Quantitative pharmacology approaches to inform treatment strategies against tuberculosis

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Chapter 3

Pharmacogenetic variability and the probability of site of action target attainment during tuberculosis meningitis treatment: A physiologically based pharmacokinetic modeling and simulations study

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Abstract

Objective and Methods: Our objective was to investigate the role of patient pharmacogenetic variability in determining site of action target attainment during tuberculous meningitis (TBM) treatment. Rifampin and isoniazid PBPK model that included *SLCO1B1* and NAT2 effects on exposures respectively were obtained from literature, modified, and validated using available cerebrospinal-fluid (CSF) concentrations. Population simulations of isoniazid and rifampin concentrations in brain interstitial fluid and probability of target attainment according to genotypes and *M. tuberculosis* MIC levels, under standard and intensified dosing, were conducted.

Results: The rifampin and isoniazid model predicted steady-state drug concentration within brain interstitial matched with the observed CSF concentrations. At MIC level of 0.25 mg/L, 57% and 23% of the patients with wild type and heterozygous *SLCO1B1* genotype respectively attained the target in CNS with rifampin standard dosing, improving to 98% and 91% respectively with 35 mg/kg dosing. At MIC level of 0.25 mg/L, 33% of fast acetylators attained the target in CNS with isoniazid standard dosing, improving to 90% with 7.5 mg/kg dosing.

Conclusion: In this study, the combined effects of pharmacogenetic and *M. tuberculosis* MIC variability were potent determinants of target attainment in CNS. The potential for genotype-guided dosing during TBM treatment should be further explored in prospective clinical studies.

Introduction

Central nervous system infection is the most severe manifestation of TB, with approximately one-half of affected patients suffering severe neurologic disability or death[1,2]. In the absence of known or suspected drug-resistant disease, TB treatment guidelines recommend standard dosing of isoniazid and rifampin as part of the first-line regimen[3]. Clinical trials of intensified dosing of rifampin for tuberculosis meningitis (TBM) have yielded mixed results[4–6], perhaps owing to differences in the dosing regimen of the intensified arm[7]. There still remains considerable uncertainty regarding the optimal initial treatment of TBM patients[6].

For the treating clinician, limited information is available to guide the selection of a drug regimen for a TBM patient. The susceptibility of *M. tuberculosis* to a given anti-TB drug is typically established with phenotypic resistance testing at a "breakpoint" MIC, with a delay of several weeks after cultures are obtained[8]. While these breakpoint MIC values have been interrogated in the treatment of pulmonary TB[9], the relationship between MIC breakpoint and clinical response in the treatment of TBM patients is less examined[2]. Furthermore, there is an emerging understanding of the contribution of host genetics to the pharmacokinetic (PK) variability of both isoniazid and rifampin[10]. For isoniazid, this source of variability is primarily driven by the metabolizing enzyme responsible for isoniazid elimination, the N-acetyltransferase-2 (*NAT2)* gene[11]. More recently, pharmacogenetic variability in the hepatic OATP1B1 uptake transporter gene (*SLCO1B1*) has been identified as a driver of rifampin PK variability, as individuals who possessed the variant allele demonstrated increased rifampin clearance compared to individuals with the homozygous wild-type gene[12,13].

For both isoniazid and rifampin, the pharmacodynamic effect is based on achieving PK exposure at the site of infection, defined by the area under the concentration-versus-time profile (AUC), that is sufficiently greater than the MIC of the infecting *M. tuberculosis* strain[14,15]. Prior work has examined the impact of phenotypic drug resistance on the clinical outcomes of TBM, demonstrating that initial isoniazid and/or rifampin resistance is associated with death before treatment completion[16,17]. We sought to extend this work by examining the likelihood of target attainment among TBM patients with putative drug-susceptible disease, as defined by MIC levels for isoniazid and rifampin below the CLSI breakpoint[18]. We hypothesized that sub-breakpoint MIC levels would correspond to unattainable targets among TBM patients with genotypes of *SLCO1B1* (for rifampin) or *NAT2* (for isoniazid) that correspond with lower systemic exposures.

Methods

Rifampin and isoniazid PBPK modeling with genotype effects of SLCO1B1 and NAT2

A previously developed rifampin whole-body PBPK model was used as the base model[19]. The rifampin PBPK model included metabolism by enzyme arylacetamide deacetylase (AADAC), transport by organic anion-transporting polypeptide transporter (OATP1B1) and P-glycoprotein, along with the auto-induction of AADAC, OATP1B1, P-glycoprotein, and CYP3A4. Partition-coefficients from plasma to various tissues, including brain interstitial and intracellular compartments, were calculated based on Rodgers and Rowland method20. The model included efflux transporter, P- glycoprotein, mediated passive transport through blood-brain barrier[19]. The model also included the effect of hepatic OATP1B1 (encoded by the gene *SLCO1B1*) on rifampin clearance (S3.1).

To quantify the effects of *SLCO1B1* pharmacogenetic variability on rifampin exposure, we first reviewed the available literature. A clinical study that included rifampin PK and *SLCO1B1* genotypes identified an association of SLCO1B1 SNP c.463CC (rs11045819 wild type) or c.463CA (rs11045819 heterozygous) with plasma concentrations of rifampin in TB patients (n=72 pulmonary TB patients from Africa, North America, and Spain)[13]. We performed a comparison of this SNP with data collected in a prospective cohort study of 40 HIV/TB patients in Botswana and also identified an association between SLCO1B1 rs11045819 and rifampin exposure[12]. As such, only SLCO1B1 rs11045819 heterozygous vs. wild type categories were selected for evaluations in our PBPK study. The rifampin PBPK model was calibrated using data from literature[13] and the proportional effect of heterozygous category on the maximum transport rate ($Vmax_{OATP1B1}$) was estimated, with all other parameters kept unchanged from the original model. Next, we performed an external validation of the expanded rifampin PBPK model using the PK data from our Botswana study[12]. Patients in the validation dataset were categorized into heterozygous or wild-type groups based on the rs11045819 SNP (S3.2). We validated this expanded rifampin PBPK model by overlaying the model-predicted rifampin concentrations, stratified by SLCO1B1 genotype, with the observed PK data for both genotype categories. Once validated, we performed a sensitivity analysis of the expanded rifampin PBPK model. The sensitivity of the estimates in exposure metrics, including the AUC, C_{max}, and half-life were examined, after introducing 10% variation in absorption and clearance parameters.

We utilized a previously published and validated whole-body PBPK model of isoniazid to simulate PK profiles in CNS compartments during TB treatment[21]. This model incorporated a complex metabolic network, including metabolism of isoniazid by N-acylethanolamine-hydrolyzing acid amidase (NAAA) and NAT2 enzymes, along with further metabolism and transport of the metabolites by various processes. Partition-coefficients from plasma to various tissues, including brain interstitial and intracellular compartments, were calculated based on PK-Sim standard method as incorporated in the software[22].

Additional external validation of the rifampin and isoniazid for the purpose of our analysis was performed by comparing brain interstitial drug predictions against observed drug concentrations measured in cerebrospinal fluid (CSF) collected from TB patients who received various doses of rifampin and isoniazid[5,23,24]. Upon completion of the external validations, the rifampin and isoniazid PBPK model, which included *SLCO1B1* and NAT2 covariate effects on drug exposures, respectively, were used for simulations and CNS target attainment evaluations.

Model codes

The isoniazid PBPK model was unchanged from the previously published version[21] and is available at the GitHub repository https://github.com/HenrikCordes/isoniazid-PBPK-model. The updated rifampin PBPK model with SLCO1B1 genotype effect is available at the GitHub repository https://github.com/krinaj/RIF-INH-PBPK-Models. Additional details about the isoniazid and rifampin PBPK model development, validation, and parameter estimates are available in literature [19,20].

Observed MIC distributions in M. tuberculosis isolates cultured from CSF in TBM patients

To understand the potential benefit of intensified dosing regimens at the population level, we directly measured the rifampin and isoniazid MIC levels in collection of *M. tuberculosis* isolates that had been obtained from TBM patients in the U.S. state of New Jersey over a 12-year period. In support of statewide molecular epidemiology efforts, the Kreiswirth laboratory routinely performs DNA fingerprinting on all *M. tuberculosis* isolates across the state of New Jersey, recording the anatomic site of culture for each of isolate in the collection[25]. Among those *M. tuberculosis* isolates that had been cultured from CSF and previously determined to be susceptible to both rifampin and isoniazid (n=34), we determined the MIC for rifampin and isoniazid by agar diffusion[26].

Target attainment under standard and intensified dosing schemes of isoniazid and rifampin

Isoniazid and rifampin concentrations in venous blood plasma and brain interstitial fluids were simulated using PBPK models. The simulated population contained 1,000 virtual adult TBM patients with body weight sampled from prior distribution of body weight from TB patients[12]. Additionally, other physiological and anatomical parameters were varied as described previously to generate the virtual population[21]. Next, we performed separate simulations (n=1,000) for each *NAT2* (slow, intermediate, and fast acetylators) and *SLCO1B1* (wild-type and heterozygous) genotype[27]. Under each dosing scheme (standard or intensified), the isoniazid or rifampin $AUC_{0\text{-}24}$ following the 10^{th} dose was calculated for brain interstitial fluid compartment.

Next, we calculated the $AUC_{0\text{-}24}$/MIC ratio corresponding to each MIC value for the infecting *M. tuberculosis* strain. Since all MIC values were falling below the breakpoint that defines drug susceptibility or resistance, we also calculated target attainment at higher MIC referring to drug-resistant strains[23]. For each MIC value, we estimated probabilities of target attainment in brain interstitial fluid for both drugs, under standard and intensified dosing strategies. For rifampin, the target was defined as an $AUC_{0\text{-}24}$/MIC ratio of 30, corresponding to a 1 $\log_{10}$ CFU/mL decrease in *M. tuberculosis* bacterial load[28]. Based on the same criteria, the isoniazid target was defined as an $AUC_{0\text{-}24}$/MIC ratio of 43.5[14]. We selected intensified dosing strategies based on published clinical trial experiences[23,24,29]. Additionally, based on observed MIC distributions at the population level, cumulative fraction of response under standard and intensified dosing strategies was estimated by sampling from observed distribution of MIC values in CSF of TB patients.

Software

Physiologically-based PK modeling and simulation was performed in PK-Sim® and Mobi® (Open Systems Pharmacology Suite, v8.0, www.open-systems-pharmacology.org). Statistical analysis and plots were generated in R (R for Windows, v4.1, https://www.r-project.org/) using RStudio (RStudio, v1-554, www.rstudio.com/).

Results

Extension of rifampin PBPK model with SLCO1B1 genotype effects

The rifampin and isoniazid PBPK models included all major contributing factors affecting systemic and CNS exposures, including, protein binding, active and passive transports into various tissues, and relevant metabolism networks. As such, these models were selected for the purpose of our analysis. The updated rifampin PBPK model described observed plasma concentrations for both patients with both wild type and heterozygous SLCO1B1 genotypes **(Figure 3.1a)**. The model suggested a 3% proportional increase in OATP1B1 V_{max} among heterozygous genotype patients, compared to wild-type genotype patients (OATP1B1 V_{max} WT = 0.37 µmol/L/min vs. OATP1B1 V_{max} WT = 0.39 µmol/L/min)[13]. All other parameters, other than OATP1B1 V_{max}, remained unchanged from the literature-based model[19]. In an external validation exercise, the simulated plasma concentration-time profile agreed well with observed rifampin PK data (R^2=0.96 and 0.93, respectively, p-value<0.0001) for both *SLCO1B1* genotypes **(Figure 3.1b)**. With a 10% change in parameter estimates, the sensitivity for key rifampin PK parameters was low (between -1 and 1), which further supported the reliability of the rifampin expanded PBPK model.

Model-predicted isoniazid and rifampin exposures in CNS, stratified by genotype

The rifampin and isoniazid PBPK models predicted steady-state drug concentration within brain interstitial compartment matched well with observed CSF drug concentrations **(Figure 3.2, Figure 3.4)**. With the standard rifampin dose of 10 mg/kg orally once daily, the mean AUC_{0-24} ratio for brain interstitial fluid: plasma was predicted to be approximately 0.36 and 0.24 for wild-type and heterozygous groups, respectively. For the standard isoniazid dose (5 mg/kg), the mean AUC_{0-24} ratio for brain interstitial fluid: plasma was predicted to be approximately 0.76 for fast acetylators and 0.78 for both intermediate and slow acetylators.

Figure 3.1 Development and validation of an expanded rifampin PBPK model to include SLCO1B1 genotype. (A) Development of the model to include SLCO1B1 covariate effects (n=72 patients from Weiner et al, 2010[13]. (B) Validation of the expanded rifampin PBPK model (n=40 patients from Vinnard et al, 2017[12]. Rifampin PBPK model described plasma concentrations time profiles for both SLCO1B1 wild type and heterozygous groups well. Black points with error bars represent mean and SD of observed data, black points represent individual concentrations data, black line represent median of predicted, and grey shading represent 95% confidence interval of the predictions.

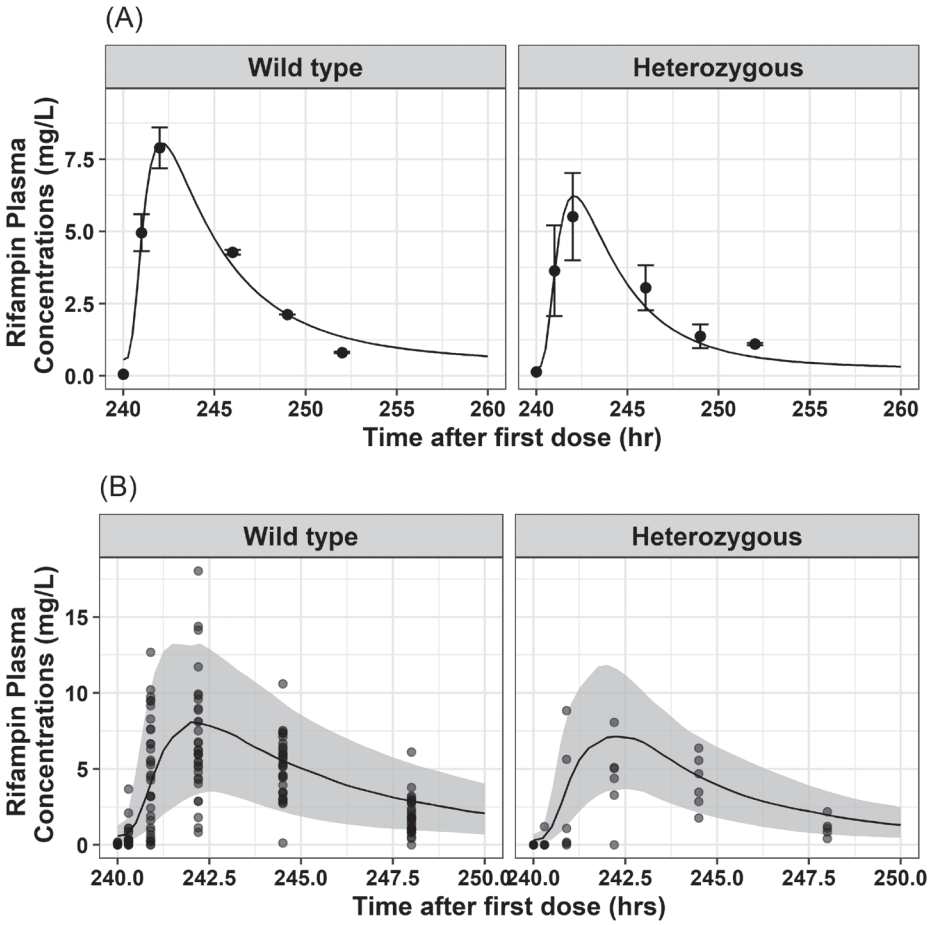


Figure 3.2 Validation of the rifampin and isoniazid PBPK models for predictions of drug exposures in the CSF. The PBPK models predicted rifampin and isoniazid steady-state concentrations in brain interstitial compartment matched well with the observed concentrations data from CSF of TB patients[23,24].

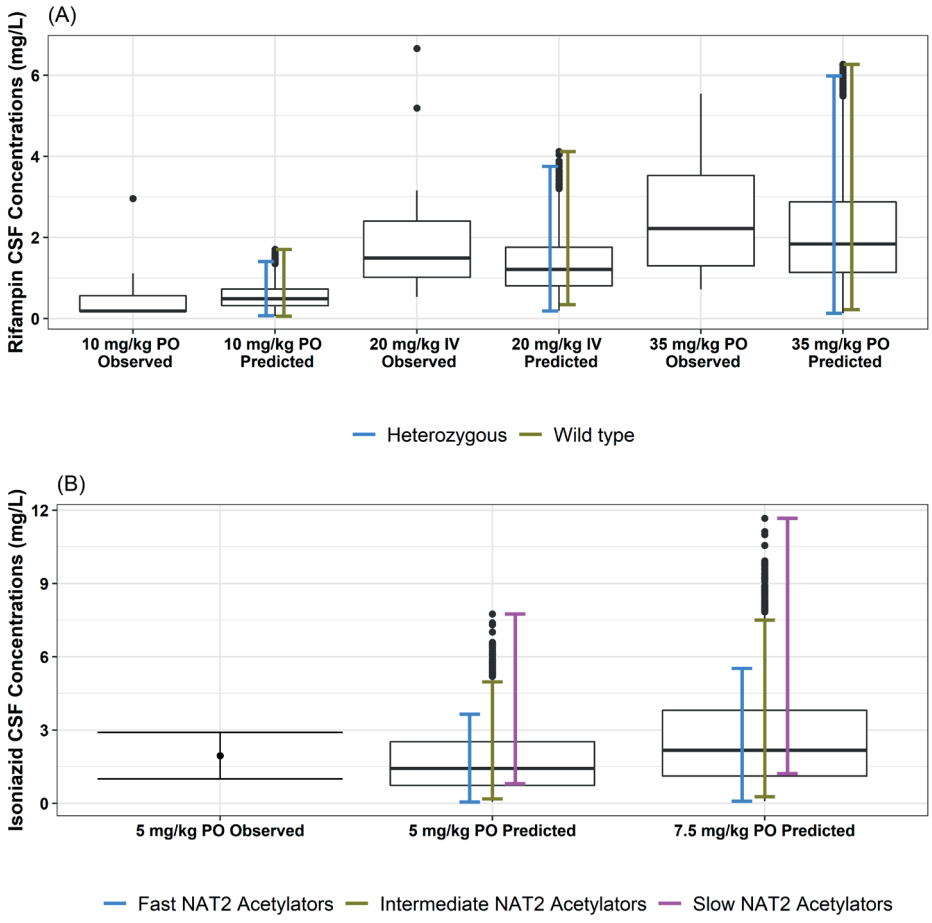
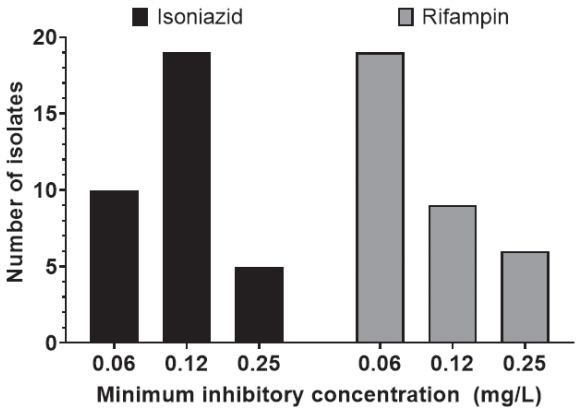


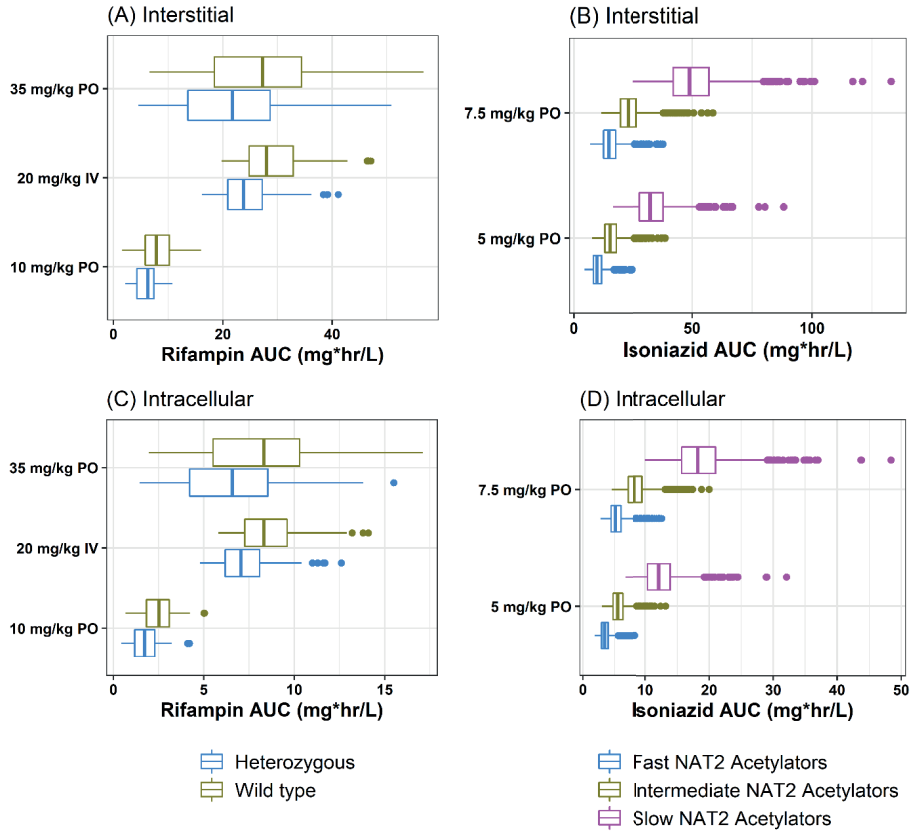
Figure 3.3 Distribution of minimum inhibitory concentration levels of isoniazid and rifampin among M. tuberculosis isolates that were cultured from CSF in New Jersey over a 12 -year period.



Probability of target attainment in CNS under standard and intensified treatments

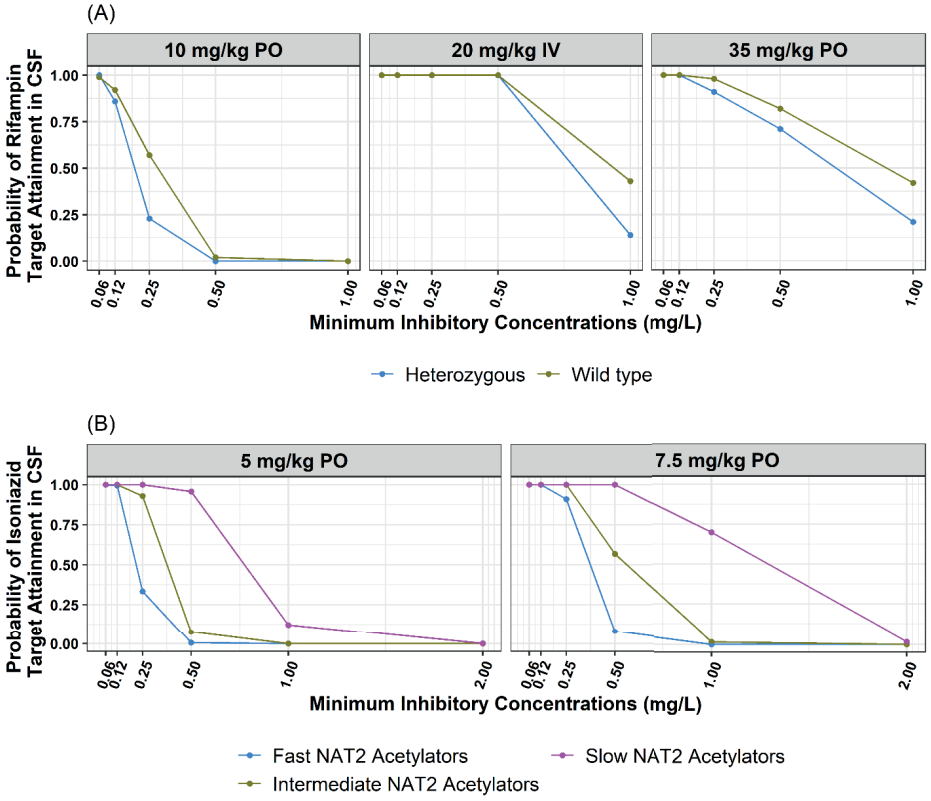
Distribution of MIC levels for rifampin and isoniazid in a collection of *M. tuberculosis* isolates that had been cultured from the CSF of patients is presented in **Figure 3.3**. With standard and intensified rifampin dosing, the probabilities of successful rifampin target attainment in brain interstitial fluid are shown in **Figure 3.5A.** At rifampin MIC level of 0.125 mg/L, 92% of patients with wild-type *SLCO1B1* genotype attained the rifampin target in brain interstitial fluid, compared with 86% of the patients with heterozygous *SLCO1B1* genotype. At a rifampin MIC level of 1 mg/L, none of the patients with either *SLCO1B1* genotype were predicted to achieve rifampin target in brain interstitial fluid. With intensified rifampin dosing of 35 mg/kg and MIC level of 1 mg/L, 42% and 21% of patients with wild-type and heterozygous *SLCO1B1* genotype, respectively, attained the rifampin target in brain interstitial fluid. With standard and intensified rifampin dosing, the probabilities of successful isoniazid target attainment in brain interstitial fluid are shown in **Figure 3.5B**. At an isoniazid MIC level that is less than or equal to 0.125 mg/L, nearly all TBM patients regardless of *NAT2* genotypes attained the target in brain interstitial fluid at the standard dosing. At an isoniazid MIC level of 1 mg/L, none of the fast or intermediate acetylators and only 12% of slow acetylator patients attained the target in brain interstitial fluid at the standard dosing. At the same MIC, intensified dosing predicted to provide target attainment in none of the fast acetylators, 2% of intermediate acetylators, and 68% of slow acetylators.

Figure 3.4 Predicted steady state rifampin and isoniazid AUC_{0-24} (mg·hr/L) in the CNS compartments stratified by dosing regimen and genotype. (A) rifampin brain interstitial, (B) isoniazid brain interstitial, (C) rifampin brain intracellular, (D) rifampin brain interstitial. All dosing regimens were administered once daily.



Based on observed MIC distributions at the population level **(Figure 3.3)**, cumulative fraction of response under standard and intensified dosing strategies was estimated by sampling MIC values from observed distribution of MIC values in CSF of TB patients to calculate target attainment probabilities. For the drug-susceptible strains, there was 86% and 99% overall probability of PD target attainment in brain interstitial fluid with standard dosing and intensified dosing of rifampin, respectively. Similarly, for the drug-susceptible strains, there was a 92% and 99% overall probability of target attainment in brain interstitial fluid with standard dosing and intensified dosing of isoniazid, respectively.

Figure 3.5 Target attainment probabilities in brain interstitial compartment under standard and intensified dosing regimens for rifampin and isoniazid stratified by *SLCO1B1* and NAT2 genotypes, respectively. All dosing regimen assumed once daily therapy.



Discussion

Our objective was to evaluate the probability of target attainment in the CNS during TBM treatment with a first-line regimen that includes isoniazid and rifampin. We used a PBPK modeling approach to incorporate two independent sources of variability: host pharmacogenetics and pathogen MIC levels. Using this approach, we tested the hypothesis that sub-breakpoint MIC levels for isoniazid and rifampin would correspond to essentially unattainable targets among patients with fast elimination genotypes. While our findings support this hypothesis, they also demonstrate that the clinical benefit of intensified dosing regimens are concentrated at certain MIC levels for the infecting *M. tuberculosis* strain.

Adequate PK exposures of anti-TB drugs in the CNS are crucial for treatment success for TBM patients[30]. Current bioanalytical sampling methods do not allow measurements of drug exposure from various CNS sites of TB lesions, such as brain intracellular tuberculomas, and CSF drug concentrations may be used as a summary measure of CNS drug exposure[31]. The whole-body PBPK model that was used in this analysis includes blood cells, plasma, interstitial space, and tissue space for each organ/compartment; drug partitioning into these spaces is based on physicochemical parameters of the drug and physiological parameters of the species. Furthermore, the rifampin PBPK model also includes P-glycoprotein transporter effects at the blood-brain barrier[19]. As such, our PBPK model-based approach in this analysis is useful to predict anti-TB drug target attainment at CNS sites of action in TBM patients, and advances prior understandings based on CSF concentration-time profiles[32–34].

In clinical trials of pulmonary TB patients, intensified dosing of rifampin (up to 50 mg/kg oral) led to fast sterilization activity increasing toxicity[23,29,35]. In TBM patient populations, clinical trials of intensified rifampin dosing have shown mixed results. Rifampin doses up to 15 mg/kg did not show improved survival in a study conducted in Vietnamese patients (n=817)[4]. In contrast, a clinical trial of intensified rifampin dosing among Indonesian TBM patients (n=122) led to improvements in mortality without an increased rate of adverse events, with dose increases up to 30 mg/kg[5]. A model-based meta-analysis has found that even doses beyond 30 mg/kg may be expected to improve clinical response[33]. Our work also suggests that unmeasured MIC variability may be a major driver of clinical response, with an additional contribution of *SLCO1B1* pharmacogenetic variability in some populations. Importantly, the MIC variability in the current study was entirely sub-breakpoint, meaning that these isolates would be classified as drug-susceptible by the clinical laboratory. With the PBPK model-based simulations, we were able to demonstrate that standard dosing would achieve markedly low probabilities for target attainment for drug-resistant strains by setting MIC to higher values. We propose that future prospective clinical trials of TBM treatment regimens prioritize the capacity for secondary analyses based on these additional sources of variability.

As patient genotyping methods advance to reach a greater number of bedsides in geographic areas with a high burden of TB disease, the potential tradeoffs between personalized medicine and standardized treatment regimens will require greater consideration, regarding incremental benefits and resource utilization. Much attention has been focused on the support of clinical decision-making provided

by DNA sequencing of *M. tuberculosis* strains, for example to identify mutants likely to confer phenotypic drug resistance[36]. Yet parallel efforts are underway to identify the patient's genotypic determinants of TB treatment response, including the use of the *LTA4H* genotype to select patients for adjunctive corticosteroid treatment[37], currently studied in a prospective clinical trial[38]. Our findings suggest that these patient genotyping efforts should be expanded to evaluate prospectively the impact of SNPs related to *NAT2* and/or *SLCO1B1* activity during TBM treatment. This information could be combined with *M. tuberculosis* mutational analysis to identify those patients most likely to benefit from intensified drug therapy, and perhaps to guide further the selection of the intensified dose in the regimen.

A key finding of the current work was the difference in drug exposures between brain interstitial fluid and brain intracellular. According to one model of TBM pathogenesis, the early bloodstream dissemination of *M. tuberculosis* may lead to foci of infection established in the meninges and brain parenchyma, following a vascular distribution[39]. As these tubercles enlarge, there is potential for rupture into the sub-arachnoid space, leading to the signs and symptoms of meningitis, most commonly in a basilar distribution[40]. Yet the tubercles themselves are found in the brain or meningeal tissue, and enlargement without rupture leads to the formation of tuberculomas, which may become clinically apparent as space-occupying lesions. Delayed sterilization of deep CNS anatomic sites during TB treatment, as a consequence of sub-optimal PK exposures, could contribute to the observed risk of paradoxical reaction during TBM treatment[41]. The current PBPK model calculated brain interstitial to intracellular partition coefficients based on standard PBPK modeling methods[42]. As such, the model may not contain all relevant mechanistic details pertaining drug penetration in the brain intracellular compartment. Although further work may be needed to implement all relevant mechanisms of brain intracellular penetration for anti-tuberculosis drugs, our relatively simple adaptation of whole-body PBPK model provide a quantitative estimate of the PK exposures of isoniazid and rifampin in brain intracellular, relative to brain interstitial fluid.

Our study had several notable limitations. The pharmacogenetic association of *SLCO1B1* variability with lower rifampin exposures was based on analysis from two independent clinical studies, and we recognize that heterozygous alleles at additional loci likely relate to rifampin PK variability[43]. In pharmacogenetic studies that were reported subsequent to the work used in our PBPK model development and validation, the rs11045819 allele was found to be rare in certain populations[44]. Linkage disequilibrium analyses, both between- and within- populations, will be

essential to improve understanding of the SNPs tags that correspond to gene function[45]. For simplicity, we assigned the drug dose (mg) based on body weight (kg), rather than using dosing bands that allow for fixed-dose combination, and the additional impact of weight-based dosing bands would be of interest in a future study[46]. Furthermore, recent clinical trials have also studied even higher rifampin doses than we selected for simulation purposes, up to 50 mg/kg[47]. Strengths of our approach included the utilization of previously validated PBPK models for each drug, the formal validation of the *SLCO1B1* genotype as a novel covariate effect in the rifampin PBPK model, and the additional measurements of MIC distributions for isoniazid and rifampin among *M. tuberculosis* isolates cultured from TBM patients.

In summary, our PBPK-based approach demonstrated that the likelihood of target attainment during TBM treatment is jointly influenced by host pharmacogenetics and pathogen MIC variability. Within a PK-PD framework, the combination of these factors also identifies those patients most likely to benefit from intensified drug therapy. We propose that prospective clinical trials of TBM therapies should routinely capture these determinants of clinical response.

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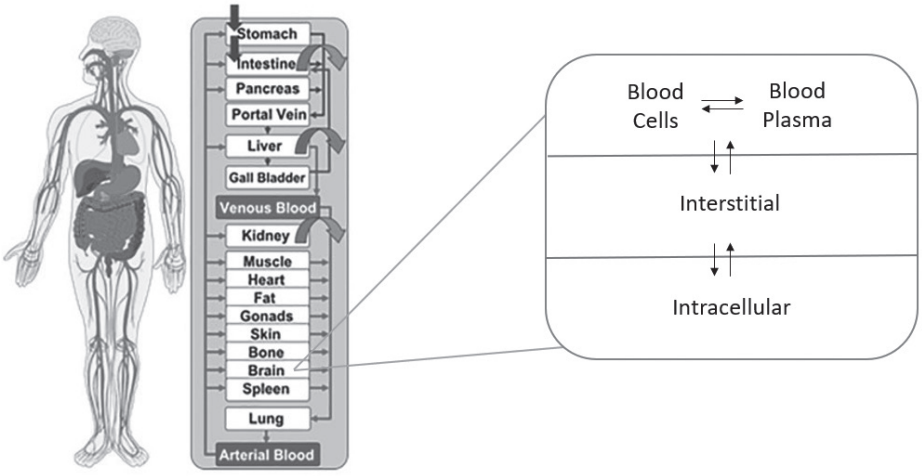
Supplementary Materials

S3.1. Generic Structure and Relevant Mechanistic Details of the PBPK Models for Rifampin and Isoniazid. The whole-body PBPK models for isoniazid and rifampin contains the relevant organs that play key roles in pharmacokinetics of drugs[1]. The organs are represented by their volume and connected with each other by arterial and venous blood flows. Each organ, including brain, is further divided into blood, interstitial, and intracellular compartments. Reproduced from Thiel et al., 2015 and Kuepfer et al., 2016 under Creative Commons Attribution[2,3.] Additionally, the rifampin and isoniazid PBPK models included all major contributing factors affecting systemic and CNS exposures, including, protein binding, active diffusion, passive transport, and relevant distribution and metabolism networks[4,5].



S3.2. Selection of the SNP Variant for Inclusion in Rifampin PBPK Analysis. Prior work has identified association of SLCO1B1 c.463CC (rs11045819 wild type) or c.463CA (rs11045819 heterozygous) genotypes with serum concentrations of rifampin in TB patients[6]. In our study, all SNPs identified in SLCO1B1 recognized in were evaluated for each subject[7]. Here, we performed a linkage disequilibrium analysis to characterize the association between various SLCO1B1 SNPs observed in our study data. A total of 32/40 patients had at least one heterozygous SNP. Four patients had heterozygous rs11045819 which was previously associated with lower rifampin Cmax. We identified other SNPs that were possibly associated with rs11045819 via linkage disequilibrium analysis. Two patients who did not have heterozygous rs11045819 SNP, but one or more associated SNP also had lower rifampin Cmax values in our dataset Additionally, two patients who had heterozygous rs4149080 had lower rifampin Cmax. Previously, Sloan et al., 2017 observed that rs4149032 to be possibly associated with lower rifampin exposure however, our study did not demonstrate similar finding[8]. Patients who had rs11045819 heterozygous SNP were flagged in our dataset as SLCO1B1 heterozygous for evaluation in the PBPK model.

Linkage Disequilibrium Heatmap for SLCO1B1 SNPs

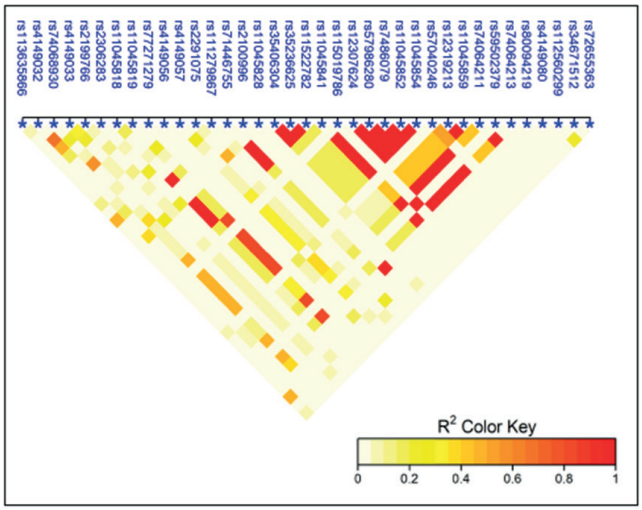
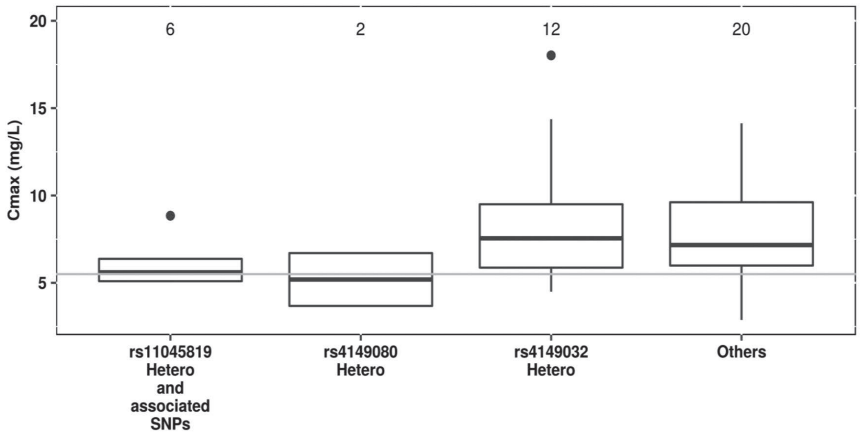


Table S3.3. List of SLCO1B1 SNPs associated with RS11045819

SLCO1B1 SNPs	rs11045819 (r^2)
rs11045841	0.82
rs11045852	0.82
rs11045854	0.82
rs12307624	0.82
rs57986280	0.82
rs74064211	0.82
rs74064213	0.82
rs74068930	0.57
rs7486079	0.82

S3.4. Observed Cmax Stratified by SLCO1B1 SNP Groups



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