Some synonymous and non-synonymous gyrA mutations in Mycobacterium tuberculosis lead to systematic false-resistance results to fluoroquinolones with the Hain GenoType MTBDRsl assays.

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Some Synonymous and Nonsynonymous gyrA Mutations in *Mycobacterium tuberculosis* Lead to Systematic False-Positive Fluoroquinolone Resistance Results with the Hain GenoType MTBDRsl Assays


ABSTRACT In this study, using the Hain GenoType MTBDRsl assays (versions 1 and 2), we found that some nonsynonymous and synonymous mutations in *gyrA* in *Mycobacterium tuberculosis* result in systematic false-resistance results to fluoroquinolones by preventing the binding of wild-type probes. Moreover, such mutations can prevent the binding of mutant probes designed for the identification of specific resistance mutations. Although these mutations are likely rare globally, they occur in approximately 7% of multidrug-resistant tuberculosis strains in some settings.

KEYWORDS *Mycobacterium tuberculosis*, Hain GenoType MTBDRsl, fluoroquinolones

As part of its recommendation for a shorter treatment regimen for multidrug-resistant tuberculosis (MDR TB), the World Health Organization (WHO) recently endorsed version 2 of the Hain GenoType MTBDRsl as the first genotypic drug susceptibility testing (DST) assay for detecting resistance to fluoroquinolones and to the second-line injectable drugs kanamycin, amikacin, and capreomycin (1–5). Specifically, the WHO has endorsed its use instead of phenotypic methods as an initial direct test for ruling in resistance in patients with either MDR TB or confirmed resistance to rifampin. The precise correlation between genotype and phenotype for some muta-
tions, however, remains unclear, which complicates the interpretation of this assay (5). The WHO is currently reviewing the available evidence to address this point.

The only documented instance of systematic false-positive fluoroquinolone resistance results with the MTBDRsl was caused by the \textit{gyrA} \textit{Acc/Gcc T80A gCg/gGg A90G} double mutations relative to the \textit{Mycobacterium tuberculosis} \textit{H37Rv} laboratory strain, given that the A90G mutation prevents the binding of the WT2 band of this assay (Fig. 1) (6–9). Several independent studies, which used a variety of techniques, demonstrated that these double mutations do not confer resistance to any of the four fluoroquinolones currently used for the treatment of TB (i.e., ofloxacin, levofloxacin, moxifloxacin, and gatifloxacin) and may even result in hypersusceptibility (6, 7, 9–15). Unfortunately, most of the strains with double mutants were not typed, which left two key questions largely unanswered. First, it remains unclear whether these strains are monophyletic or polyphyletic. Second, there is only limited evidence on how widespread the group(s) of strains with these mutations is.

There are several pieces of circumstantial evidence regarding these mutations. Only 10 primary research studies from our internal database of 265 in which \textit{gyrA} was studied reported these double mutations, although it should be noted that not all of these studies covered codon 80 (6–15). This suggested that these mutations are not widespread globally. Based on studies that found the T80A mutation to be a marker for the \textit{M. tuberculosis} Uganda genotype (formerly known as \textit{Mycobacterium africanum} subtype II but now known to be a sublineage within Euro-American \textit{M. tuberculosis} lineage 4), we speculated that the \textit{gyrA} double mutant strains might constitute a subgroup of the Uganda genotype (16, 17). This hypothesis appeared to be consistent with the results of two studies from the Republic of the Congo and the Democratic Republic of the Congo, which reported the highest frequency of these double mutants (in 60% [9/15] versus 7.2% [15/209] of MDR TB cases from Brazzaville and Pointe-Noire versus Kinshasa, respectively) (7, 8). This was further supported by mycobacterial interspersed repetitive unit–variable-number tandem repeat (MIRU-VNTR) results (7, 15).

To clarify the exact relationship of these double mutants with regard to the wider \textit{M. tuberculosis} complex (MTC) diversity, we analyzed the genomes of 1,974 previously published MTC strains (14). This identified a single T80A+90G double mutant, which, as expected, resulted in a false-positive result with the MTBDRsl assay (Table 1, C00014838). We then analyzed this strain in a wider collection of 94 Uganda or Uganda-like strains, including 27 T80A+A90G double mutants (or variants thereof), which confirmed that this double mutation was a marker for a subgroup of Uganda strains (Fig. 2; see also Table S1 in the supplemental material). Of these 28 double mutant strains (or variants thereof), 25 originated from the Democratic Republic of Congo in a study of acquired drug resistance, nested in routine surveillance conducted.
<table>
<thead>
<tr>
<th>Strain/plasmid name</th>
<th>gyrA mutation(s)</th>
<th>WT1</th>
<th>WT2</th>
<th>WT3</th>
<th>MUT1</th>
<th>MUT2</th>
<th>MUT3A</th>
<th>MUT3B</th>
<th>MUT3C</th>
<th>MUT3D</th>
<th>Comment</th>
<th>Interpretation of result</th>
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<td>WT2 and MUT2 binding prevented</td>
<td>True resistant, but 91P mutation not identified</td>
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</table>

aUnless otherwise stated, testing was done with version 1 of the assay. WT or MUT bands (Fig. 1) were deemed positive if they were as strong as or stronger than the amplification control band, as stipulated in the instructions for use (24, 40). Plasmids were used to investigate combinations of mutations that could arise but, to our knowledge, have not been reported to date. In this context, plasmids 1 to 12 served as controls to demonstrate that plasmids could be used instead of genomic DNA. Plasmids 10a, 11a, 11b, and 12a indicate that the known A90V or S91P resistance mutations were detected but not identified by the corresponding mutant probes in the T80A/H11001 A90G, A90A, or I92I strain background. It should be noted, however, that if the strain population is not homogeneous, the effects of these mutations may differ from those simulated in these experiments (see Supplemental Methods in the supplemental material).
bAlso observed in a strain from China (44).cThe two samples were from the same patient.
dTested with version 2 of the assay.eOne strain had a D94G minority mutation, which resulted in the binding of probe MUT3C. In this case, this was not a false-resistant result.
H37Rv reference sequence.
Ser at codon 95 is an H37Rv-specific mutation (17). All subsequent gyrA plasmids have the aGc/aCc 59ST change. The gyrA Gag/Cag E21Q polymorphism was not taken into consideration, since it lay outside the area targeted by probes, as shown in Fig. 1 (45).
MUT3B did not identify D94T, contrary to the package insert (44). This was in agreement with observations from other studies that used version 1 or 2 of the assay (1, 9, 23, 46–49), although the mutation was identified in some cases (1).
Assuming that the S91P mutation causes resistance in a T80A/H11001 A90G background, which is not necessarily the case, as discussed in the Fig. 2 legend.
A90V mutation in a gcG/gcA A90A background.
from 2006 to 2009 for drug resistance in Kinshasa (18). Specifically, strains were drawn from a collection of 324 phenotypically rifampin-resistant isolates, resulting in a frequency of 7.7% (25/324), which is in line with the aforementioned frequency of 7.2% in Kinshasa during the period of 2011 to 2013 (8).

Synonymous mutations have been shown in other contexts to cause systematic false-positive results, such as those for rifampin when using genotypic DST assays such as the Hain GenoType MTBDRplus or Cepheid Xpert MTB/RIF (19, 20). To date, the equivalent phenomenon had not been described with the MTBDRsI assay. We therefore screened the aforementioned 1,974 genomes and the Sanger sequencing data of 104 MDR TB strains from Medellín (Colombia) and unpublished data, which identified six different synonymous mutations in the fluoroquinolone resistance-determining region of gyrA (14, 21). Two of the synonymous mutations (caC/caT H85H and ctG/ctA L96L) did not cause false-resistance results by preventing the corresponding wild-type bands from binding (Table 1). In contrast, the remaining four did, including a mutation at another nucleotide position of codon 96 (Ctg/Ttg) (Table 1), which was found in seven Haarlem strains from Colombia that were closely related based on 24-locus MIRU-VNTR, resulting in a systematic false-resistance rate of 6.7% (7/104) in Medellín.
Furthermore, we showed that the T80A+90G double mutations and the synonymous gcG/gcA A90A and atC/atT I92I mutations prevented the binding of not only their corresponding wild-type band(s) but also that of the Tcg/Ccg S91P probe (Table 1). Similarly, if the A90V resistance mutation arose in the A90A background (i.e., by a further change in the triplet gCG/gTA), it would not be detected by the gCg/gTg A90V probe.

The consequences of these findings depend on a variety of factors. The aforementioned mutations that result in systematic false-positive results are likely rare globally (i.e., <1% based on the total number of strains initially screened for this study). Nevertheless, they can be frequent locally. Synonymous mutations in particular are not selected against, which means that it is only a matter of time until the MTBDRs\text\textsuperscript{s} is used in a region where it has a poor positive predictive value, as would be the case in Medellín. As a result, the absence of binding of wild-type probes without concomitant binding of a mutant probe is a true marker of resistance in most settings, because this binding pattern identifies (i) valid resistance mutations, such as G88C and G88A, that can be inferred only by the absence of WT1, (ii) D94Y, which, contrary to the package insert, was not detected by MUT3B (Table 1), and (iii) mutations that are targeted by specific mutant probes but to which the mutant probes do not bind for unknown reasons (i.e., when the absence of wild-type probes acts as a failsafe method) (22, 23). In other words, simply ignoring wild-type bands would likely result in a significant loss of MTBDRs\text\textsuperscript{s} sensitivity.

In the MTBDRs\text\textsuperscript{s} instructions, Hain acknowledges that synonymous mutations can result in false-resistant results, but the instructions do not comment on the T80A+90G mutation or on the effects of synonymous and nonsynonymous mutations on the binding of mutant probes (24). The WHO report that endorsed the assay did not discuss the consequences of systematic false-resistant results (3, 4). In light of the potentially severe consequences of systematic false-resistance results, we propose that in cases where fluoroquinolone resistance is inferred from the absence of a wild-type band alone, appropriate confirmatory testing is undertaken immediately. This would not only be beneficial to the patient but also may prove cost-effective overall for the TB control program (i.e., by avoiding the unnecessary use of more toxic, less effective, and often more expensive drugs, thereby minimizing transmission and enabling preventive therapy of contacts with fluoroquinolones [9, 25]). Given that systematic false-positives are rare in most settings, we would advise not discontinuing fluoroquinolone treatment while confirmatory testing is being carried out, provided this testing is done rapidly (e.g., using targeted sequencing of the locus in question to identify synonymous mutations, the T80A+90G mutations, or any resistance mutations). Ideally, this should be complemented with phenotypic DST to identify heteroresistance that is missed by Sanger sequencing, which cannot detect mutations that occur in below 10 to 15% of the total population (26). Alternatively, fluoroquinolones could be kept in the regimen but not counted as an effective agent until systematic false-positives are excluded.

Although not investigated here, these highlighted issues likely apply to some, if not all, other commercial genotypic DST assays for fluoroquinolones, which are manufactured by Autoimmun Diagnostika, NIPRO, Seegene, YD Diagnostics, and Zeesan Biotech (27–32). Our findings therefore underline the need for diagnostic companies, including Cepheid, which is currently adapting its GeneXpert system for fluoroquinolone testing, to consider the genetic diversity within the MTC at the development stage and to monitor test performance after uptake in clinical settings (19, 33, 34). Importantly, this also applies to software tools designed to automate the analysis of whole-genome sequencing data. In fact, three of the current tools (KvarQ, Mykrobe Predictor TB, and TB Profiler) misclassified strain BTB-08-045 with \text\textsuperscript{gyrA} T80A+90G as resistant to at least one fluoroquinolone because the respective mutation catalogues of these tools list A90G as a resistance mutation, whereas the tools CASTB and PhyResSE correctly classified the strain (35–39).
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REFERENCES


