Wild-Type and Non-Wild-Type Mycobacterium tuberculosis MIC Distributions for the Novel Fluoroquinolone Antofloxacin Compared with Those for Ofloxacin, Levofloxacin, and Moxifloxacin

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Antofloxacin (AFX) is a novel fluoroquinolone that has been approved in China for the treatment of infections caused by a variety of bacterial species. We investigated whether it could be repurposed for the treatment of tuberculosis by studying its in vitro activity. We determined the wild-type and non-wild-type MIC ranges for AFX as well as ofloxacin (OFX), levofloxacin (LFX), and moxifloxacin (MFX), using the microplate alamarBlue assay, of 126 clinical Mycobacterium tuberculosis strains from Beijing, China, of which 48 were OFX resistant on the basis of drug susceptibility testing on Löwenstein-Jensen medium. The MIC distributions were correlated with mutations in the quinolone resistance–determining regions of gyrA (Rv0006) and gyrB (Rv0005). Pharmacokinetic/pharmacodynamic (PK/PD) data for AFX were retrieved from the literature. AFX showed lower MIC levels than OFX but higher MIC levels than LFX and MFX on the basis of the tentative epidemiological cutoff values (ECOFFs) determined in this study. All strains with non-wild-type MICs for AFX harbored known resistance mutations that also resulted in non-wild-type MICs for OFX but higher MIC levels than LFX and MFX on the basis of the tentative epidemiological cutoff values (ECOFFs) determined in this study. Moreover, our data suggested that the current critical concentration of OFX for Löwenstein-Jensen medium that was recently revised by the World Health Organization might be too high, resulting in the misclassification of phenotypically non-wild-type strains with known resistance mutations as wild type. On the basis of our exploratory PK/PD calculations, the current dose of AFX is unlikely to be optimal for the treatment of tuberculosis, but higher doses could be effective.

Received 18 February 2016 Returned for modification 24 March 2016 Accepted 10 June 2016


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standard. Suspensions were further diluted (1:25) with 7H9 broth. H37Rv was used as a control.

Genotypic analyses. We sequenced the quinolone resistance-determining regions (QRDRs) of gyrA (Rv0006) and gyrB (Rv0005) and called mutations relative to the sequence of the H37Rv reference genome (GenBank accession number AL123456.3) using the 2002 numbering for gyrB (5–7). We usually sequenced isolates recovered from the drug-free LJ slopes, but where no resistance mutations were found in phenotypically resistant strains, sequencing was repeated with isolates recovered from the OFX-containing LJ slope to detect low-frequency mutations (8, 9). Strains belonging to the East Asian lineage were identified on the basis of RD105 (10).

RESULTS

A total of 92.9% (117/126) of the strains in this study belonged to the East Asian lineage (see Table S1 in the supplemental material) (11). We found that the MIC distributions for all four fluoroquinolones were bimodal (Fig. 1A to D), where the more susceptible of the two distributions represented the phenotypically wild-type distributions, whereas the remaining strains were, by definition, phenotypically non-wild type. Based on visual inspection, we therefore set tentative epidemiological cutoff values (ECOFFs) for MIC determination using the MABA method at 2, 1, 0.5, and 0.25 μg/ml for OFX, AFX, LFX, and MFX, respectively (12). Not all phenotypically wild-type strains were identical genotypically (i.e., all 126 Chinese strains harbored the known gyrA S95T mutation that does not correlate with resistance [7, 13]), but after the exclusion of this polymorphism, we found a nearly perfect correlation between the tentative ECOFFs and nonsynonymous mutations in the two subunits of DNA gyrase, encoded by gyrA and gyrB.

All gyrA mutations detected in this study were classical resistance mutations that fell into the QRDR and resulted in an MIC increase above the tentative ECOFF for all four fluoroquinolones (Fig. 1A; see also Table S1 in the supplemental material) (7, 14). This was in line with the fact that all gyrA mutants tested resistant to OFX on LJ, although retesting of seven strains that were initially discrepant was required to achieve complete agreement (Table 1). In line with a recent systematic review, the D94G and A90V mutations were the most frequent and the second most frequent mutations, respectively, whereas other changes (e.g., G88C) occurred in only a single strain (15). Theoretically, all of these mutations could have been detected with the genotypic DST assays of Hain Lifescience, Nipro, and YD Diagnostics, whereas the assays of AID and Seegene would have missed the two resistant strains with mutations at codon 88 (see Table S1 in the supplemental material) (16–22). In practice, however, some resistance mutations might have been missed, given that the detection limits of these assays, albeit unknown, are almost certainly higher than the critical proportion of 1% (e.g., strain 14114 was heteroresistant, and its D94G mutation was detectable only using Sanger sequencing of an isolate from the drug-containing slope [see Table S1 in the supplemental material]) (23–25).

As expected, gyrB mutations were rare and usually coincided with gyrA mutations (in 5/6 cases); thus, they did not improve markedly the sensitivity of detecting phenotypically non-wild-type strains (48/49 strains had a gyrA mutation) (15). Strain 14117 was the sole exception. It harbored only a gyrB mutation (T500N), was found to be susceptible to OFX on LJ, and had MABA MICs that corresponded to the aforementioned ECOFFs for the four respective fluoroquinolones (Table 1). The mutation in question fell just outside of the gyrB QRDR, as defined by Maruri et al. (7), which spans codons 461 to 499, but inside the QRDR based on the findings of Pantel et al. (26), which extends to codon 501. Using the recently developed version 2 of the Hain Lifescience Genotype MTBDR assay, which covers codons 497 to 502 of gyrB, an isolate with this mutation would also have been interpreted to be resistant (22). We therefore repeated DST for this strain, whereupon the MICs for AFX, LFX, and MFX increased by 1 doubling dilution and the strain consequently became phenotypically non-wild-type, whereas the OFX MIC and LJ result remained unchanged (Table 1).

DISCUSSION

The aim of DST is usually to distinguish resistant strains, patients infected with which are likely to fail treatment, from susceptible strains, patients infected with which have a high likelihood of clinical success (an intermediate category is sometimes possible) (27). The clinical breakpoints (known as critical concentrations [CCs] in the tuberculosis field) employed for this purpose should be based on clinical, pharmacokinetic/pharmacodynamic, and, ideally, clinical outcome data, which, for a variety of reasons, are difficult to obtain for tuberculosis drugs (27). As a result, an important aim of DST for the majority of tuberculosis drugs is to distinguish wild-type from non-wild-type strains [i.e., strains with elevated MICs compared with those for strains that (i) have never been exposed to the agent or class of agent in question and (ii) are not Intrinsically resistant] using the ECOFF, which represents the highest concentration of the wild-type distribution determined by modern microbiological principles pioneered by the European Committee on Antimicrobial Susceptibility Testing (EUCAST) (12, 23, 27–30). In other words, the ECOFF represents the lowest possible CC and some non-wild-type strains might remain treatable, as proposed for MFX, albeit on the basis of limited evidence (i.e., the CC of 2 μg/ml set by the World Health Organization [WHO] is higher than the ECOFF) (9, 29, 31).

Setting conclusive ECOFFs and validating MABA as a method for routine DST were beyond the scope of this study, which would have required a larger number of phylogenetically diverse strains from multiple laboratories and more extensive reproducibility testing, as specified by EUCAST and the International Organization for Standardization (ISO) (12, 28, 32, 33). Nevertheless, our MABA results were sufficiently robust compared with those of LJ DST and the genotypic results to set tentative ECOFFs. Accordingly, AFX had a lower ECOFF than OFX in vitro but an ECOFF higher than the ECOFFs of LFX and MFX. All gyrA mutations correlated with non-wild-type MICs for all fluoroquinolones. Consequently, clinicians should consider the possibility that the use of AFX to treat infections caused by E. coli, K. pneumoniae, and staphylococci at the doses currently suggested might result in the selection of fluoroquinolone resistance in M. tuberculosis in coinfected patients.

We had only one strain that had a gyrB mutation without a mutation in gyrA. The fact that four different amino acid changes had been observed at the gyrB codon in question (T500A/N/P) constitutes a potential signal for drug selection (7, 34, 35). In line with this observation, allelic exchange experiments with T500N in an Erdman background increased the MIC from wild-type levels to the CC for OFX and LFX and just above the CC for MFX (36). The results of the equivalent experiment in an H37Rv background were identical for OFX and LFX, but no increase in MIC was
observed for MFX (36). In accordance with the results of the in vitro selection experiments and the aforementioned allelic exchange experiments, this suggested that the MIC of the strain with gyrB T500N was close to the ECOFF, which, due to biological and technical variability (e.g., for reproducibility, the ISO guidelines allow ±1 dilution of the mode for ≥95% of the results), would likely result in a poor reproducibility of DST (32, 37–39). Irrespective of whether this slightly elevated MIC increases the likelihood of treatment failure, it is possible that it increases the likelihood of selecting for higher levels of fluoroquinolone resistance due to a

FIG 1 Wild-type and non-wild-type MIC distributions for the four fluoroquinolones under investigation relative to their gyrA and gyrB genotypes (see Table S1 in the supplemental material). The tentative ECOFF represents the upper limit of the wild-type distribution. All clinical strains, with the exception of H37Rv, harbored the gyrA S95T mutation that is known not to confer fluoroquinolone resistance and was consequently excluded from the analysis (13).
gyrA mutation or a secondary gyrB mutation, as observed for streptomycin (36, 40, 41). Larger data sets, ideally with longitudinal samples from the same patients, would be required to clarify this possibility (i.e., to determine in which order gyrA and gyrB mutations arose in double mutants, such as the five strains observed in this study [Fig. 1; see also Table S1 in the supplemental material]).

Using the published area under the concentration-time curve from time zero to 24 h (AUC0−24) of 47.59 ± 7.85 mg · h/liter for the currently approved dose of AFX (i.e., a 200-mg daily dose following a 400-mg loading dose) and protein binding of 17.5%, the unbound [AUC0−24/MIC ratio for the wild-type MICs of 0.064 to 1 µg/ml would range from 613.46 ± 101.19 h to 39.26 ± 6.48 h (42, 43). Although there is no consensus on the precise [AUC0−24/MIC ratio that best predicts in vivo efficacy, ratios of >100 at the upper end of the wild-type distribution are likely required to maximize clinical success (44, 45). Given that the currently recommended dose of AFX is unusually low (probably because of a narrow clinical indication) compared with the doses of the other fluoroquinolones used to treat tuberculosis, the target [AUC0−24/MIC of >100 at an increased dose is likely achievable, but this would have to be evaluated in clinical trials, where side effects would have to be monitored carefully.

Our study also has implications for DST for OFX on LJ. Although the absolute concentration method has not been validated by the WHO for second-line drugs, it is used clinically with the CC recommended for the proportion method (29). In our case, we employed a CC of 2 µg/ml, which corresponded to the old CC for this drug for the proportion method, which the WHO recently increased to 4 µg/ml, although the rationale for this change is unclear (29). In light of the excellent correlation between the LJ DST results and MABA MICs for all four fluoroquinolones, which is in line with the findings of previous studies, this suggested that the revised CC is likely too high for the absolute concentration method, resulting in non-wild-type strains being misclassified as wild type (46, 47). This, together with prior studies that raised doubts regarding the validity of some CCs, underlined the fact that the WHO should start to apply modern microbiological principles and, crucially, to publish the evidence used to set CCs, as has been the case for EUCAST for many years (12, 27, 39).

**ACKNOWLEDGMENTS**

Anhui Huanqiu Pharmaceutical Co. provided AFX for this study, but this work was designed, conducted, and analyzed independently of the company. T.S. is a member of the EUCAST Subgroup on Antimycobacterial Susceptibility Testing, J.P., S.J.P., and C.U.K. have collaborated with Illumina Inc. on a number of scientific projects. J.P. has received funding for travel and accommodation from Pacific Biosciences Inc. and Illumina Inc. S.J.P. has received funding for travel and accommodation from Illumina Inc. C.U.K. is a consultant for the Foundation for Innovative New Diagnostics and was a technical advisor for the Tuberculosis Guideline Development Group of the World Health Organization. The Bill & Melinda Gates Foundation and Janssen Pharmaceutica covered C.U.K.’s travel and accommodation to present at meetings. The European Society of Mycobacteriology awarded C.U.K. the Gertrud Meissner Award, which is sponsored by Hain Lifescience.

The work was supported by research funding from the Infectious Diseases Special Project, Minister of Health of China (2016ZX10003001-12), and Beijing Municipal Administration of Hospitals Clinical Medicine Development of Special Funding Support (ZYLK201304). The strains used in this project were obtained from the Beijing Bio-Bank of Clinical Resources on Tuberculosis (D909050704640000), Beijing Chest Hospital. In addition, this study was supported by the Health Innovation Challenge Fund (HICF-T5-342 and WT098600), a parallel funding partnership between the United Kingdom Department of Health and Wellcome Trust. T.S. was supported by grants from the Swedish Heart and Lung Foundation and the Marianne and Marcus Wallenberg Foundation.

The views expressed in this publication are those of the authors and not necessarily those of the Department of Health, Public Health England, or the Wellcome Trust.

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