-	-	-	-
4-63	-	-	-	-
4-64	-	-	-	-
4-65	-	-	-	-
4-66	-	-	-	-

Isolate ID	-10	-12	-14	-37
H37Rv	G	C	C	G
4-67	-	-	-	-
4-68	-	-	-	-
4-69	-	-	-	-
4-70	-	-	-	-
4-71	-	-	-	-
4-72	-	-	-	-
4-73	-	-	-	-
4-74	-	-	-	-
4-75	-	-	-	-
4-76	-	-	-	-
4-77	-	-	-	-
4-78	-	-	-	-
4-79	-	-	-	-
4-80	-	-	-	-
4-81	-	-	-	-
4-82	-	-	-	-
4-83	-	-	-	-
4-84	-	-	-	-
4-85	-	-	-	-
4-86	-	-	-	-
4-87	-	-	-	-
4-88	-	-	-	-
4-89	-	-	-	-
4-90	-	-	-	-
4-91	-	-	-	-
4-92	-	-	-	-
4-93	-	-	-	-
4-94	-	-	-	-
4-95	-	-	-	-
4-96	-	-	-	-
4-97	-	-	-	-
4-98	-	-	-	-
4-99	-	-	-	-
4-100	-	-	-	-

Table 6.27 – Drug susceptibility testing data of isolates from India

Isolate ID	RIF	INH	FQL	AMI
1-1	Resistant	Resistant	Resistant	Resistant
1-2	Resistant	Resistant	Resistant	Resistant
1-3	Resistant	Resistant	Resistant	Resistant
1-4	Resistant	Resistant	Resistant	Resistant
1-5	Resistant	Resistant	Resistant	Resistant
1-6	Resistant	Resistant	Resistant	Resistant
1-7	Resistant	Resistant	Resistant	Resistant
1-8	Resistant	Resistant	Resistant	Resistant
1-9	Resistant	Resistant	Resistant	Resistant
1-10	Resistant	Resistant	Resistant	Resistant
1-11	Resistant	Resistant	Resistant	Resistant
1-12	Resistant	Resistant	Resistant	Resistant
1-13	Resistant	Resistant	Resistant	Resistant
1-14	Resistant	Resistant	Resistant	Resistant
1-15	Resistant	Resistant	Resistant	Resistant
1-16	Resistant	Resistant	Resistant	Resistant
1-17	Resistant	Resistant	Resistant	Resistant
1-18	Resistant	Resistant	Resistant	Resistant
1-19	Resistant	Resistant	Resistant	Resistant
1-20	Resistant	Resistant	Resistant	Resistant
1-21	Resistant	Resistant	Resistant	Resistant
1-22	Resistant	Resistant	Resistant	Resistant
1-23	Resistant	Resistant	Resistant	Resistant
1-24	Resistant	Resistant	Resistant	Resistant
1-25	Resistant	Resistant	Resistant	Resistant
1-26	Resistant	Resistant	Resistant	Resistant
1-27	Resistant	Resistant	Resistant	Resistant
1-28	Resistant	Resistant	Resistant	Resistant
1-29	Resistant	Resistant	Resistant	Resistant
1-30	Resistant	Resistant	Resistant	Resistant
1-31	Resistant	Resistant	Resistant	Resistant
1-32	Resistant	Resistant	Resistant	Resistant
1-33	Resistant	Resistant	Resistant	Resistant

Table 6.27 – Drug susceptibility testing data of isolates from India (continued)

Isolate ID	RIF	INH	FQL	AMI
1-34	Resistant	Resistant	Resistant	Resistant
1-35	Resistant	Resistant	Resistant	Resistant
1-36	Resistant	Resistant	Resistant	Resistant
1-37	Resistant	Resistant	Resistant	Resistant
1-38	Resistant	Resistant	Resistant	Resistant
1-39	Resistant	Resistant	Resistant	Resistant
1-40	Resistant	Resistant	Resistant	Resistant
1-41	Resistant	Resistant	Resistant	Resistant
1-42	Resistant	Resistant	Resistant	Resistant
1-43	Resistant	Resistant	Resistant	Resistant
1-44	Resistant	Resistant	Resistant	Resistant
1-45	Resistant	Resistant	Resistant	Resistant
1-46	Resistant	Resistant	Resistant	Resistant
1-47	Resistant	Resistant	Resistant	Resistant
1-48	Resistant	Resistant	Resistant	Resistant
1-49	Resistant	Resistant	Resistant	Resistant
1-50	Resistant	Resistant	Resistant	Resistant
1-51	Resistant	Resistant	Resistant	Resistant
1-52	Resistant	Resistant	Resistant	Resistant
1-53	Resistant	Resistant	Resistant	Resistant
1-54	Resistant	Resistant	Resistant	Resistant
1-55	Resistant	Resistant	Resistant	Resistant
1-56	Resistant	Resistant	Resistant	Resistant
1-57	Resistant	Resistant	Resistant	Resistant
1-58	Resistant	Resistant	Resistant	Resistant
1-59	Resistant	Resistant	Resistant	Resistant
1-60	Resistant	Resistant	Resistant	Resistant
1-61	Resistant	Resistant	Resistant	Resistant
1-62	Resistant	Resistant	Resistant	Resistant
1-63	Resistant	Resistant	Resistant	Resistant
1-64	Resistant	Resistant	Resistant	Resistant
1-65	Resistant	Resistant	Resistant	Resistant
1-66	Resistant	Resistant	Resistant	Resistant

Table 6.27 – Drug susceptibility testing data of isolates from India (continued)

Isolate ID	RIF	INH	FQL	AMI
1-67	Resistant	Resistant	Resistant	Resistant
1-68	Resistant	Resistant	Resistant	Resistant
1-69	Resistant	Resistant	Resistant	Resistant
1-70	Resistant	Resistant	Resistant	Resistant
1-71	Resistant	Resistant	Resistant	Resistant
1-72	Resistant	Resistant	Resistant	Resistant
1-73	Resistant	Resistant	Resistant	Resistant
1-74	Resistant	Resistant	Resistant	Resistant
1-75	Resistant	Resistant	Resistant	Resistant
1-76	Resistant	Resistant	Resistant	Resistant
1-77	Resistant	Resistant	Resistant	Resistant
1-78	Resistant	Resistant	Resistant	Resistant
1-79	Resistant	Resistant	Resistant	Resistant
1-80	Resistant	Resistant	Resistant	Resistant
1-81	Resistant	Resistant	Resistant	Resistant
1-82	Resistant	Resistant	Resistant	Resistant
1-83	Resistant	Resistant	Resistant	Resistant
1-84	Resistant	Resistant	Resistant	Resistant
1-85	Resistant	Resistant	Resistant	Resistant
1-86	Resistant	Resistant	Resistant	Resistant
1-87	Resistant	Resistant	Resistant	Resistant
1-88	Resistant	Resistant	Resistant	Resistant
1-89	Resistant	Resistant	Resistant	Resistant
1-90	Resistant	Resistant	Resistant	Resistant
1-91	Resistant	Resistant	Resistant	Resistant
1-92	Resistant	Resistant	Resistant	Resistant
1-93	Susceptible	Susceptible	Susceptible	Susceptible
1-94	Susceptible	Susceptible	Susceptible	Susceptible
1-95	Susceptible	Susceptible	Susceptible	Susceptible
1-96	Susceptible	Susceptible	Susceptible	Susceptible

Table 6.28 – Drug susceptibility testing data of isolates from Moldova

Isolate ID	RIF	INH	FQL	AMI
2-1	Resistant	Resistant	Resistant	Susceptible
2-2	Resistant	Resistant	Resistant	Susceptible
2-3	Resistant	Resistant	Susceptible	Resistant
2-4	Resistant	Resistant	Resistant	Resistant
2-5	Resistant	Resistant	Resistant	Resistant
2-6	Resistant	Resistant	Resistant	Susceptible
2-7	Resistant	Resistant	Susceptible	Resistant
2-8	Resistant	Resistant	Susceptible	Resistant
2-9	Resistant	Resistant	Resistant	Resistant
2-10	Resistant	Resistant	Resistant	Susceptible
2-11	Resistant	Resistant	Susceptible	Resistant
2-12	Resistant	Resistant	Resistant	Susceptible
2-13	Resistant	Resistant	Resistant	Susceptible
2-14	Resistant	Resistant	Resistant	Susceptible
2-15	Resistant	Resistant	Resistant	Susceptible
2-16	Resistant	Resistant	Resistant	Resistant
2-17	Resistant	Resistant	Resistant	Susceptible
2-18	Resistant	Resistant	Resistant	Resistant
2-19	Resistant	Resistant	Resistant	Resistant
2-20	Resistant	Resistant	Resistant	Susceptible
2-21	Resistant	Resistant	Resistant	Susceptible
2-22	Resistant	Resistant	Resistant	Susceptible
2-23	Resistant	Resistant	Resistant	Susceptible
2-24	Resistant	Resistant	Resistant	Resistant
2-25	Resistant	Resistant	Resistant	Resistant
2-26	Resistant	Resistant	Resistant	Resistant
2-27	Resistant	Resistant	Resistant	Resistant
2-28	Resistant	Resistant	Susceptible	Resistant
2-29	Resistant	Resistant	Resistant	Resistant
2-30	Resistant	Resistant	Resistant	Resistant
2-31	Resistant	Resistant	Resistant	Resistant
2-32	Resistant	Resistant	Resistant	Resistant
2-33	Resistant	Resistant	Susceptible	Resistant

Table 6.28 – Drug susceptibility testing data of isolates from Moldova (continued)

Isolate ID	RIF	INH	FQL	AMI
2-34	Resistant	Resistant	Susceptible	Resistant
2-35	Resistant	Resistant	Resistant	Susceptible
2-36	Resistant	Resistant	Resistant	Susceptible
2-37	Resistant	Resistant	Resistant	Resistant
2-38	Resistant	Resistant	Resistant	Resistant
2-39	Resistant	Resistant	Resistant	Susceptible
2-40	Resistant	Resistant	Susceptible	Resistant
2-41	Resistant	Resistant	Resistant	Susceptible
2-42	Resistant	Resistant	Resistant	Resistant
2-43	Resistant	Resistant	Resistant	Resistant
2-44	Resistant	Resistant	Resistant	Resistant
2-45	Resistant	Resistant	Resistant	Susceptible
2-46	Resistant	Resistant	Resistant	Resistant
2-47	Resistant	Resistant	Susceptible	Susceptible
2-48	Resistant	Resistant	Susceptible	Resistant
2-49	Resistant	Resistant	Resistant	Susceptible
2-50	Resistant	Resistant	Resistant	Susceptible
2-51	Resistant	Resistant	Resistant	Susceptible
2-52	Resistant	Resistant	Resistant	Susceptible
2-53	Resistant	Resistant	Resistant	Susceptible
2-54	Resistant	Resistant	Resistant	Susceptible
2-55	Resistant	Resistant	Resistant	Susceptible
2-56	Resistant	Resistant	Susceptible	Resistant
2-57	Resistant	Resistant	Resistant	Resistant
2-58	Resistant	Resistant	Resistant	Resistant
2-59	Resistant	Resistant	Susceptible	Susceptible
2-60	Resistant	Resistant	Resistant	Resistant
2-61	Resistant	Resistant	Resistant	Susceptible
2-62	Resistant	Resistant	Resistant	Resistant
2-63	Resistant	Resistant	Resistant	Resistant
2-64	Resistant	Resistant	Resistant	Resistant
2-65	Resistant	Resistant	Resistant	Resistant
2-66	Resistant	Resistant	Resistant	Susceptible

Table 6.28 – Drug susceptibility testing data of isolates from Moldova (continued)

Isolate ID	RIF	INH	FQL	AMI
2-67	Resistant	Resistant	Resistant	Susceptible
2-68	Resistant	Resistant	Resistant	Susceptible
2-69	Resistant	Resistant	Resistant	Resistant
2-70	Resistant	Resistant	Resistant	Resistant
2-71	Resistant	Resistant	Susceptible	Resistant
2-72	Resistant	Resistant	Resistant	Susceptible
2-73	Susceptible	Susceptible	Susceptible	Susceptible
2-74	Susceptible	Susceptible	Susceptible	Susceptible
2-75	Susceptible	Susceptible	Susceptible	Susceptible
2-76	Susceptible	Susceptible	Susceptible	Susceptible
2-77	Susceptible	Susceptible	Susceptible	Susceptible
2-78	Susceptible	Susceptible	Susceptible	Susceptible
2-79	Resistant	Resistant	Resistant	Susceptible
2-80	Resistant	Resistant	Resistant	Susceptible
2-81	Resistant	Resistant	Resistant	Resistant
2-82	Resistant	Resistant	Resistant	Resistant
2-83	Resistant	Resistant	Resistant	Susceptible
2-84	Resistant	Resistant	Resistant	Resistant
2-85	Resistant	Resistant	Resistant	Susceptible
2-86	Resistant	Resistant	Resistant	Resistant
2-87	Resistant	Resistant	Susceptible	Resistant
2-88	Susceptible	Susceptible	Susceptible	Susceptible

Table 6.29 – Drug susceptibility testing data of isolates from Philippines

Isolate ID	RIF	INH	FQL	AMI
3-2	Resistant	Resistant	Susceptible	Resistant
3-3	Resistant	Resistant	Susceptible	Resistant
3-4	Resistant	Resistant	Resistant	Resistant
3-5	Resistant	Resistant	Susceptible	Resistant
3-6	Resistant	Resistant	Resistant	Resistant
3-7	Resistant	Resistant	Resistant	Resistant
3-8	Resistant	Resistant	Resistant	Resistant
3-9	Resistant	Resistant	Resistant	Resistant
3-10	Resistant	Resistant	Resistant	Susceptible
3-11	Resistant	Resistant	Resistant	Susceptible
3-12	Susceptible	Susceptible	Resistant	Susceptible
3-13	Resistant	Resistant	Resistant	Susceptible
3-14	Resistant	Resistant	Resistant	Susceptible
3-15	Resistant	Resistant	Resistant	Susceptible
3-16	Susceptible	Resistant	Resistant	Susceptible
3-17	Resistant	Resistant	Resistant	Susceptible
3-18	Resistant	Resistant	Resistant	Susceptible
3-19	Resistant	Resistant	Resistant	Susceptible
3-20	Resistant	Resistant	Resistant	Susceptible
3-21	Resistant	Resistant	Resistant	Susceptible
3-22	Resistant	Resistant	Resistant	Susceptible
3-23	Resistant	Resistant	-	Resistant
3-24	Susceptible	Susceptible	Susceptible	Susceptible
3-25	Susceptible	Susceptible	Susceptible	Susceptible
3-26	Susceptible	Susceptible	Susceptible	Susceptible
3-27	Susceptible	Susceptible	Susceptible	Susceptible
3-28	Resistant	Resistant	-	Susceptible
3-29	Resistant	Resistant	Resistant	Susceptible
3-30	Resistant	Resistant	Resistant	Susceptible
3-31	Resistant	Resistant	Resistant	Susceptible
3-32	Resistant	Resistant	-	Susceptible
3-33	Resistant	Resistant	-	Susceptible
3-34	Resistant	Resistant	Resistant	Susceptible

Table 6.29 – Drug susceptibility testing data of isolates from Philippines (continued)

Isolate ID	RIF	INH	FQL	AMI
3-35	Resistant	Resistant	-	Resistant
3-36	Resistant	Resistant	-	Resistant
3-37	Resistant	Resistant	Resistant	Susceptible
3-38	Resistant	Resistant	-	Resistant
3-39	Resistant	Resistant	-	Susceptible
3-40	Resistant	Resistant	Susceptible	Susceptible
3-41	Resistant	Resistant	Susceptible	Susceptible
3-42	Resistant	Resistant	Susceptible	Susceptible
3-43	Resistant	Resistant	-	Susceptible
3-44	Resistant	Resistant	Susceptible	Susceptible
3-45	Resistant	Resistant	Susceptible	Susceptible
3-46	Resistant	Resistant	Susceptible	Susceptible
3-47	Resistant	Resistant	Susceptible	Susceptible
3-48	Resistant	Resistant	Susceptible	Susceptible
3-49	Resistant	Resistant	-	Susceptible
3-50	Susceptible	Susceptible	Susceptible	Susceptible
3-51	Susceptible	Susceptible	Susceptible	Susceptible
3-52	Susceptible	Susceptible	Susceptible	Susceptible
3-53	Resistant	Resistant	Resistant	Susceptible
3-54	Susceptible	Susceptible	Susceptible	Susceptible
3-55	Susceptible	Susceptible	Susceptible	Susceptible
3-56	Resistant	Resistant	-	Susceptible
3-57	Susceptible	Susceptible	Susceptible	Susceptible
3-58	Resistant	Susceptible	Susceptible	Susceptible
3-59	Susceptible	Susceptible	Susceptible	Susceptible
3-60	Susceptible	Resistant	Resistant	Susceptible
3-61	Resistant	Resistant	-	Resistant
3-62	Resistant	Resistant	Resistant	Resistant
3-63	Resistant	Resistant	Resistant	Resistant
3-64	Resistant	Resistant	-	Resistant
3-65	Resistant	Resistant	-	Resistant
3-66	Resistant	Resistant	Susceptible	Resistant
3-67	Resistant	Resistant	Resistant	Resistant

Table 6.29 – Drug susceptibility testing data of isolates from Philippines (continued)

Isolate ID	RIF	INH	FQL	AMI
3-68	Resistant	Resistant	Resistant	Resistant
3-69	Resistant	Resistant	-	Resistant
3-70	Resistant	Resistant	-	Resistant
3-71	Resistant	Resistant	Susceptible	Resistant
3-72	Susceptible	Resistant	Resistant	Susceptible
3-73	Susceptible	Susceptible	Susceptible	Susceptible
3-74	Resistant	Resistant	Resistant	Susceptible
3-76	Resistant	Resistant	Resistant	Susceptible
3-77	Resistant	Resistant	Resistant	Susceptible
3-78	Resistant	Resistant	Resistant	Susceptible
3-79	Resistant	Resistant	Resistant	Susceptible
3-80	Susceptible	Resistant	Resistant	Susceptible
3-81	Susceptible	Susceptible	Susceptible	Susceptible
3-82	Resistant	Resistant	Resistant	Susceptible
3-83	Resistant	Resistant	Susceptible	Susceptible
3-84	Resistant	Resistant	Susceptible	Susceptible
3-85	Resistant	Resistant	-	Susceptible
3-86	Resistant	Resistant	Susceptible	Susceptible
3-87	Resistant	Resistant	Susceptible	Susceptible
3-88	Resistant	Resistant	-	Susceptible
3-89	Resistant	Resistant	Susceptible	Susceptible
3-90	Resistant	Resistant	Susceptible	Susceptible
3-91	Resistant	Resistant	Susceptible	Susceptible
3-92	Resistant	Resistant	Susceptible	Susceptible
3-93	Resistant	Resistant	-	Susceptible
3-94	Resistant	Resistant	Susceptible	Susceptible
3-95	Resistant	Resistant	-	Susceptible
3-96	Resistant	Resistant	-	Susceptible
3-97	Susceptible	Susceptible	-	Susceptible
3-98	Susceptible	Susceptible	Susceptible	Susceptible
3-99	Susceptible	Susceptible	Susceptible	Susceptible
3-100	Susceptible	Susceptible	-	Susceptible

Table 6.29 – Drug susceptibility testing data of isolates from Philippines (continued)

Isolate ID	RIF	INH	FQL	AMI
3-101	Resistant	Resistant	Susceptible	Resistant
3-102	Resistant	Resistant	Resistant	Susceptible
3-103	Susceptible	Susceptible	Resistant	Susceptible
3-104	Resistant	Resistant	Resistant	Susceptible
3-105	Resistant	Resistant	Resistant	Susceptible
3-106	Resistant	Resistant	Resistant	Susceptible
3-107	Resistant	Resistant	Resistant	Susceptible
3-108	Resistant	Resistant	Resistant	Susceptible
3-109	Resistant	Resistant	Resistant	Susceptible
3-110	Susceptible	Resistant	Susceptible	Susceptible
3-111	Resistant	Susceptible	Susceptible	Susceptible
3-112	Susceptible	Susceptible	Susceptible	Susceptible
3-113	Resistant	Resistant	Susceptible	Susceptible
3-114	Resistant	Resistant	-	Susceptible
3-115	Resistant	Resistant	Susceptible	Susceptible
3-116	Resistant	Resistant	-	Susceptible
3-117	Susceptible	Resistant	Susceptible	Susceptible
3-118	Resistant	Resistant	Susceptible	Susceptible
3-119	Resistant	Resistant	Susceptible	Susceptible
3-120	Resistant	Resistant	-	Susceptible
3-121	Resistant	Resistant	Susceptible	Susceptible
3-122	Resistant	Resistant	-	Susceptible
3-123	Resistant	Resistant	-	Susceptible
3-124	Resistant	Resistant	Susceptible	Susceptible
3-125	Resistant	Resistant	Susceptible	Susceptible

Table 6.30 – Drug susceptibility testing data of isolates from South Africa

Isolate ID	RIF	INH	FQL	AMI
4-1	Resistant	Resistant	Resistant	Resistant
4-2	Resistant	Resistant	Resistant	Resistant
4-3	Resistant	Resistant	Resistant	Resistant
4-4	Resistant	Resistant	Resistant	Resistant
4-5	Resistant	Resistant	Resistant	Resistant
4-6	Resistant	Resistant	Resistant	Resistant
4-7	Resistant	Resistant	Resistant	Resistant
4-8	Resistant	Resistant	Resistant	Resistant
4-9	Resistant	Resistant	Resistant	Resistant
4-10	Resistant	Resistant	Resistant	Resistant
4-11	Resistant	Resistant	Resistant	Resistant
4-12	Resistant	Resistant	Resistant	Resistant
4-13	Resistant	Resistant	Resistant	Resistant
4-14	Resistant	Resistant	Resistant	Resistant
4-15	Resistant	Resistant	Resistant	Resistant
4-16	Resistant	Resistant	Resistant	Resistant
4-17	Resistant	Resistant	Resistant	Resistant
4-18	Resistant	Resistant	Resistant	Resistant
4-19	Resistant	Resistant	Resistant	Resistant
4-20	Resistant	Resistant	Resistant	Resistant
4-21	Resistant	Resistant	Resistant	Resistant
4-22	Resistant	Resistant	Resistant	Resistant
4-23	Resistant	Resistant	Resistant	Resistant
4-24	Resistant	Resistant	Resistant	Resistant
4-25	Resistant	Resistant	Resistant	Resistant
4-26	Resistant	Resistant	Resistant	Resistant
4-27	Resistant	Resistant	Resistant	Resistant
4-28	Resistant	Resistant	Resistant	Resistant
4-29	Resistant	Resistant	Resistant	Resistant
4-30	Resistant	Resistant	Resistant	Resistant
4-31	Resistant	Resistant	Resistant	Resistant
4-32	Resistant	Resistant	Resistant	Resistant
4-33	Resistant	Resistant	Resistant	Resistant

Table 6.30 – Drug susceptibility testing data of isolates from South Africa (continued)

Isolate ID	RIF	INH	FQL	AMI
4-34	Resistant	Resistant	Resistant	Resistant
4-35	Resistant	Resistant	Resistant	Resistant
4-36	Resistant	Resistant	Resistant	Resistant
4-37	Resistant	Resistant	Resistant	Resistant
4-38	Resistant	Resistant	Resistant	Resistant
4-39	Resistant	Resistant	Resistant	Resistant
4-40	Resistant	Resistant	Resistant	Resistant
4-41	Resistant	Resistant	Resistant	Resistant
4-42	Resistant	Resistant	Resistant	Resistant
4-43	Resistant	Resistant	Resistant	Resistant
4-44	Resistant	Resistant	Resistant	Resistant
4-45	Resistant	Resistant	Resistant	Resistant
4-46	Resistant	Resistant	Resistant	Resistant
4-47	Resistant	Resistant	Resistant	Resistant
4-48	Resistant	Resistant	Resistant	Resistant
4-49	Resistant	Resistant	Resistant	Resistant
4-50	Resistant	Resistant	Resistant	Resistant
4-51	Resistant	Resistant	Resistant	Resistant
4-52	Resistant	Resistant	Resistant	Resistant
4-53	Resistant	Resistant	Resistant	Resistant
4-54	Resistant	Resistant	Resistant	Resistant
4-55	Resistant	Resistant	Resistant	Resistant
4-56	Resistant	Resistant	Resistant	Resistant
4-57	Resistant	Resistant	Resistant	Resistant
4-58	Resistant	Resistant	Resistant	Resistant
4-59	Resistant	Resistant	Resistant	Resistant
4-60	Resistant	Resistant	Resistant	Resistant
4-61	Resistant	Resistant	Resistant	Resistant
4-62	Resistant	Resistant	Resistant	Resistant
4-63	Resistant	Resistant	Resistant	Resistant
4-64	Resistant	Resistant	Resistant	Resistant
4-65	Resistant	Resistant	Resistant	Resistant
4-66	Resistant	Resistant	Resistant	Resistant

Table 6.30 – Drug susceptibility testing data of isolates from South Africa (continued)

Isolate ID	RIF	INH	FQL	AMI
4-67	Resistant	Resistant	Resistant	Resistant
4-68	Resistant	Resistant	Resistant	Resistant
4-69	Resistant	Resistant	Resistant	Resistant
4-70	Resistant	Resistant	Resistant	Resistant
4-71	Resistant	Resistant	Resistant	Resistant
4-72	Resistant	Resistant	Resistant	Resistant
4-73	Resistant	Resistant	Resistant	Resistant
4-74	Resistant	Resistant	Resistant	Resistant
4-75	Resistant	Resistant	Susceptible	Resistant
4-76	Resistant	Resistant	Susceptible	Resistant
4-77	Susceptible	Resistant	Susceptible	Resistant
4-78	Susceptible	Susceptible	Susceptible	Susceptible
4-79	Resistant	Resistant	Resistant	Resistant
4-80	Susceptible	Susceptible	Susceptible	Susceptible
4-81	Susceptible	Susceptible	Susceptible	Susceptible
4-82	Susceptible	Susceptible	Susceptible	Susceptible
4-83	Susceptible	Susceptible	Susceptible	Susceptible
4-84	Susceptible	Susceptible	Susceptible	Susceptible
4-85	Susceptible	Susceptible	Susceptible	Susceptible
4-86	Resistant	Resistant	Resistant	Resistant
4-87	Resistant	Resistant	Resistant	Resistant
4-88	Resistant	Resistant	Resistant	Resistant
4-89	Resistant	Resistant	Resistant	Resistant
4-90	Resistant	Resistant	Resistant	Resistant
4-91	Resistant	Resistant	Resistant	Resistant
4-92	Resistant	Resistant	Resistant	Resistant
4-93	Resistant	Resistant	Resistant	Resistant
4-94	Resistant	Resistant	Resistant	Resistant
4-95	Resistant	Resistant	Susceptible	Resistant
4-96	Resistant	Resistant	Resistant	Resistant
4-97	Resistant	Resistant	Resistant	Resistant
4-98	Resistant	Resistant	Resistant	Resistant
4-99	Resistant	Resistant	Susceptible	Resistant
4-100	Resistant	Resistant	Resistant	Resistant

Table 6.31 – Classification of isolates from India into four different resistance groups

Isolate ID	RIF	FQL	AMI	INH
1-1	Resistant	Resistant	Resistant	Discordant
1-2	Resistant	Discordant	Discordant	Resistant
1-3	Resistant	Resistant	Discordant	Resistant
1-4	Resistant	Resistant	Resistant	Resistant
1-5	Resistant	Resistant	Resistant	Resistant
1-6	Discordant	Discordant	Discordant	Discordant
1-7	Resistant	Resistant	Resistant	Discordant
1-8	Resistant	Resistant	Resistant	Discordant
1-9	Resistant	Resistant	Resistant	Resistant
1-10	Resistant	Resistant	Resistant	Resistant
1-11	Resistant	Resistant	Resistant	Resistant
1-12	Resistant	Resistant	Resistant	Resistant
1-13	Resistant	Resistant	Resistant	Resistant
1-14	Resistant	Resistant	Discordant	Resistant
1-15	Resistant	Discordant	Resistant	Resistant
1-16	Resistant	Resistant	Resistant	Resistant
1-17	Resistant	Resistant	Resistant	Resistant
1-18	Resistant	Resistant	Resistant	Resistant
1-19	Resistant	Resistant	Resistant	Resistant
1-20	Resistant	Resistant	Discordant	Resistant
1-21	Discordant	Resistant	Resistant	Resistant
1-22	Resistant	Resistant	Resistant	Resistant
1-23	Resistant	Resistant	Resistant	Resistant
1-24	Discordant	Resistant	Discordant	Resistant
1-25	Resistant	Resistant	Resistant	Discordant
1-26	Resistant	Resistant	Discordant	Discordant
1-27	Resistant	Resistant	Resistant	Discordant
1-28	Resistant	Resistant	Discordant	Resistant
1-29	Resistant	Resistant	Resistant	Discordant
1-30	Resistant	Resistant	Resistant	Resistant
1-31	Resistant	Resistant	Resistant	Resistant
1-32	Resistant	Resistant	Resistant	Discordant
1-33	Resistant	Discordant	Resistant	Resistant

Table 6.31 – Classification of isolates from India into four different resistance groups (continued)

Isolate ID	RIF	FQL	AMI	INH
1-34	Resistant	Resistant	Resistant	Resistant
1-35	Resistant	Resistant	Resistant	Resistant
1-36	Resistant	Resistant	Resistant	Resistant
1-37	Resistant	Resistant	Discordant	Resistant
1-38	Resistant	Resistant	Resistant	Resistant
1-39	Resistant	Resistant	Resistant	Resistant
1-40	Resistant	Resistant	Discordant	Resistant
1-41	Resistant	Resistant	Resistant	Resistant
1-42	Resistant	Resistant	Resistant	Resistant
1-43	Resistant	Discordant	Resistant	Resistant
1-44	Resistant	Resistant	Resistant	Resistant
1-45	Resistant	Resistant	Resistant	Resistant
1-46	Resistant	Resistant	Resistant	Resistant
1-47	Resistant	Resistant	Resistant	Resistant
1-48	Resistant	Resistant	Resistant	Resistant
1-49	Resistant	Resistant	Resistant	Resistant
1-50	Resistant	Resistant	Discordant	Resistant
1-51	Resistant	Resistant	Resistant	Resistant
1-52	Resistant	Resistant	Resistant	Resistant
1-53	Resistant	Resistant	Resistant	Resistant
1-54	Resistant	Resistant	Resistant	Resistant
1-55	Resistant	Resistant	Resistant	Resistant
1-56	Resistant	Resistant	Resistant	Resistant
1-57	Resistant	Resistant	Resistant	Resistant
1-58	Resistant	Resistant	Resistant	Resistant
1-59	Resistant	Resistant	Resistant	Resistant
1-60	Resistant	Resistant	Discordant	Resistant
1-61	Resistant	Resistant	Resistant	Resistant
1-62	Resistant	Resistant	Resistant	Resistant
1-63	Resistant	Discordant	Resistant	Resistant
1-64	Resistant	Resistant	Resistant	Resistant
1-65	Resistant	Resistant	Resistant	Resistant
1-66	Resistant	Resistant	Resistant	Resistant

Table 6.31 – Classification of isolates from India into four different resistance groups (continued)

Isolate ID	RIF	FQL	AMI	INH
1-67	Resistant	Resistant	Resistant	Resistant
1-68	Resistant	Resistant	Discordant	Resistant
1-69	Resistant	Resistant	Discordant	Resistant
1-70	Resistant	Discordant	Discordant	Resistant
1-71	Resistant	Resistant	Resistant	Resistant
1-72	Resistant	Resistant	Resistant	Resistant
1-73	Resistant	Resistant	Resistant	Resistant
1-74	Resistant	Resistant	Resistant	Resistant
1-75	Resistant	Resistant	Resistant	Resistant
1-76	Resistant	Discordant	Resistant	Resistant
1-77	Resistant	Resistant	Resistant	Resistant
1-78	Resistant	Resistant	Resistant	Resistant
1-79	Resistant	Resistant	Resistant	Resistant
1-80	Resistant	Resistant	Resistant	Resistant
1-81	Resistant	Resistant	Resistant	Resistant
1-82	Resistant	Discordant	Discordant	Resistant
1-83	Resistant	Resistant	Discordant	Resistant
1-84	Resistant	Resistant	Resistant	Resistant
1-85	Discordant	Discordant	Discordant	Resistant
1-86	Resistant	Resistant	Resistant	Resistant
1-87	Resistant	Resistant	Resistant	Resistant
1-88	Resistant	Resistant	Discordant	Resistant
1-89	Resistant	Resistant	Resistant	Resistant
1-90	Resistant	Resistant	Resistant	Resistant
1-91	Resistant	Resistant	Resistant	Resistant
1-92	Resistant	Resistant	Resistant	Resistant
1-93	Susceptible	Susceptible	Susceptible	Reverse
1-94	Susceptible	Susceptible	Susceptible	Reverse
1-95	Susceptible	Susceptible	Susceptible	Reverse
1-96	Susceptible	Susceptible	Susceptible	Reverse

Table 6.32 – Classification of isolates from Moldova into four different resistance groups

Isolate ID	RIF	FQL	AMI	INH
2-1	Discordant	Resistant	Susceptible	Resistant
2-2	Resistant	Discordant	Susceptible	Resistant
2-3	Resistant	Reverse	Resistant	Resistant
2-4	Resistant	Discordant	Resistant	Resistant
2-5	Resistant	Resistant	Resistant	Resistant
2-6	Resistant	Discordant	Susceptible	Resistant
2-7	Resistant	Reverse	Resistant	Resistant
2-8	Resistant	Susceptible	Resistant	Resistant
2-9	Discordant	Resistant	Resistant	Resistant
2-10	Resistant	Discordant	Susceptible	Resistant
2-11	Resistant	Susceptible	Resistant	Resistant
2-12	Resistant	Discordant	Reverse	Resistant
2-13	Resistant	Resistant	Susceptible	Resistant
2-14	Resistant	Resistant	Susceptible	Resistant
2-15	Resistant	Resistant	Reverse	Resistant
2-16	Resistant	Resistant	Resistant	Resistant
2-17	Resistant	Resistant	Reverse	Resistant
2-18	Resistant	Resistant	Resistant	Resistant
2-19	Resistant	Discordant	Resistant	Resistant
2-20	Resistant	Discordant	Reverse	Resistant
2-21	Resistant	Resistant	Reverse	Resistant
2-22	Resistant	Resistant	Reverse	Resistant
2-23	Resistant	Resistant	Reverse	Resistant
2-24	Resistant	Resistant	Resistant	Resistant
2-25	Resistant	Discordant	Resistant	Resistant
2-26	Resistant	Resistant	Susceptible	Resistant
2-27	Resistant	Discordant	Resistant	Resistant
2-28	Resistant	Susceptible	Resistant	Resistant
2-29	Resistant	Resistant	Discordant	Resistant
2-30	Resistant	Resistant	Resistant	Resistant
2-31	Resistant	Resistant	Resistant	Resistant
2-32	Resistant	Resistant	Resistant	Resistant
2-33	Resistant	Reverse	Resistant	Resistant

Table 6.32 – Classification of isolates from Moldova into four different resistance groups (continued)

Isolate ID	RIF	FQL	AMI	INH
2-34	Resistant	Reverse	Resistant	Resistant
2-35	Resistant	Resistant	Reverse	Resistant
2-36	Resistant	Resistant	Reverse	Resistant
2-37	Resistant	Resistant	Resistant	Resistant
2-38	Resistant	Resistant	Resistant	Resistant
2-39	Resistant	Discordant	Discordant	Resistant
2-40	Resistant	Reverse	Resistant	Resistant
2-41	Resistant	Resistant	Susceptible	Resistant
2-42	Resistant	Resistant	Resistant	Resistant
2-43	Resistant	Resistant	Resistant	Resistant
2-44	Resistant	Resistant	Resistant	Resistant
2-45	Resistant	Resistant	Reverse	Resistant
2-46	Resistant	Discordant	Resistant	Resistant
2-47	Resistant	Susceptible	Reverse	Resistant
2-48	Resistant	Susceptible	Resistant	Resistant
2-49	Resistant	Resistant	Reverse	Resistant
2-50	Resistant	Resistant	Susceptible	Resistant
2-51	Resistant	Resistant	Reverse	Resistant
2-52	Resistant	Resistant	Reverse	Resistant
2-53	Resistant	Discordant	Reverse	Resistant
2-54	Resistant	Resistant	Reverse	Resistant
2-55	Resistant	Resistant	Reverse	Resistant
2-56	Resistant	Susceptible	Resistant	Resistant
2-57	Resistant	Resistant	Resistant	Resistant
2-58	Resistant	Resistant	Resistant	Resistant
2-59	Resistant	Susceptible	Reverse	Resistant
2-60	Resistant	Resistant	Resistant	Resistant
2-61	Resistant	Discordant	Reverse	Resistant
2-62	Resistant	Resistant	Resistant	Resistant
2-63	Resistant	Resistant	Resistant	Resistant
2-64	Resistant	Discordant	Resistant	Resistant
2-65	Resistant	Resistant	Discordant	Resistant
2-66	Resistant	Resistant	Reverse	Resistant

Table 6.32 – Classification of isolates from Moldova into four different resistance groups (continued)

Isolate ID	RIF	FQL	AMI	INH
2-67	Resistant	Resistant	Resistant	Resistant
2-68	Resistant	Resistant	Reverse	Resistant
2-69	Resistant	Resistant	Resistant	Resistant
2-70	Resistant	Resistant	Resistant	Resistant
2-71	Resistant	Reverse	Resistant	Resistant
2-72	Resistant	Resistant	Reverse	Resistant
2-73	Susceptible	Susceptible	Susceptible	Susceptible
2-74	Susceptible	Susceptible	Susceptible	Susceptible
2-75	Susceptible	Susceptible	Susceptible	Susceptible
2-76	Susceptible	Susceptible	Susceptible	Susceptible
2-77	Susceptible	Susceptible	Susceptible	Susceptible
2-78	Susceptible	Susceptible	Susceptible	Susceptible
2-79	Resistant	Resistant	Susceptible	Resistant
2-80	Resistant	Discordant	Susceptible	Resistant
2-81	Discordant	Discordant	Discordant	Resistant
2-82	Resistant	Discordant	Resistant	Resistant
2-83	Resistant	Discordant	Reverse	Resistant
2-84	Resistant	Resistant	Discordant	Resistant
2-85	Resistant	Discordant	Reverse	Resistant
2-86	Resistant	Resistant	Resistant	Resistant
2-87	Resistant	Reverse	Resistant	Resistant
2-88	Reverse	Reverse	Reverse	Reverse

Table 6.33 – Classification of isolates from the Philippines into four different resistance groups

Isolate ID	RIF	FQL	AMI	INH
3-2	Resistant	Susceptible	Resistant	Resistant
3-3	Resistant	Susceptible	Resistant	Resistant
3-4	Resistant	Resistant	Resistant	Resistant
3-5	Resistant	Susceptible	Resistant	Resistant
3-6	Discordance	Discordant	Discordant	Discordant
3-7	Resistant	Resistant	Resistant	Resistant
3-8	Resistant	Resistant	Resistant	Discordant
3-9	Resistant	Discordant	Discordant	Resistant
3-10	Resistant	Discordant	Susceptible	Resistant
3-11	Resistant	Resistant	Susceptible	Resistant
3-12	Susceptible	Discordant	Susceptible	Susceptible
3-13	Resistant	Resistant	Susceptible	Resistant
3-14	Resistant	Discordant	Susceptible	Resistant
3-15	Discordance	Discordant	Susceptible	Discordant
3-16	Susceptible	Discordant	Susceptible	Discordant
3-17	Resistant	Discordant	Susceptible	Resistant
3-18	Resistant	Resistant	Susceptible	Resistant
3-19	Resistant	Resistant	Susceptible	Resistant
3-20	Resistant	Resistant	Susceptible	Resistant
3-21	Resistant	Discordant	Susceptible	Resistant
3-22	Resistant	Resistant	Susceptible	Resistant
3-23	Resistant	-	Resistant	Resistant
3-24	Susceptible	Susceptible	Susceptible	Susceptible
3-25	Susceptible	Susceptible	Susceptible	Susceptible
3-26	Susceptible	Susceptible	Susceptible	Susceptible
3-27	Susceptible	Susceptible	Susceptible	Susceptible
3-28	Resistant	-	Susceptible	Discordant
3-29	Resistant	Resistant	Susceptible	Discordant
3-30	Resistant	Discordant	Susceptible	Resistant
3-31	Resistant	Resistant	Susceptible	Resistant
3-32	Resistant	-	Susceptible	Resistant
3-33	Resistant	-	Susceptible	Resistant
3-34	Resistant	Discordant	Susceptible	Resistant

Table 6.33 – Classification of isolates from the Philippines into four different resistance groups (continued)

Isolate ID	RIF	FQL	AMI	INH
3-35	Resistant	-	Resistant	Resistant
3-36	Resistant	-	Resistant	Resistant
3-37	Discordance	Discordant	Susceptible	Resistant
3-38	Resistant	-	Resistant	Resistant
3-39	Resistant	-	Susceptible	Discordant
3-40	Resistant	Susceptible	Susceptible	Resistant
3-41	Resistant	Susceptible	Susceptible	Resistant
3-42	Resistant	Susceptible	Susceptible	Discordant
3-43	Resistant	-	Susceptible	Resistant
3-44	Resistant	Susceptible	Susceptible	Resistant
3-45	Discordance	Susceptible	Susceptible	Resistant
3-46	Resistant	Susceptible	Susceptible	Resistant
3-47	Resistant	Susceptible	Susceptible	Resistant
3-48	Resistant	Susceptible	Susceptible	Resistant
3-49	Resistant	-	Susceptible	Resistant
3-50	Susceptible	Susceptible	Susceptible	Susceptible
3-51	Susceptible	Susceptible	Susceptible	Susceptible
3-52	Susceptible	Susceptible	Susceptible	Susceptible
3-53	Resistant	Resistant	Susceptible	Resistant
3-54	Susceptible	Susceptible	Susceptible	Susceptible
3-55	Susceptible	Susceptible	Susceptible	Resistant
3-56	Resistant	-	Susceptible	Discordant
3-57	Susceptible	Susceptible	Susceptible	Susceptible
3-58	Discordance	Susceptible	Susceptible	Reverse
3-59	Susceptible	Susceptible	Susceptible	Susceptible
3-60	Reverse	Resistant	Susceptible	Resistant
3-61	Resistant	-	Resistant	Resistant
3-62	Resistant	Resistant	Resistant	Discordant
3-63	Discordance	Discordant	Discordant	Resistant
3-64	Resistant	-	Resistant	Resistant
3-65	Resistant	-	Resistant	Resistant
3-66	Resistant	Susceptible	Discordant	Resistant
3-67	Resistant	Resistant	Discordant	Resistant

Table 6.33 – Classification of isolates from the Philippines into four different resistance groups (continued)

Isolate ID	RIF	FQL	AMI	INH
3-68	Resistant	Discordant	Resistant	Resistant
3-69	Resistant	-	Resistant	Resistant
3-70	Resistant	-	Resistant	Resistant
3-71	Resistant	Susceptible	Resistant	Resistant
3-72	Reverse	Resistant	Susceptible	Resistant
3-73	Reverse	Reverse	Susceptible	Susceptible
3-74	Resistant	Discordant	Susceptible	Resistant
3-76	Resistant	Resistant	Susceptible	Discordant
3-77	Resistant	Resistant	Susceptible	Resistant
3-78	Resistant	Discordant	Susceptible	Resistant
3-79	Resistant	Resistant	Susceptible	Discordant
3-80	Susceptible	Resistant	Susceptible	Resistant
3-81	Susceptible	Susceptible	Susceptible	Susceptible
3-82	Resistant	Discordant	Susceptible	Resistant
3-83	Resistant	Susceptible	Susceptible	Resistant
3-84	Resistant	Susceptible	Susceptible	Resistant
3-85	Resistant	-	Susceptible	Resistant
3-86	Resistant	Susceptible	Susceptible	Discordant
3-87	Resistant	Susceptible	Susceptible	Resistant
3-88	Resistant	-	Susceptible	Resistant
3-89	Resistant	Susceptible	Susceptible	Resistant
3-90	Resistant	Reverse	Susceptible	Resistant
3-91	Resistant	Susceptible	Susceptible	Resistant
3-92	Resistant	Susceptible	Susceptible	Resistant
3-93	Resistant	-	Susceptible	Resistant
3-94	Resistant	Susceptible	Susceptible	Resistant
3-95	Resistant	-	Susceptible	Resistant
3-96	Resistant	-	Susceptible	Resistant
3-97	Susceptible	-	Susceptible	Reverse
3-98	Susceptible	Susceptible	Susceptible	Reverse
3-99	Susceptible	Susceptible	Susceptible	Reverse
3-100	Reverse	-	Susceptible	Reverse

Table 6.33 – Classification of isolates from the Philippines into four different resistance groups (continued)

Isolate ID	RIF	FQL	AMI	INH
3-101	Resistant	Susceptible	Resistant	Resistant
3-102	Resistant	Resistant	Susceptible	Resistant
3-103	Susceptible	Discordant	Susceptible	Susceptible
3-104	Resistant	Resistant	Susceptible	Resistant
3-105	Resistant	Resistant	Susceptible	Discordant
3-106	Resistant	Discordant	Susceptible	Resistant
3-107	Resistant	Resistant	Susceptible	Resistant
3-108	Resistant	Resistant	Susceptible	Resistant
3-109	Resistant	Resistant	Susceptible	Resistant
3-110	Susceptible	Susceptible	Susceptible	Resistant
3-111	Resistant	Susceptible	Susceptible	Reverse
3-112	Discordance	Susceptible	Susceptible	Reverse
3-113	Resistant	Susceptible	Susceptible	Resistant
3-114	Resistant	-	Susceptible	Discordant
3-115	Resistant	Susceptible	Susceptible	Discordant
3-116	Resistant	-	Susceptible	Resistant
3-117	Susceptible	Susceptible	Susceptible	Resistant
3-118	Resistant	Susceptible	Susceptible	Resistant
3-119	Resistant	Susceptible	Susceptible	Resistant
3-120	Resistant	-	Susceptible	Resistant
3-121	Resistant	Susceptible	Susceptible	Resistant
3-122	Resistant	-	Reverse	Resistant
3-123	Resistant	-	Susceptible	Discordant
3-124	Resistant	Susceptible	Susceptible	Resistant
3-125	Resistant	Susceptible	Susceptible	Resistant

Table 6.34 – Classification of isolates from South Africa into four different resistance groups

Isolate ID	RIF	FQL	AMI	INH
4-1	Resistant	Resistant	Resistant	Resistant
4-2	Resistant	Resistant	Resistant	Resistant
4-3	Resistant	Discordant	Discordant	Resistant
4-4	Resistant	Discordant	Resistant	Resistant
4-5	Resistant	Resistant	Resistant	Resistant
4-6	Resistant	Resistant	Resistant	Resistant
4-7	Resistant	Resistant	Resistant	Resistant
4-8	Resistant	Resistant	Resistant	Resistant
4-9	Resistant	Resistant	Resistant	Resistant
4-10	Resistant	Resistant	Resistant	Resistant
4-11	Resistant	Resistant	Resistant	Resistant
4-12	Resistant	Resistant	Resistant	Resistant
4-13	Resistant	Resistant	Resistant	Resistant
4-14	Resistant	Resistant	Discordant	Discordant
4-15	Resistant	Resistant	Resistant	Resistant
4-16	Resistant	Resistant	Resistant	Resistant
4-17	Resistant	Resistant	Resistant	Resistant
4-18	Resistant	Resistant	Discordant	Resistant
4-19	Resistant	Resistant	Resistant	Resistant
4-20	Resistant	Resistant	Resistant	Resistant
4-21	Resistant	Resistant	Resistant	Resistant
4-22	Resistant	Resistant	Resistant	Resistant
4-23	Resistant	Resistant	Resistant	Resistant
4-24	Resistant	Resistant	Resistant	Resistant
4-25	Resistant	Resistant	Resistant	Resistant
4-26	Resistant	Resistant	Resistant	Resistant
4-27	Resistant	Resistant	Resistant	Resistant
4-28	Resistant	Resistant	Resistant	Resistant
4-29	Resistant	Resistant	Resistant	Resistant
4-30	Resistant	Resistant	Resistant	Resistant
4-31	Resistant	Resistant	Resistant	Resistant
4-32	Resistant	Resistant	Resistant	Resistant
4-33	Resistant	Resistant	Resistant	Resistant

Table 6.34 – Classification of isolates from South Africa into four different resistance groups (continued)

Isolate ID	RIF	FQL	AMI	INH
4-34	Resistant	Resistant	Resistant	Resistant
4-35	Resistant	Resistant	Resistant	Resistant
4-36	Resistant	Resistant	Resistant	Resistant
4-37	Resistant	Resistant	Resistant	Resistant
4-38	Resistant	Resistant	Resistant	Resistant
4-39	Resistant	Resistant	Resistant	Resistant
4-40	Resistant	Resistant	Resistant	Resistant
4-41	Resistant	Resistant	Resistant	Resistant
4-42	Resistant	Resistant	Resistant	Resistant
4-43	Resistant	Resistant	Resistant	Resistant
4-44	Discordant	Discordant	Discordant	Resistant
4-45	Resistant	Resistant	Resistant	Resistant
4-46	Resistant	Resistant	Resistant	Resistant
4-47	Resistant	Resistant	Resistant	Resistant
4-48	Resistant	Resistant	Resistant	Resistant
4-49	Resistant	Resistant	Resistant	Resistant
4-50	Resistant	Resistant	Resistant	Resistant
4-51	Resistant	Resistant	Resistant	Resistant
4-52	Resistant	Resistant	Resistant	Resistant
4-53	Resistant	Resistant	Resistant	Resistant
4-54	Resistant	Resistant	Resistant	Resistant
4-55	Resistant	Resistant	Resistant	Resistant
4-56	Resistant	Resistant	Resistant	Resistant
4-57	Resistant	Resistant	Discordant	Resistant
4-58	Resistant	Resistant	Resistant	Resistant
4-59	Resistant	Discordant	Resistant	Resistant
4-60	Resistant	Resistant	Resistant	Resistant
4-61	Resistant	Resistant	Resistant	Resistant
4-62	Resistant	Resistant	Resistant	Resistant
4-63	Resistant	Resistant	Resistant	Resistant
4-64	Resistant	Resistant	Resistant	Resistant
4-65	Resistant	Resistant	Resistant	Resistant
4-66	Resistant	Resistant	Resistant	Resistant

Table 6.34 – Classification of isolates from South Africa into four different resistance groups (continued)

Isolate ID	RIF	FQL	AMI	INH
4-67	Resistant	Resistant	Resistant	Resistant
4-68	Resistant	Resistant	Resistant	Resistant
4-69	Discordant	Discordant	Discordant	Discordant
4-70	Resistant	Resistant	Resistant	Resistant
4-71	Resistant	Resistant	Resistant	Resistant
4-72	Resistant	Resistant	Resistant	Resistant
4-73	Resistant	Resistant	Resistant	Resistant
4-74	Resistant	Resistant	Resistant	Resistant
4-75	Resistant	Susceptible	Resistant	Resistant
4-76	Resistant	Susceptible	Resistant	Resistant
4-77	Susceptible	Susceptible	Resistant	Resistant
4-78	Susceptible	Susceptible	Susceptible	Susceptible
4-79	Discordant	Discordant	Discordant	Resistant
4-80	Susceptible	Susceptible	Susceptible	Susceptible
4-81	Susceptible	Susceptible	Susceptible	Susceptible
4-82	Susceptible	Susceptible	Susceptible	Susceptible
4-83	Susceptible	Susceptible	Susceptible	Susceptible
4-84	Susceptible	Susceptible	Susceptible	Susceptible
4-85	Susceptible	Susceptible	Susceptible	Susceptible
4-86	Resistant	Resistant	Resistant	Resistant
4-87	Resistant	Resistant	Discordant	Resistant
4-88	Resistant	Resistant	Resistant	Resistant
4-89	Resistant	Resistant	Resistant	Resistant
4-90	Resistant	Resistant	Resistant	Discordant
4-91	Resistant	Resistant	Resistant	Resistant
4-92	Resistant	Resistant	Resistant	Resistant
4-93	Resistant	Resistant	Resistant	Resistant
4-94	Resistant	Resistant	Resistant	Resistant
4-95	Resistant	Susceptible	Resistant	Resistant
4-96	Resistant	Resistant	Resistant	Resistant
4-97	Resistant	Discordant	Resistant	Resistant
4-98	Resistant	Resistant	Resistant	Resistant
4-99	Resistant	Susceptible	Resistant	Resistant
4-100	Resistant	Resistant	Resistant	Resistant