Evaluation of Methods for Rapid Detection of Resistance to Isoniazid and Rifampin in Mycobacterium tuberculosis Isolates Collected in the Caribbean\textsuperscript{Y}

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The rapid identification of drug-resistant strains of Mycobacterium tuberculosis is crucial for the timely initiation of appropriate antituberculosis therapy. The performance of the Genotype MTBDRplus assay was compared with that of the Bactec 460 TB system, a “gold standard” culture-based method. The Genotype MTBDRplus assay was quicker and more cost-effective for the detection of rifampin resistance, but it was not as good for the detection of isoniazid-resistant strains in our setting.

The major serious challenges associated with the management of tuberculosis in Caribbean countries are diagnosis of the infection, drug resistance, and the paucity of reports on the prevalence of drug resistance. Although laboratories in many of these countries have the ability to perform smear microscopy, there is still a shortage of a laboratory capability for the performance of accurate, rapid culture and drug susceptibility tests (DSTs). As a result, many cases with low bacillary loads are misdiagnosed, underdiagnosed, or poorly treated.

The rapid detection of drug-resistant Mycobacterium tuberculosis strains facilitates early access to the appropriate therapy, reduces rates of transmission, and improves treatment outcomes (12). M. tuberculosis resistance to isoniazid (INH) and rifampin (RIF), which are two of the most important antituberculosis drugs, often results in treatment failure and death (6); hence, the detection of resistance to these agents is crucial.

The phenotypic DST method is routinely performed only after a pure, viable culture is obtained, and this usually takes 4 to 6 weeks, resulting in long diagnostic delays (7). The administration of inappropriate therapy during the period of delay may lead to the acquisition of further drug resistance as well as the dissemination of drug-resistant strains through person-to-person transmission. To improve treatment and prevent the transmission of drug-resistant M. tuberculosis strains, effective alternative diagnostic tests that will enable the rapid detection of drug resistance after the collection of specimens from infected patients are required. This study was carried out to determine the turnaround time, cost, and reliability of the Genotype MTBDRplus assay, a relatively new molecular test, in comparison with those of the Bactec 460 TB system, a “gold standard” conventional method, for the identification and the detection of susceptibility to INH and RIF of M. tuberculosis isolates from the Caribbean.

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\textbf{MATERIALS AND METHODS}

Eighty-one samples (26 sputum specimens and 55 culture material specimens on Lowenstein-Jensen medium) received at the Caribbean Epidemiology Centre of Trinidad and Tobago from several Caribbean islands for further confirmatory tests were used for this study. These were processed by standard microbiological methods (9, 11) to identify and confirm the presence of M. tuberculosis as well as to carry out the DSTs (3, 14). Informed consent was not required since no detailed patient information was known and the results were not linked to a patient identifier at the center.

The Genotype MTBDRplus assay (Hain Lifescience, Nehren, Germany), which is based on a DNA strip technology that permits the molecular identification of isolates of the M. tuberculosis complex and their susceptibilities to RIF and INH, were performed either with the cultured sample on Lowenstein-Jensen material or directly from the sputum specimen, according to the manufacturer’s instruction and as reported elsewhere (8; product insert, Hain Lifescience).

The turnaround time, which is time required to process, inoculate, identify, and perform the DST with the M. tuberculosis isolate, was measured. The costs of the reagents needed to perform either the MTBDRplus or the Bactec procedure were determined. These costs did not include the cost for labor (the technologists’ hands-on time) or for the purchase of any major equipment, such as the Bactec 460 system, microscopes, power supplies, and other infrastructural elements. Quality control of the procedure was performed by using aliquots of DNA extracts of pansusceptible Mycobacterium tuberculosis ATCC 27294 isolates. The data were analyzed by using Epi Info software (version 3.4.3) (5).

Comparisons were done by chi-square analysis and Fisher’s exact test. A $P$ value of $\leq 0.05$ was considered significant.

\textbf{RESULTS AND DISCUSSION}

In this study, evaluation of the performance characteristics of a molecular test and a conventional test that is an efficient, cost-effective, and timely method for use in determining whether M. tuberculosis isolates are resistant to INH and RIF revealed that the MTBDRplus assay performed very well only for the detection of RIF resistance, while the Bactec 460 system performed well for the detection of both RIF and INH resistance. Resistance to RIF, which is conferred by mutations in the rpoB gene, was correctly identified in 23 of 24 isolates (95.8%) by use of the Genotype MTBDRplus assay. This good
performance of the MTBDRplus assay for the detection of RIF resistance agrees with the findings of previous reports (8, 13, 16). The MTBDRplus assay allowed the rapid and specific detection of most mutations that confer resistance to RIF and, to a lesser extent, INH. Collective observations have indicated that mutations in the *rpoB* gene may account for >96% of the resistance to RIF (2, 8, 15), and a similar observation was also made for the Caribbean strains tested in this study.

The rate of INH resistance detection by the MTBDRplus method was a very disappointing 34.6%, and for multidrug-resistant isolates the rate of resistance detection rate was even less (29.4%). This observation is not unique, since the molecular mechanisms required for INH resistance are not fully understood and about 25 to 30% of the phenotypic INH resistance–associated mutations are still unaccounted for (10). It has been reported that the MTBDRplus assay was unable to detect low levels of INH resistance (1, 15); the assay also detects *M. tuberculosis* isolates in which resistance originates only in the *rpoB* gene and showed a AGC→ACA mutation (Table 1).

The low rate of detection of INH resistance by the MTBDRplus method in the present study may be due to the fact that only a single concentration of INH was used (0.1 μg/ml) or that the Caribbean strains harbor resistance mutations at unidentified gene regions. The changes in the *M. tuberculosis* *rpoB* and *katG* genes that denote susceptibility or resistance in the isolates detected by Genotype MTBDRplus test are shown in Table 1. The *rpoB* gene codons most frequently involved in mutations were S531L (57.1%) and S516L (20%) in isolates resistant to RIF. Twenty isolates carried the most common mutation, Ser531→Leu. A similar result was reported by Cavusoglu et al. (4), but our result was not in agreement with the findings of Barnard et al., who reported that most mutations occur at several other codons (2). As for INH resistance, of the nine resistant isolates that the Genotype MTBDRplus detected, 78% of them carried a mutation at the S315T1 codon of the *katG* gene and showed a AGC→ACC mutation, and 22% showed a AGC→ACA mutation (Table 1).

In conclusion, the high sensitivity of RIF resistance detection is a merit point for the MTBDRplus test, as it can be used for the detection of RIF resistance, which is a surrogate marker for multiple-drug resistance in *M. tuberculosis* isolates. In our study, the results for the detection of INH resistance were not as good as those for the detection of RIF resistance and may be a setback of this assay as a method for the detection of INH resistance in *M. tuberculosis* isolates; but the assay detects resistance only when the origin of resistance is in the *M. tuberculosis* *rpoB*, *katG*, and *inhA* regions.

Although the MTBDRplus assay has limitations, as is the case with any DNA-based assay that screens the nucleic acid sequence and not the amino acid sequence, it is possible that mutations that do not cause an amino acid exchange (silent mutations) will still result in the absence of one of the wild-type probes. Also, the assay detects resistance only when the origin of resistance is in the *M. tuberculosis* *rpoB*, *katG*, and *inhA* regions.

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