**ABSTRACT**

Rapid diagnosis of tuberculosis (TB) and multidrug-resistant (resistance to at least rifampin and isoniazid) *Mycobacterium tuberculosis* (MDR-TB) is one of the cornerstones for global TB control as it allows early epidemiological and therapeutic interventions. The slow growth of the tubercle bacillus is the greatest obstacle to rapid diagnosis of the disease. However, considerable progress has recently been made in developing novel diagnostic tools, especially molecular methods (commercial and ‘in-house’), for direct detection in clinical specimens. These methods, based on nucleic acid amplification (NAA) of different targets, aim to identify the *M. tuberculosis* complex and detect the specific chromosome mutations that are most frequently associated with phenotypic resistance to multiple drugs. In general, commercial methods are recommended since they have a better level of standardization, reproducibility and automation. Although some aspects such as cost-efficiency and the appropriate setting for the implementation of these techniques are not yet well established, organizations such as the WHO are strongly supporting the implementation and universal use of these new molecular methods. This chapter summarizes current knowledge and the available molecular methods for rapid diagnosis of TB and anti-tuberculous drug resistance in clinical microbiology laboratories.

© 2011 Elsevier España, S.L. All rights reserved.

---

**Keywords:**

- Tuberculosis
- Molecular diagnosis
- Rapid detection of drug resistance

---

**Resumen**

El diagnóstico rápido de la enfermedad tuberculosa y la resistencia múltiple a los fármacos antituberculosos (al menos isoniazida y rifampicina) en *Mycobacterium tuberculosis* complex (MDR-TB) es una de las piedras angulares en el control de esta enfermedad, ya que permite una acción epidemiológica y terapéutica precoz. El crecimiento lento del bacilo tuberculoso es uno de los mayores impedimentos para un diagnóstico rápido. En los últimos años ha existido un importante avance en el desarrollo de nuevas herramientas diagnósticas, sobre todo moleculares (comerciales y caseras), para el diagnóstico directo de muestra clínica. Estos métodos se basan en la amplificación de diversas dianas de ácidos nucleicos (AAN), para la identificación de *M. tuberculosis* complex y la detección de las mutaciones cromosómicas más frecuentemente relacionadas con la resistencia fenotípica a diversos fármacos. En general, entre las múltiples técnicas existentes, se recomiendan los métodos comerciales por su mayor estandarización, reproducibilidad y automatización. A pesar de que aspectos como el coste-efectividad y las indicaciones para la adecuada implementación de estas técnicas no están del todo bien establecidos, organizaciones como la OMS están apoyando de forma firme la aplicación y utilización universal de estos nuevos métodos moleculares. Este capítulo resume el conocimiento actual y los métodos moleculares disponibles para el diagnóstico rápido de la TB y la resistencia a los fármacos en los laboratorios de microbiología clínica.

© 2011 Elsevier España, S.L. Todos los derechos reservados.
Introduction

Delayed diagnosis of tuberculosis (TB) and multi-drug resistant forms of the disease constitute one of the biggest obstacles to effective control of TB worldwide. Recently, the Stop TB Partnership, a network of concerned governments, organizations and donors led by the World Health Organization (WHO) (http://www.stoptb.org/stop_tb_initiative/), outlined a global plan to halve TB prevalence and mortality by 2015 and eliminate the disease as a public health problem by 2050. Multidisciplinary approaches, including studies of TB epidemiology, comparative genomics, evolution and host-pathogen interaction, will be necessary in order to develop better tools and strategies to control and eliminate TB. In this context, several rapid and accurate diagnostic methods have recently appeared, and they will be briefly discussed in this chapter.

Rapid detection of Mycobacterium tuberculosis

Although the presumptive diagnosis of TB is often based on clinical suspicion and radiological data, a definitive diagnosis of disease and drug resistance requires microbiological assays. Laboratory diagnosis of TB has traditionally been based on smear microscopy, culture and phenotypic identification. While the quickest, easiest and cheapest method available is acid-fast staining, its low sensitivity (45%-80% of positive cultures) has limited its usefulness, especially in geographical areas of lower incidence, in extrapulmonary forms (paucibacillary) of TB, and in HIV-infected patients. It should also be noted that a significant percentage (17%) of transmission occurs from smear-negative pulmonary tuberculosis patients. A further point is that despite having overall specificity the smear has a low positive predictive value (50%-80%) in areas of higher incidence of non-tuberculous mycobacteria (NTM) clinical isolates.

By contrast, the culture technique is still regarded as the reference method due to its sensitivity and the fact that further studies can be conducted with the isolated mycobacteria (identification, sensitivity and epidemiological typing). However, the slow growth of the tubercle bacillus is a major obstacle to rapid disease diagnosis. Indeed, while the last two decades have witnessed spectacular improvements to the culture method through the use of new media and automated systems such as Bactec 460TB (Becton Dickinson Diagnostics, Sparks, USA), MB/BacT ALERT (bioMérieux, Marcy-l’Etoile, France), MGIT 960 (Becton Dickinson Diagnostics) and VersaTREK (Trek Diagnostic System, Westlake, USA), several weeks are still required to obtain the final laboratory confirmation, and even longer in the case of conventional phenotypic identification procedures. Therefore, in recent years new methods have been developed for the rapid diagnosis of active TB, the best alternative being the molecular or genotypic techniques.

Chromatographic methods

Direct M. tuberculosis identification from clinical samples has been attempted by using different chromatography methods to detect tuberculostearic acid (TBSA) alone or in combination with other structural components of the mycobacterial cell wall. Several fairly fast and sensitive methods have been developed so far,9 one of the most interesting of which is fast gas chromatography mass spectrometry (GC-MS). However, because TBSA is not specific to species and its detection requires a differential diagnosis between Mycobacterium and Nocardia species and other Gram-positive bacilli, which also contain the same acid, other lipids have been studied and proposed. Among these, hexacosanoic acid in combination with TBSA appears to be quite specific for the presence of M. tuberculosis. However, although chromatographic methods may have some utility for mycobacterial identification from positive cultures, such as in the case of the new immunochromatographic assays based on the MPT-64 antigen, they do not yet represent a significant alternative for the rapid diagnosis of tuberculosis from clinical specimens.

Phagotypic methods

During the last decade a number of bacteriophages with specific affinity for mycobacteria have appeared for the rapid diagnosis of tuberculosis. Since 1947, over 250 different types of mycobacteriophages have been isolated and described, and they have constituted important tools for the genetic manipulation of mycobacteria. However, a degree of clinical utility has only been shown by two of the phage-based approaches developed to date, namely the Luciferase Reporter Phage Assay (LRP) and the Phage Amplified Assay (PhaB or MAB). The most important difference between these methods concerns the detection of phage-infected mycobacterial cells. LRP relies on the emitted light that is encoded by the gene for luciferase (fflux), which is inserted into the phage genome. By contrast, PhaB or MAB is based on the presence of viable M. tuberculosis complex cells after phage amplification (Mycobacteriophage D29) in Mycobacterium smegmatis.

LRP has proven useful in differentiating M. tuberculosis and NTM from culture and, especially, in susceptibility tests to isoniazid and rifampin. PhaB or MAB has been commercialized (FASTPlaque-TB or the variant PhageTeK MB, Biotec Laboratories Ltd, Ipswich, Suffolk, UK) for diagnosing tuberculosis in respiratory specimens, and has also been studied for antimicrobial susceptibility testing in M. tuberculosis. Both techniques are generally quick and simple, requiring little training and technical equipment, and they are relatively inexpensive. However, although they have demonstrated good specificity, several problems of sensitivity have been encountered in most studies. Their routine application has therefore been somewhat delayed, and it remains to be seen what their real usefulness will be in the diagnosis of tuberculosis or the detection of resistance to anti-tuberculosis drugs.

Genotypic methods

Numerous molecular techniques (commercial and ‘in-house’) and various applications of them are now available for the microbiological diagnosis of mycobacterial infections. Although DNA probes were the first major innovation in the molecular diagnosis of tuberculosis, the direct detection from clinical samples of M. tuberculosis and specific mutations correlating with resistance requires methods based on amplifying specific sequences of nucleic acids (NAA). These techniques have several advantages, such as a fast turnaround time and feasibility for automation. However, a number of disadvantages emerge when applying these methods directly to clinical specimens, for example, problems with inhibitors, sensitivity in smear-negative samples and DNA extraction.

Although the clinical utility of these methods has been widely discussed, solid evidence and a global consensus regarding their implementation has yet to be definitively achieved. This is due in part to the wide variety of techniques available, as well as to the lack of standardization between studies, most of which use culture as the gold standard, which theoretically has a lower sensitivity than nucleic acid amplification (NAA) tests. Furthermore, the lack of assessment of clinical aspects in most studies has led to some confusion regarding how, with whom and when to use this technology. Nevertheless, the current findings regarding the use of NAA tests to diagnose tuberculosis suggest that: a) they can quickly detect the presence of M. tuberculosis in 50%-85% of acid-fast bacillus (AFB) smear-negative and culture-positive specimens; b) the positive predictive value in AFB smear-positive specimens is higher (95%) than that of microscopy in geographical areas with a large number of NTM isolates; and c) in general, these molecular methods can diagnose TB
several weeks earlier than culture in 80%-90% of patients with a high level of TB suspicion.21-23

NAA tests include a wide variety of 'in house' methods with multiple protocols of nucleic acid extraction and amplification (PCR) of different genetic targets (IS6110, rpoB, hsp65, 16S rDNA or MPB64). However, although these 'in house' amplification tests have generally improved in recent years, the recommendation is to use commercial tests that have a greater level of standardization and reproducibility.20,23,24

All NAA methods require further post-amplification analysis by electrophoretic observation of the amplified fragment or hybridization, restriction or sequencing.18,20,21 The analysis based on sequencing (16S rDNA) or restriction (such as PCR-RFLP of the hsp65 gene or 16S-23S spacer region) could theoretically be used on clinical specimens. However, for the diagnosis of tuberculosis the most developed and commercialized methods are based on hybridization assays, and these are briefly described below, especially the newly marketed systems (Table 1).

**Conventional DNA amplification by PCR.** The Amplicor Mycobacterium tuberculosis test (Roche Diagnostic System Inc., Basel, Switzerland) is one of the oldest marketed techniques to rely on standard PCR. It is a DNA-based test that amplifies a specific segment of the 16S rRNA gene, followed by hybridization and colorimetric detection. This method may be automated (Cobas Amplicor) and was approved in 1996 by the US Food and Drug Administration (FDA) for use in respiratory samples that have positive AFB smears.24 Numerous studies have reported high sensitivity in smear-positive respiratory specimens (87%-100%), the figure being lower in smear-negative cases (40%-73%) and extrapulmonary samples (27%-98%). The specificity of this method ranges from 91% to 100%.20,24,26,27

**Transcription-mediated amplification (TMA).** The commercial Amplified M. tuberculosis Direct Test (AMTD; Gen-Probe Inc., San Diego, CA, USA) is a rapid isothermal (42 °C) method based on the amplification of 16S rRNA. Reverse transcriptase is used to copy rRNA to a cDNA-RNA hybrid, and the chemiluminescent method is then applied to detect the M. tuberculosis complex by specific DNA probes. The AMTD was the first test to be approved by the FDA (1995) for smear-positive respiratory specimens, and in 2000 the FDA recommendation was extended to smear-negative samples.23 There is now evidence that AMTD shows high specificity (95%-100%) and high sensitivity (91%-100%) for smear-positive respiratory samples, although the latter is lower for smear-negative (65%-93%) and extrapulmonary samples (63%-100%). The most important disadvantages are the lack of internal amplification control (IAC) and no possibility of automation.20,24,26,27

**Ligase chain reaction (LCR).** The LCX M. tuberculosis assay (Abbott Laboratories, Chicago, IL, USA) is a semi-automated DNA amplification method using LCR for direct detection, from clinical samples, of chromosomal gene encoding the M. tuberculosis protein antigen b. However, although good specificity (90%-100%) and sensitivity (65%-90%) were reported in several studies from respiratory specimens, this product was withdrawn from the European market in 2002.20,26,27,28

**Strand displacement amplification (SDA).** The BD ProbeTec ET Direct TB System (DTB; Becton Dickinson) was introduced in 1998 as a semi-automated technique for rapid detection of MTBC in respiratory samples. It is an isothermal (52.5 °C) enzymatic amplification process for generating multiple copies of target sequences of the IS6110 and 16S rRNA genes, whose amplification product is detected by the fluorescent method. Evaluations in respiratory samples have shown a sensitivity of 90%-100% in smear-positive samples and 30%-85% in smear-negative ones, with high specificity (90%-100%).20,24,26,27

**Solid-phase hybridization assays.** Three line probe assays are commercially available: the INNO-LiPA Rif. TB kit (Innogenetics, Gent, Belgium), the GenoType Mycobacterium Direct (MD) assay (Hain Lifescience, Nehren, Germany). Although the first two systems can detect and identify M. tuberculosis complex from clinical samples their major use is with positive cultures and for the detection of rifampin and isoniazid (by GenoType MTBDRplus only) resistance (see below). However, the GenoType MD assay is specific for the direct detection of RNA in clinical specimens of M. tuberculosis complex and other common NTM (Mycobacterium avium, Mycobacterium intracellulare, Mycobacterium kansasii and Mycobacterium malmoense) by the NASBA amplification method. The limited data available to date indicate good sensitivity and specificity in respiratory specimens, with the potential advantage that this assay can detect five clinically common mycobacterial species.20-31

**Real-time PCR (RT-PCR).** These techniques are based on simultaneous amplification of different DNA targets and fluorometric detection by labelled probes (for example, TaqMan, molecular beacons, bioprobes or FRET). These tests have a number of important advantages, especially their rapidity and fewer cross-contamination problems; this is because the processes, after DNA extraction, occur in a single tube. In recent years, numerous commercial techniques, such as the Cobas TaqMan MTB test (Roche Diagnostic System), have been developed with high overall sensitivity and specificity, especially in smear-positive respiratory samples (Table 1).19,20,24,26,32 Among these, the GeneXpert MTB/RIF (Cepheid, Sunnyvale, CA, USA and FIND Diagnostics, Geneva, Switzerland) has recently been introduced as a semi-quantitative nested RT-PCR in vitro.
Rapid diagnosis of anti-tuberculous drug resistance

The rapid emergence of multidrug-resistant Mycobacterium tuberculosis (MDR-TB: resistance to at least rifampin and isoniazid) and extensively drug-resistant tuberculosis (XDR-TB: MDR plus resistance to fluoroquinolone and one of the three injectable second-line drugs, amikacin, kanamycin and capreomycin) poses a serious threat to the treatment of tuberculosis. The World Health Organization estimates that 500,000 new cases of MDR-TB occur globally every year and more than 45 countries have reported XDR cases.

Because genetic resistance to an anti-tuberculosis drug is due to spontaneous chromosomal mutations the MDR/XDR phenotype is caused by sequential accumulation of mutations in different genes involved in individual drug resistance. This drug resistance may be attributable to direct transmission of drug-resistant strains (primary resistance) or to de novo acquisition of resistance during individual patient treatment (secondary resistance), i.e. due to inappropriate treatment or poor adherence to treatment.

A delay in diagnosing MDR-TB associated with standard drug susceptibility testing methods is likely to contribute to the acquisition of further drug resistance, as well as to the dissemination of drug-resistant strains through person-to-person transmission. By contrast, the rapid detection of drug-resistant strains facilitates early access to the appropriate therapy, reduces transmission rates and improves treatment outcomes. The long turnaround time and laboriousness of drug susceptibility testing methods has therefore stimulated the search for alternative and faster techniques. New genotypic methods search for the genetic determinants of resistance rather than the resistance phenotype. In this regard, the WHO has recommended the worldwide use of rapid genotypic assays for the rapid diagnosis of MDR-TB. Those genotypic assays should be able to detect the mutations responsible for isoniazide (INH) and rifampin (RMP) resistance. Moreover, if XDR-TB is to be ruled out, then the mutations responsible for resistance to streptomycin (STR), amikacin (AMK), kanamycin (KAN), capreomycin (CM) and fluoroquinolones should also be screened for.

Mutations confined to a short 81bp DNA region of the rpoB gene, encoding the β-subunit of RNA polymerase and spanning codons 507-533, have been found in ~95% of RMP-resistant strains. Mutations in rpoB generally result in high-level resistance to RMP and cross resistance to all rifamycins. However, specific mutations in codons 511, 516, 518 and 522 result in a phenotype of lower-level resistance to RMP and rifapentin, and retained susceptibility to rifabutin and rifalazil.40 As RMP monoresistance is relatively rare, molecular detection of mutations in this region (RDRD, rifampin resistance determining region) is a good indicator of MDR-TB. It should be noted that a recent paper by Zaczek et al41 reported that direct molecular identification for RMP-resistant M. tuberculosis clinical isolates is only possible for strains carrying selected mutations in RpoB. The identification of other mutations suggests that investigated strains might be resistant to this drug, in other words, these mutations require a specific genetic background to develop resistance.

The molecular mechanisms of resistance to INH are more complex. They have been associated with a variety of mutations which affect one or several genes involved in mycolic acid biosynthesis or that are overexpressed as a response to the build-up or cellular toxicity of INH. Mutations in the katG gene are responsible for 60%-70% of INH-resistant strains, with the most frequent mutation occurring at codon 315 (S315T, serine-to-threonine substitution). The S315T alteration located within the active site of katG prevents KatG-mediated activation of INH and results in a high level of resistance. Mutations in the mabA-inhA regulatory region that exhibit both low-level INH resistance and ethionamide resistance account for 8%-20% of INH resistance. A C-to-T substitution at nucleotide -15 results in the overexpression of inhA, a NADH-dependent enoyl-acyl reductase involved in mycolic acid synthesis, and INH resistance arises as a result of drug titration.42 In our experience, a rapid genotypic assay including the 315-katG codon and -15 nt of the mabA-inhA regulatory region would cover 62% of isoniazid-resistant strains in Barcelona.43

STR acts on the ribosome, inhibiting the translation of mRNA and, therefore, disrupting protein synthesis. Mutations associated with STR resistance in M. tuberculosis have been identified in the rpsL and rrs genes, which encode the ribosomal proteins S12 and 16S rRNA, respectively. More than half the STR-resistant clinical isolates present mutations associated with these genes.44 The most common mutations in the rpsL gene have been detected in codons 43 and 48, and in two specific regions (the 530 loop and 912 regions) of the rrs gene.45 In our experience, mutations in the rpsL and rrs genes are detected in 37.7% of STR-resistant M. tuberculosis isolates46. There is also a strong correlation between the level of resistance and the type and position of mutations.46,47 High-level resistance has mainly been associated with rpsL gene alterations, whereas intermediate and low levels of resistance have been linked with mutations in the rrs gene and wild-type patterns.46,47

Only a few studies have investigated the genetic background of AMK, KAN and CM resistance.48-50 Resistance to AMK and CM is associated with mutations in the rrs gene, especially in the region between nucleotides 1.400 and 1.500, each of which are responsible for a specific resistance pattern. Mutations G1484T and A1401G were between nucleotides 1.400 and 1.500, each of which are responsible for a specific resistance pattern. Mutations in the rpsL gene, which are genes that encode the respective subunits of the DNA topoisomerase gyrase.52 Most mutations accumulate in a short discrete region known as the quinolone resistance-determining region (QDRD). It has been observed that certain isolates show a mixture of wild-type and multiple mutant alleles of gyrA (heteroresistant isolates).53 Heteroresistance is considered a preliminary stage of full resistance.

In summary, a genotypic method to detect INH resistance should be based on the analysis of the 315-katG codon and -15 nt of the mabA-inhA regulatory region. For RMP resistance the method should explore the short 81bp DNA region of the rpoB gene. In this context, it has to be stressed that RMP resistance is a surrogate marker for
MDR-TB. Finally, detection of XDR-TB would be based on the study of\textit{rpsL}, \textit{rrs} and \textit{tlyA}, for resistance to STR, AMK, KAN and CM, and of\textit{gyrA} and \textit{gyrB}, for fluoroquinolone resistance.

Several molecular methods have been proposed to detect the specific mutations correlating with resistance in the amplified products: DNA sequencing, PCR-single-strand conformation polymorphism, PCR-heteroduplex formation, RT-PCR or solid-phase hybridization assays. As solid-phase hybridization assays and RT-PCR have been commercialized and are widely used in clinical laboratories, they will be reviewed in some detail.

### Solid-phase hybridization assays

**Line probe assays**. Line probe assays are a family of novel DNA strip tests that use PCR and reverse hybridization methods. Results are determined by colorimetric development. They have been designed to identify \textit{M. tuberculosis} complex and simultaneously detect genetic mutations related to drug resistance. Amplified DNA can be obtained from cultured strains or clinical samples. Commercially available kits include the INNO-LiPA Rif. TB kit (Innogenetics, Gent, Belgium), the GenoType MTBDRplus assay and the GenoType MTBDRsl assay (Hain Lifescience).54 The INNO-LiPA Rif. TB kit hybridizes the amplified DNA to ten oligonucleotide probes (one specific for the \textit{M. tuberculosis} complex, and nine encompassing the core region of the \textit{rpoB} gene: five overlapping wild-type S probes and four R probes for detecting specific mutations) that are immobilized on a nitrocellulose strip.55 A number of studies have evaluated the diagnostic accuracy of LiPA for detecting resistance in several settings (Table 2). A recent metaanalysis suggests that the LiPA assay is highly sensitive and specific for detecting rifampin-resistant \textit{M. tuberculosis} in culture.

### Table 2

**Description of studies that have evaluated line probe assays**

<table>
<thead>
<tr>
<th>Author (year) Country</th>
<th>Reference test</th>
<th>Sample</th>
<th>Susceptible/resistant</th>
<th>Sensitivity</th>
<th>Specificity</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Genotype MTBDRplus assay (Hain Lifescience, Nehren, Germany)</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Isoniazid</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lacoma (2008) Spain</td>
<td>Bactec460TB Isolate</td>
<td>14/48</td>
<td>73</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Mohito (2008) Italy</td>
<td>Bactec460TB Isolate</td>
<td>0/173</td>
<td>79</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Hilleman (2007) Germany</td>
<td>Bactec460TB Isolate</td>
<td>50/75</td>
<td>92</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Evans (2009) South Africa</td>
<td>DNA sequencing Isolate</td>
<td>90/123</td>
<td>83.8</td>
<td>98.9</td>
<td></td>
</tr>
<tr>
<td>Lacoma (2008) Spain</td>
<td>Bactec460TB Clinical specimen</td>
<td>21/30</td>
<td>93</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Causse (2008) Spain</td>
<td>MGIT Clinical specimen</td>
<td>22/37</td>
<td>94.6</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Hilleman (2007) Germany</td>
<td>Bactec460TB Clinical specimen</td>
<td>31/41</td>
<td>90.2</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Rifampin</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lacoma (2008) Spain</td>
<td>Bactec460TB Isolate</td>
<td>50/12</td>
<td>91.7</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Hilleman (2007) Germany</td>
<td>Bactec460TB Isolate</td>
<td>50/75</td>
<td>98.7</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Evans (2009) South Africa</td>
<td>DNA sequencing Isolate</td>
<td>131/92</td>
<td>90.8</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Lacoma (2008) Spain</td>
<td>Bactec460TB Clinical specimen</td>
<td>22/29</td>
<td>100</td>
<td>95.4</td>
<td></td>
</tr>
<tr>
<td>Causse (2008) Spain</td>
<td>MGIT Clinical specimen</td>
<td>23/36</td>
<td>100</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Hilleman (2007) Germany</td>
<td>Bactec460TB Clinical specimen</td>
<td>41/31</td>
<td>96.8</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td><strong>INNO-LiPA Rif. TB kit (Innogenetics, Gent, Belgium)</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ahmad (2002) Kuwait</td>
<td>Bactec460TB Isolate</td>
<td>29/12</td>
<td>97</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>De Oliveira (1998) Brazil</td>
<td>Proportion Isolate</td>
<td>113/15</td>
<td>97</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Gamboa (1998) Spain</td>
<td>Bactec460TB Isolate</td>
<td>46/13</td>
<td>100</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Hirano (1999) Japan</td>
<td>Proportion Isolate</td>
<td>90/26</td>
<td>92</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Johansen (2003) Denmark</td>
<td>Bactec460TB Isolate</td>
<td>35/24</td>
<td>97</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Lemus (2004) Belgium</td>
<td>Bactec460TB Isolate</td>
<td>10/10</td>
<td>100</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Rossau (1997) Belgium</td>
<td>Proportion Isolate</td>
<td>203/61</td>
<td>98</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Sintchenko (1999) Australia</td>
<td>Bactec460TB Isolate</td>
<td>22/11</td>
<td>96</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Somoskovi (2003) USA</td>
<td>Proportion Isolate</td>
<td>64/37</td>
<td>95</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Srivastava (2004) India</td>
<td>MIC Isolate</td>
<td>45/10</td>
<td>82</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Tracevska (2002) Latvia</td>
<td>Bactec460TB Isolate</td>
<td>34/19</td>
<td>100</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Traore (2000) Belgium</td>
<td>Proportion Isolate</td>
<td>266/145</td>
<td>99</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>De Beenhouwer (1995) Belgium</td>
<td>Proportion Clinical specimen</td>
<td>21/46</td>
<td>91</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Gamboa (1998) Spain</td>
<td>Bactec460TB Clinical specimen</td>
<td>46/13</td>
<td>98</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Johansen (2003) Denmark</td>
<td>Bactec460TB Clinical specimen</td>
<td>26/21</td>
<td>100</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>Watterson (1998) England</td>
<td>Bactec460TB Clinical specimen</td>
<td>10/24</td>
<td>80</td>
<td>100</td>
<td></td>
</tr>
</tbody>
</table>

*Modified from references 56 and 57.*
and, to a slightly lesser degree, in clinical specimens. The Genotype MTBDRplus assay detects mutations in the rpoB gene for rifampin resistance, in the katG gene (S315T) for high-level INH resistance and in the promoter region of the inhA gene (nucleotides -8, -15, and -16) for low-level INH resistance. Various studies on the kit’s accuracy have been performed and summarized in a recent meta-analysis.\(^5\) Sensitivities for the detection of rifampin resistance range from 91% to 100%, whereas in the case of INH they range from 73% to 94%. The main limitation for the detection of INH resistance is that the molecular mechanisms behind some INH-resistant \(M.\) \(tuberculosis\) isolates are not known. Differences in the observed sensitivity could be due to the distribution of resistance-associated mutations in the different studies.\(^6\) The Genotype Mycobacterium \(tuberculosis\) second line \((\text{MTBDR}^\text{SL})\) assay was developed with a specific focus on the most prevalent \(gyrA, rsr\) and \(embB\) mutations. Although few studies have been published to date, this new assay may represent a reliable tool for the detection of fluoroquinolone and amikacin/capreomycin resistance, and, to a lesser extent, ethambutol resistance. In combination with a molecular test for the detection of RMP and INH resistance, the potential to detect XDR-TB can also be postulated.\(^7\)

**Conflict of interest**

The authors declare they have not any conflict of interest.

**References**


