Evaluation of the COBAS TaqMan MTB Test for Direct Detection of 
*Mycobacterium tuberculosis* Complex in Respiratory Specimens

Yuan-Chieh Yang¹, Po-Liang Lu¹,², Su Chiao Huang,¹ Yi-Shan Jenh³, Ruwen Jou⁴, Tsung Chain Chang³

Department of Laboratory Medicine,¹ and Department of Internal Medicine,²

Kaohsiung Medical University Hospital, Kaohsiung, Taiwan; Department of Medical Laboratory Science and Biotechnology, College of Medicine, National Cheng Kung University, Tainan, Taiwan;⁵ Reference Laboratory of Mycobacteriology, Center for Disease Control, Department of Health, Taipei, Taiwan⁴

Running title: EVALUATION OF COBAS TAQMAN MTB TEST

Corresponding author: Tsung Chain Chang

Mailing address: 1 University Road, Department of Medical Laboratory Science and Biotechnology, College of Medicine, National Cheng Kung University, Tainan 701, Taiwan.

Phone: 886-6-2353535 ext. 5790. Fax: 886-6-2363956.

E-mail: tsungcha@mail.ncku.edu.tw
ABSTRACT

The COBAS TaqMan MTB Test, based on real-time PCR technology, was evaluated for the direct detection of *Mycobacterium tuberculosis* complex (MTBC) in respiratory specimens. A total of 1093 samples from 446 patients, including 118 acid-fast smear positive and 975 acid-fast smear negative specimens, were investigated. Diagnostic cultures performed with 7H11 agar, Löwenstein-Jensen medium, and BACTEC MGIT 960 system, were considered as the reference methods. When discrepant results between the COBAS TaqMan MTB Test and culture occurred, additional results from the BD MGIT TBe Identification Test and GenoType Mycobacterium CM performed on growth-positive and acid-fast-positive MGIT tubes and review of patient’s medical history were used for discrepant analysis. The overall sensitivity, specificity, positive, and negative predictive values for the COBAS TaqMan MTB Test were 91.5%, 98.7%, 91.5%, and 98.7%, respectively. In general, the performance of the new COBAS TaqMan MTB Test was comparable to the replaced COBAS AMPLICOR MTB system. The most prominent feature of the new system was its extraordinary high sensitivity (79.5%) for detecting MTBC in smear-negative specimens; out of 44 smear negative but culture positive specimens, 35 were positive by the new system. The COBAS TaqMan MTB assay, including DNA extraction, can be completed within 3 h.
INTRODUCTION

Tuberculosis (TB) is one of the most threatening curable infectious diseases. The disease afflicts approximately 8.6 million patients and causes about 2 million deaths annually (25). The increasing global burden of mycobacteriosis is associated with improper antibiotic therapy and immunocompromised patients, such as those with AIDS (1). Early diagnosis of TB and the prompt use of adequate antibiotics to interrupt transmission remain the top priorities for TB control (6).

The conventional diagnosis of mycobacterial infections is based primarily on demonstrating the presence of the acid-fast bacilli (AFB) in the smear, followed by a positive culture and identification of the isolate by biochemical characteristics. In the past decades, several commercial systems are gaining popular for direct detection of MTBC in clinical specimens. For instance, the COBAS AMPLICOR MTB Test (Roche, Basel, Switzerland), the Amplified M. tuberculosis Direct Test (Gen-Probe, San Diego, Ca.), the BDProbe Tec ET system (Becton, Dickinson and Company, Sparks, Md.) and the GenXpert MTB/RIF system (Cepheid, Sunnyvale, Ca.). These systems, being able to reduce the diagnostic time from weeks to hours, have been acquiring great attention in TB diagnosis. In general, the specificity of these systems is very high while the sensitivity varied widely (18). For most commercial tests, the assay sensitivities (87.5%-100%) seem to be satisfactory for AFB smear-positive
specimens, but the sensitivities (50.0% to 70.8%) varied greatly for AFB smear-negative samples (18).

The COBAS AMPLICOR MTB assay for direct detection of MTBC in pulmonary specimens is popular in the developing and developed countries and many studies have been conducted worldwide to evaluate the system (10, 11, 15, 18). The COBAS AMPLICOR MTB assay is based on amplification of a segment of the 16S rRNA gene followed by colorimetric detection of the PCR product by probe hybridization (18). The AMPLICOR assay was approved by the FDA for testing on smear-positive respiratory samples. Recently, Roche Diagnostics (Taipei, Taiwan) introduced a new system (COBAS TaqMan MTB Test), based on real-time PCR technology, to replace the COBAS AMPLICOR MTB assay. According to the user’s instructions from Roche (5), the total agreement rate was 98.3% (95% confidence interval 97.1-99.1%) between the new and old systems. The new system is recommended for analyzing respiratory samples, including smear-positive and -negative specimens. However, so far, there is only one study published to evaluate the performance of the COBAS TaqMan MTB Test by testing a limited number of specimens (13). The aim of this study was to evaluate the new system by using a large number of respiratory specimens.
MATERIALS AND METHODS

Clinical specimens and processing. In an open prospective study in the spring of 2010, a total of 1093 respiratory specimens (1036 sputum, 39 bronchial and tracheal aspirate, and 18 bronchial alveolar lavage samples) were sent to the Division of Clinical Microbiology, Department of Laboratory Medicine, Kaohsiung Medical University Hospital (KMUH) for mycobacterial testing. The collection of these clinical samples for this study was approved by the Review Board Committee of KUMH. The specimens were collected from 446 patients with clinical signs of pulmonary TB or in order to exclude the possibility of TB infection. Specimens were digested and decontaminated by the N-acetyl-L-cysteine-NaOH method, and neutralized with phosphate buffer (67 mM, pH 6.8) and centrifuged (12). The sediment was resuspended in 2.0 ml of the same phosphate buffer. An aliquot of the suspension was stained with an auramine fluorescent stain. The status of those deemed positive was confirmed by the Kinyoun acid fast staining method and classified into AFB +/-, 1+, 2+, 3+ or 4+ based on standard procedures (2). Portions (0.5 ml) of the sediment from each specimen were used to inoculate a Löwenstein-Jensen (LJ) tube, a 7H11 agar plate, and a BACTEC MGIT 960 tube (Becton, Dickinson and Company, Taipei, Taiwan) supplemented with oleic acid, albumin, dextrose, catalase (BBL MGIT OADC) and PANTA Plus (both products
Culture conditions and MTBC identification. The LJ tubes and 7H11 agar plates were incubated at 37°C for 8 weeks and examined weekly for positive cultures. The identification of the mycobacterial isolates as MTBC is based mainly on routine morphological and biochemical assays (24) and confirmed by amplification of the 65-kDa heat shock protein followed by restriction enzyme analysis (23). The MGIT tubes were incubated at 35°C and monitored automatically every 60 min for fluorescence intensity. The tubes were incubated until positive or for 42 days. Positive tubes were removed from the MGIT 960 instrument, and smears for AFB stain were prepared. The smears were first screened with the auramine fluorescent stain and confirmed by the Kinyoun acid fast stain. If the smear was AFB positive, subculture was made on the 7H11 agar plate and LJ slant for recovery of mycobacteria, and an aliquot (0.1 ml) of the broth was used for testing of the presence of MTBC specific protein (MPT64) using the BD MGIT TBc Identification Test (Becton, Dickinson and Company) according to the manufacturer’s instructions. The immunochromatographic test provides results in 15 minutes. In addition, an 0.2 ml aliquot of the growth-positive and AFB-positive broth from each MGIT tube was used for DNA extraction using the Gentra Puregene DNA extraction kit (QIAGENE, Valencia, Ca.) following the manufacturer’s instructions, except that a preceding step of heat
inactivation (80°C for 5 min) was included. The DNA was kept for further testing by using a line probe hybridization kit (GenoType Mycobacterium CM, Hain Lifesience GmbH, Germany). In addition to MTBC, the GenoType kit also can detect more than 10 species of nontuberculous mycobacteria (16). The results of BD MGIT TBc Identification and Mycobacterium CM assays were used as supporting evidences for the presence of MTBC when discrepant results between the COBAS TaqMan MTB Test and culture occurred.

**COBAS TaqMan MTB Test.** The COBAS TaqMan MTB Test is used for the detection of MTBC in liquefied, decontaminated, and concentrated respiratory specimens. The test utilizes the TaqMan 48 Analyzer for automated amplification and detection. The test includes two major steps: (1) preparation of specimen DNA, and (2) real-time PCR. The assay permits the detection of amplified MTBC amplicon and internal control DNA, which is amplified and detected simultaneously with the specimen. A 100 µl aliquot of the liquefied, decontaminated, and concentrated respiratory specimen from each specimen was used for testing. One MYCO (–) control (Mycobacterium negative control) and one MTB (+) control (M. tuberculosis positive control) were included in each test run. The TaqMan 48 Analyzer determined the cycle threshold value ($C_t$) for the DNA of MTBC, and checked whether the $C_t$
values of the internal control DNA, MTB (+) control, and MYCO (–) control were within normal ranges. The internal control DNA was used to detect polymerase inhibitors that might present in specimens. In this study, PCR inhibitors were found in about 1% specimens (10 samples), and these specimens were 1:10 diluted and retested as recommended (5).

**Analysis of discrepant results.** Conventional culture was primarily considered as the “gold standard” for performance calculation. When discrepant results between the COBAS TaqMan MTB Test and culture occurred, the test results from the adjunct BD MGIT TBC Identification and GenoType Mycobacterium CM assays were taken into consideration for resolving discrepancies. For example, if a specimen was TaqMan MTB test positive but culture negative, the specimen was considered to contain MTBC if the BD MGIT TBC Identification assay and/or the GenoType Mycobacterium CM test were also positive for MTBC. In addition, patient’s clinical pictures, including the chest symptoms, X ray, and history of antibiotics administered, whenever those data were available, were taken into account for discrepant analysis. Patient’s clinical history was classified into five groups according to the recommendations of the American Thoracic Society (3) with small modifications. The five groups were: group 1 (exclusion of TB), negative tuberculin skin test, smear and
culture negative, definitive other diagnosis obtained by culture, or on the basis of clinical presentation; group 2 (TB infection), smear and culture negative, not clinically active (positive tuberculin skin test and/or history of tuberculosis); group 3 (TB infection), smear positive or negative, culture negative, clinically active (positive tuberculin skin test, history of TB, radiological or clinical signs of active TB, exclusion of other definitive cultures, improvement under antituberculous chemotherapy); group 4 (TB infection), smear negative or positive, culture positive; and group 5 (TB infection), smear and culture positive. If a specimen was positive by the COBAS test but was negative by culture and the two adjunct tests, the specimen was still determined to contain MTBC if the patient clinical history was classified in group 3.

**Performance analysis.** The sensitivity, specificity, positive predictive value (PPV), and negative predictive value (NPV) of the COBAS TaqMan MTB Test were calculated after discrepant analysis. The 95% confidence interval was calculated according to Gardner and Altman (9).
RESULTS

**Smear-positive specimens.** A total of 118 specimens from 52 patients were AFB smear-positive. Of these samples, the COBAS TaqMan MTB assay yielded 115 concordant results (94 positives and 21 negatives) with culture after resolving discrepancies (Table 1). The TaqMan MTB assay produced three false negatives (T03092, T03609, and T04270), since MTBC was isolated from these samples by culture. In addition, clinical history indicated that the three specimens were from patients in clinical group 5. Before discrepancy resolving, 10 specimens were found to be false positive by the COBAS TaqMan MTB assay (Table 2). Of the 10 samples, specimens T03876 and T03951 were determined to be true positives by the COBAS system, since both samples were MTBC positive by the GenoType CM test and specimen T03951 was also BD MGIT TBc test positive. Clinical history also indicated that the two specimens were from patients with TB infection (group 4). However, *M. abscessus* was detected in specimen T03951 by culture and by the GenoType CM test. Therefore, specimen T03951 was recognized as a mixed culture of MTBC and *M. abscessus*, with MTBC being detected by the COBAS TaqMan, GenoType, and BD MGIT TBc assays while *M. abscessus* being detected by culture and the GenoType assay.

The remaining eight false positives (T03148, T03587, T04256, T04869, T05989,
T05990, T06228, and T06229) produced by the COBAS TaqMan MTB test were also considered to be true positives after reviewing patient’s medical history, although these samples were MTBC negative as determined by three other methods (culture, the GenoType and BD MGIT TBc assays). The eight specimens were from patients who had TB history and/or typical signs of TB, and were classified in clinical group 3 (TB infection) (Table 2). After resolving discrepancies, the sensitivity, specificity, PPV, and NPV for the COBAS system for smear-positive specimens were 96.9%, 100%, 100%, and 87.5%, respectively (Table 1). It was noted that specimens T05989 and T05990 were from the same patient, while specimens T06228 and T06229 from another patient.

Smear-negative specimens. A total of 975 specimens from 394 patients were AFB smear-negative. Of these specimens, the COBAS TaqMan MTB assay yielded 954 concordant results (35 positives and 919 negatives) with culture after resolving discrepancies. Before discrepant analysis, the COBAS assay produced nine false negatives and 20 false positives (Table 2). The nine false negatives (specimens T03266, T03281, T03323, T03434, T03577, T03919, T03960, T04265, and T04270) were true false negatives as MTBC was recovered from these samples by culture; six of these specimens were also positive by the BD MGIT TBc assay (Table 2). The false-positive number reduced from 20 to 12 after resolving discrepancies, eight false
positives (T03116, T03218, T03258, T03949, T04077, T04118, T04302, and T04332) were considered to be true positives, as clinical data revealed that these specimens were from patients with TB history or from highly suspected TB patients (medical group 3) (Table 2). Twelve specimens (T03090, T03215, T03329, T03389, T03464, T03508, T03798, T03897, T04043, T04058, T04193, and T04277) were from patients without any sign of TB (medical group 1) and these specimens were considered to be true false-positive by the COBAS TaqMan MTB assay. Therefore, for smear-negative specimens, the sensitivity, specificity, PPV, and NPV for the COBAS TaqMan MTB Test were 79.5%, 98.7%, 74.5%, and 99.0%, respectively, after discrepant resolution.

The most prominent feature of the COBAS TaqMan MTB Test was its extraordinary high sensitivity (79.5%) for detecting MTBC in smear-negative samples. Out of 44 specimens that were culture positive, 35 were also positive by the COBAS system. The less satisfactory PPV (74.5%) for smear-negative specimens was due to the fact that among the 47 COBAS TaqMan MTB-positive specimens, 12 were false positives (Table 1).

**Overall performance of the COBAS TaqMan MTB TEST.** If smear-positive and smear-negative specimens were taken together, a total of 1093 specimens were analyzed. The overall sensitivity, specificity, PPV, and NPV of the COBAS system were 91.5%, 98.7%, 91.5%, and 98.7%, respectively (Table 1).
The COBAS TaqMan MTB Test is a new system used to substitute for the COBAS AMPLICOR MTB assay that was the first automated nucleic acid amplification test for direct detection of MTBC in respiratory specimens. Since the introduction of nucleic acid-based test systems, the mostly concerned question has been the sensitivity of these assays, especially with smear-negative samples (18). In this study, we evaluated the performance of the new COBAS system by testing 1093 respiratory samples. During the evaluation, BD MGIT TBc Identification Test and GenoType Mycobacterium CM assays were also performed on growth-positive and AFB-positive MGIT broth. The two adjunct tests were intended to compensate culture results that were not available due to no visible growth or outgrowth by other bacteria (contamination) on the LJ slants and 7H11 agar plates. The sensitivities of the new COBAS system were 96.9%, 79.5%, and 91.5%, respectively, for smear-positive, smear-negative, and overall specimens (Table 1). For smear-positive samples, the sensitivity (96.9%) was comparable to those (87.5%-100%) of the COBAS AMPLICOR MTB test (4, 7, 8, 18-20). For detection of MTBC in smear-negative specimens, the sensitivity (79.5%) of the new system was the highest among those (51% to 71.7%, average 59.5%) reported for the COBAS AMPLICOR MTB system (Table 2). In other words, the newly launched COBAS system has a prominent ability
to detect lower loads of MTBC in smear-negative samples. However, the performance
determined in this study may vary according to the prevalence of tuberculosis in
different countries, especially the positive and negative predictive values.

In this study, the new system was able to detect MTBC in 35 out of 44
smear-negative specimens that were culture positive (Table 1). According to the
manufactures’ instructions (5), the detection limit of the COBAS TaqMan MTB assay
is 0.33-0.83 CFU (95% confidence interval) per PCR reaction. The high sensitivity for
smear-negative specimens seems to be a great improvement of the new system, since
smear-negative samples normally represent a major portion (>90%) of clinical
specimens sent to the routine laboratory for initial diagnosis or follow-up of
mycobacterial infections. Recently, a study was conducted to compare the
performance of the COBAS TaqMan MTB Test and the COBAS AMPLICOR MTB
system (13). The sensitivity, specificity, PPV, and NPV were 79.1%, 98.2%, 73.1%,
and 98.7%, respectively, for the Cobas TaqMan MTB Test. The performance was less
satisfactory then those obtained in this study (Table 1); this might be due to a small
sample size (406 specimens with only 24 being MTBC positive), discrepant results
being not resolved by other molecular methods, and patient’s medical data being not
taken into consideration for discrepancy resolving.

Instead of the Ziehl-Neelsen acid-fast staining method that is popular worldwide,
the cold staining technique (Kinyoun staining) was used in this study. A recent paper (21) indicated that the positive yields of the Ziehl-Neelsen (14.2%) and Kinyoun (13.8%) staining techniques were comparable. Therefore, the use of Kinyoun staining method might not be able to alter the proportion of smear positive to smear negative specimens in this study (Table 1).

In this study, a total of 12 false negatives were produced by the COBAS TaqMan MTB assay (Table 2), with nine of these specimens being smear negative. Of the 12 specimens, 10 exhibited positive culture results after a period of ≥28 days of incubation, indicating the low counts of mycobacteria in these samples. Negative results obtained from culture-positive specimens by molecular amplification assays are normally explained by a low load of mycobacteria, the presence of polymerase inhibitors, and an unequal distribution of mycobacteria in the test specimens (20). A total volume of 1.5 ml of the processed sample sediment was inoculated to the LJ tube, 7H11 agar plate, and BACTEC MGIT 960 tube (each 0.5 ml). If MTBC was finally found in any of the three media, the sample was declared as “culture positive”. Therefore, the total volume used for culture was 1.5 ml; this volume was 15 times of that (0.1 ml) processed for real-time PCR. Therefore, “sample volume effect” may contribute to some false-negative results of the COBAS TaqMan MTB system.

The overall specificity of the COBAS TaqMan MTB system was 98.7% (Table 1);
this value was comparable to those (91.3%-100%) reported for the COBAS AMPLICOR MTB assay (4, 7, 8, 17-20, 22). The high specificity indicated that the chance of producing false-positives in overall samples by the new system was low. The PPV of the COBAS TaqMan MTB assay for smear-positive specimens was 100% (Table 1), demonstrating the superiority of the new system for detection MTBC in AFB-positive samples. It was noted that the extraordinary high sensitivity (79.5%) of the new system for smear-negative samples was accompanied with a relatively poor PPV (74.5%) for smear-negative specimens, suggesting the possibility of cross reactions caused by non-mycobacterial microorganisms. The overall PPV (91.5%) of the new assay was, in general, comparable to the performance (73.3%-100%) of the COBAS AMPLICOR MTB system (4, 7, 8, 18-20).

The overall NPV (98.7%) of the COBAS TaqMan MTB assay was satisfactory as comparing with those (80.8%-99.2%) obtained by the COBAS AMPLICOR MTB system (4, 7, 8, 18-20). This indicates that the new system is also reliable for excluding non-TB cases. It should be noted that the new COBAS system tends to produce a higher rate of false negative in smear-positive specimens versus smear-negative samples. For smear-positive specimens, the NPV was 87.5% versus 99.0% of smear-negative specimens (Table 1). A possible explanation of the result is that some nontuberculous mycobacteria might compete for the primers used to
amplify the DNA of MTBC during the assay and thus caused false negatives. But, the amplified nontuberculous mycobacterial DNA was unable to react with the hybridization probes used in the COBAS TaqMan MTB system since 100% specificity was obtained by the COBAS system for smear-positive specimens.

In conclusion, the COBAS TaqMan MTB Test had comparable performance with the replaced COBAS AMPLICOR MTB system. The most important characteristic of the new system is its high sensitivity (79.5%) for smear-negative specimens. From the results of this study and previous reports, it is obvious that molecular methods are still not as sensitive as culture. Commercially automatic system for MTBC detection should always be performed in conjunction with microscopy and culture, and the results should be interpreted alongside the patient’s clinical data, as recommended by other authors (18). Moreover, the reagents used in the COBAS TaqMan MTB kit are packaged in 12-test, single use vials. For the most efficient use of reagents, specimens and controls should be processed in batches that are multiples of 12. The use of an expensive and automatic instrument should depend on several issues, such as the daily samples processed, engineering and technical support from the hospital, and the prevalence of TB or other mycobacteria-related diseases (18). The major strengths and weaknesses of an automatic system should be fully understood before adapting the system in the routine laboratory.
ACKNOWLEDGMENTS

This project was supported by grants from the National Science Council (NSC 99-2321-B-006-007-) and the Department of Health (DOH99-TD-B-111-102). The authors also thank the statistical help from Tsung-Hsueh Lu, Department of Public Health, College of Medicine, National Cheng Kung University.
REFERENCES


5. COBAS TaqMan MTB Test. Roche Molecular Systems, Inc., Branchburg, NJ.


<table>
<thead>
<tr>
<th>Specimens</th>
<th>COBAS TaqMan MTB Test&lt;sup&gt;a&lt;/sup&gt;</th>
<th>No. of specimens</th>
<th>Performance of the COBAS TaqMan MTB Test with culture result</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Positive</td>
<td>Negative</td>
<td>% Sensitivity (95% CI)</td>
</tr>
<tr>
<td>Smear positive (n = 118)</td>
<td>Positive</td>
<td>94</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>Negative</td>
<td>3</td>
<td>21</td>
</tr>
<tr>
<td>Smear negative (n = 975)</td>
<td>Positive</td>
<td>35</td>
<td>12</td>
</tr>
<tr>
<td></td>
<td>Negative</td>
<td>9</td>
<td>919</td>
</tr>
<tr>
<td>All (n = 1093)</td>
<td>Positive</td>
<td>129</td>
<td>12</td>
</tr>
<tr>
<td></td>
<td>Negative</td>
<td>12</td>
<td>940</td>
</tr>
</tbody>
</table>

<sup>a</sup> The results were adjusted after discrepant analysis.

<sup>b</sup> PPV, positive predictive value.

<sup>c</sup> NPV, negative predictive value.

<sup>d</sup> CI, confidence interval.
TABLE 2. Discrepant analysis of 42 respiratory specimens (38 patients) for *M. tuberculosis* complex detection

<table>
<thead>
<tr>
<th>Specimen (acid fast stain score)</th>
<th>Number of specimens</th>
<th><em>M. tuberculosis</em> complex (other mycobacteria) detected by Medical group</th>
<th>Final interpretation of the COBAS TaqMan MTB Test</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>COBAS TaqMan MTB GenoType CM&lt;sup&gt;a&lt;/sup&gt; BD MGIT TBc</td>
<td></td>
</tr>
<tr>
<td>T03092 (2+), T03609 (3+)</td>
<td>2</td>
<td>- ND&lt;sup&gt;b&lt;/sup&gt; + +</td>
<td>5 False negative</td>
</tr>
<tr>
<td>T04270 (1+)</td>
<td>1</td>
<td>- ND - +</td>
<td>5 False negative</td>
</tr>
<tr>
<td>T03876 (1+)</td>
<td>1</td>
<td>+ + -</td>
<td>4 True positive</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T03951 (2+)</td>
<td>1</td>
<td>+ + +</td>
<td>4 True positive</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T03148 (+), T03587 (2+)</td>
<td>4</td>
<td>+ ND ND -</td>
<td>3 True positive</td>
</tr>
<tr>
<td>T04256 (1+), T05990 (+)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T04869 (2+)</td>
<td>1</td>
<td>+ ND -</td>
<td>3 True positive</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T05989 (1+)</td>
<td>1</td>
<td>+ - -</td>
<td>3 True positive</td>
</tr>
<tr>
<td>T06228 (1+), T06229 (1+)</td>
<td>2</td>
<td>+ ND -</td>
<td>3 True positive</td>
</tr>
</tbody>
</table>

<sup>a</sup> Specimen culture results for the following species are indicated in parentheses: *(M. intracellulare)*, *(M. abscessus)*, *(M. abscessus)*, *(M. fortuitum)*.
<table>
<thead>
<tr>
<th>Sample IDs</th>
<th>Test Results</th>
<th>ND</th>
<th>+</th>
<th>4</th>
<th>False negative</th>
</tr>
</thead>
<tbody>
<tr>
<td>T03266 (-), T03960 (-)</td>
<td>3</td>
<td>-</td>
<td>ND</td>
<td>-</td>
<td>4</td>
</tr>
<tr>
<td>T04270 (-)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T03281 (-), T03323 (-),</td>
<td>6</td>
<td>-</td>
<td>ND</td>
<td>+</td>
<td>4</td>
</tr>
<tr>
<td>T03434 (-), T03577 (-), T03919 (-), T04265 (-)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T03116 (-), T03218 (-)</td>
<td>6</td>
<td>+</td>
<td>ND</td>
<td>ND</td>
<td>3</td>
</tr>
<tr>
<td>T03258 (-), T03949 (-), T04077 (-), T04302 (-)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T04118 (-)</td>
<td>1</td>
<td>+</td>
<td>ND</td>
<td>ND</td>
<td>3</td>
</tr>
<tr>
<td>T04332 (-)</td>
<td>1</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>3</td>
</tr>
<tr>
<td>T03090 (-), T03389 (-)</td>
<td>2</td>
<td>+</td>
<td>ND</td>
<td>-</td>
<td>1</td>
</tr>
<tr>
<td>T03215 (-)</td>
<td>1</td>
<td>+</td>
<td>ND</td>
<td>ND</td>
<td>1</td>
</tr>
<tr>
<td>T03329 (-), T03508 (-)</td>
<td>7</td>
<td>+</td>
<td>ND</td>
<td>ND</td>
<td>1</td>
</tr>
<tr>
<td>T03798 (-), T03897 (-), T04043 (-), T04058 (-), T04193 (-)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sample</td>
<td>Reaction 1</td>
<td>Reaction 2</td>
<td>Reaction 3</td>
<td>Reaction 4</td>
<td>Reaction 5</td>
</tr>
<tr>
<td>--------</td>
<td>------------</td>
<td>------------</td>
<td>------------</td>
<td>------------</td>
<td>------------</td>
</tr>
<tr>
<td>T03464</td>
<td>+</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T04277</td>
<td>+</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

(M. gordonae) (M. gordonae)

Nontuberculous mycobacteria detected by the GenoType CM were shown in parentheses.

Nontuberculous mycobacteria isolated by culture were shown in parentheses.

ND, not determined due to no growth in the MGIT tube or the tube was growth positive but AFB negative.