Host-directed therapies for tuberculosis: quantitative systems pharmacology approaches

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Review

Host-directed therapies for tuberculosis: quantitative systems pharmacology approaches

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Host-directed therapies (HDTs) that modulate host–pathogen interactions offer an innovative strategy to combat *Mycobacterium tuberculosis* (Mtb) infections. When combined with tuberculosis (TB) antibiotics, HDTs could contribute to improving treatment outcomes, reducing treatment duration, and preventing resistance development. Translation of the interplay of host–pathogen interactions leveraged by HDTs towards therapeutic outcomes in patients is challenging. Quantitative understanding of the multifaceted nature of the host–pathogen interactions is vital to rationally design HDT strategies. Here, we (i) provide an overview of key Mtb host–pathogen interactions as basis for HDT strategies; and (ii) discuss the components and utility of quantitative systems pharmacology (QSP) models to inform HDT strategies. QSP models can be used to identify and optimize treatment targets, to facilitate preclinical to human translation, and to design combination treatment strategies.

Highlights

HDTs present innovative treatment strategies to combat against Mtb infections. Key HDT mechanisms include autophagy induction, modulation of host epigenetics, and modulation of cytokine- and lymphocyte-mediated response.

QSP modelling approaches may guide development of HDTs, incorporating complexity of drug–host–pathogen interactions. Such models can be used to identify new treatment targets, facilitate translational predictions, design combination treatment strategies, and optimize dose and dosing regimen.

QSP models for the design and evaluations of HDTs should capture relevant mechanistic details of host immune response, pathogen dynamics, and pharmacokinetic and pharmacodynamic characteristics of HDTs.

Host-directed therapies: leveraging the host immune system for treatment of TB

Mtb infections are associated with approximately 1.5–2 million deaths annually worldwide. Two key challenges to successful TB treatment are long duration of treatment and emergence of drug-resistant strains [3]. In the last decade, HDT strategies have received increasing attention [4–6] to enhance treatment outcomes, shorten treatment durations, and avoid resistance development. HDTs target interactions between the host immune response and the Mtb pathogen, which reduces the likelihood for Mtb to acquire resistance against HDTs. In addition, additive effects of adjunctive HDT treatment with conventional antibiotics on bacterial elimination could help to shorten treatment duration and therefore may avoid development of resistance to conventional antibiotics [7].

The host immune response to Mtb infection is reliant on the cumulative activities of various defence mechanisms such as macrophage activation, **phagocytosis** (see Glossary), **autophagy**, antigen presentation, and cytokine and T lymphocyte production. Genotypic and phenotypic changes in Mtb during infection leading to modulation of the host response allows its survival and virulence in the host [8]. Mechanistic understanding of the multiscale nature of host–pathogen interactions is essential to identify HDT targets, to design and develop new HDT drugs, and to repurpose already marketed drugs as HDT strategy.

A major challenge in the discovery and development of HDTs for TB is the prediction of treatment responses associated with specific pharmacological modulation of an immune-response-associated target due to complex systems-level host–drug–pathogen interactions [4]. The translation of systems-level responses to HDT strategies from preclinical models to patients is challenged by interspecies

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differences in immune responses to Mtb pathogen. QSP modelling can serve as a valuable tool to identify relevant HDT targets, and to inform subsequent design of combination drug treatment strategies and dosing schedules [9–11]. The utility of quantitative modelling to improve treatment strategies for TB have been demonstrated for antibiotic therapies [11,12]. However, these approaches have not yet been developed to design HDTs.

Here, we review high-potential host–pathogen interactions of relevance for HDTs. We then outline how QSP modelling approaches can be used to predict optimal HDT strategies with a focus on required model components and the integration with available data for application in target selection, interspecies translation, and treatment optimisation.

Host–pathogen interactions as basis for HDT strategies

Several host–pathogen interactions of Mtb involved in its pathogenesis and immune system evasion offer potential targets for design of HDTs [6] (Figure 1), and are of relevance to capture in QSP modelling approaches.

Induction of autophagy

Autophagy plays an essential role in controlling Mtb infections and has been studied extensively as potential HDT strategy for Mtb [6]. Multiple intertwined pathways affecting glucose and cholesterol metabolism, such as the **AMP-activated protein kinase (AMPK) and mammalian target of rapamycin (mTOR) pathway** and **HMG-CoA reductase pathway**, are involved in regulation of autophagy (Figure 1). AMPK plays a key role in these pathways and therefore in regulation of autophagy. As an evasion mechanism, Mtb inhibits phosphorylation of AMPK protein and inhibits autophagy [13]. Apart from AMPK-mediated autophagy regulation, intracellular cholesterol is also involved in Mtb survival leading to inhibition of autophagosome maturation and autophagosome–lysosome fusion [1]. Thus, autophagy induction through inhibition of mTOR complex (mTORC)1 or by inhibition of HMG-CoA reductase represent a potential HDT strategy.

mTORC1 inhibitors

Metformin is the most evaluated mTORC1 inhibitor as potential HDT treatment for Mtb infections. Metformin inhibited the growth of intracellular Mtb *in vitro* and in mice [13,14]. Multiple reports suggest that metformin adjunctive therapy in diabetic TB patients improved therapy success rate and lowered mortality rate [15,16]. Adjunctive everolimus, an mTOR inhibitor, treatment with rifabutin-substituted standard TB therapy improved lung functions as measured by forced expiratory volume when compared to a control group in a randomised clinical trial [17]. A recent study identified protein kinase inhibitor ibrutinib as a potential mTORC1-mediated autophagy inducer in a mouse study [18]. These results provide initial proof of concept and justifying further evaluations of mTORC1 inhibitors in clinical trials.

HMG-CoA inhibitors

The HMG-CoA reductase pathway has been associated with intracellular cholesterol reduction and autophagy induction. Therapy with HMG-CoA inhibitors, such as simvastatin, pravastatin, and fluvastatin, as adjunctive therapy to conventional anti-TB drugs improved bacterial clearance by the host and improved the efficacy of first-line TB drugs by promoting autophagy in macrophage cell cultures and in mice [19,20]. Several retrospective clinical studies have identified that chronic use of statins reduced the risk of developing TB [21]. A population-based cohort analysis of data from newly diagnosed TB patients recognised no significant difference in hazard ratio between patients who were using statins in addition to standard TB treatment as compared to patients who did not use statins [22]. As chronic use of statins leads to reduced risk of TB, it may be hypothesised that factors such as drug penetration in lungs and drug affinity may play

Glossary

AMPK–mTOR pathway: pathway that involves complex interplay between various proteins and plays a key role in autophagy regulation.
Autophagy: an intracellular process involving the formation of a phagophore, elongation of the phagophore, autophagosome maturation, and fusion with lysosomes for degradation of the selected cellular material.
HMG-CoA reductase pathway: pathway involved mainly in regulation of cholesterol synthesis but also known to be involved in regulation of autophagy [1].
Phagocytosis: cellular process involving engulfment of large particles, including bacteria, into the cells.
Pharmacodynamics: describes the concentration–effect–time profile of drugs and is determined by drug pharmacology and physiology of the organism [2].
Pharmacokinetics: describes the concentration–time profile of drugs and is determined by absorption, distribution, metabolism, and elimination processes.

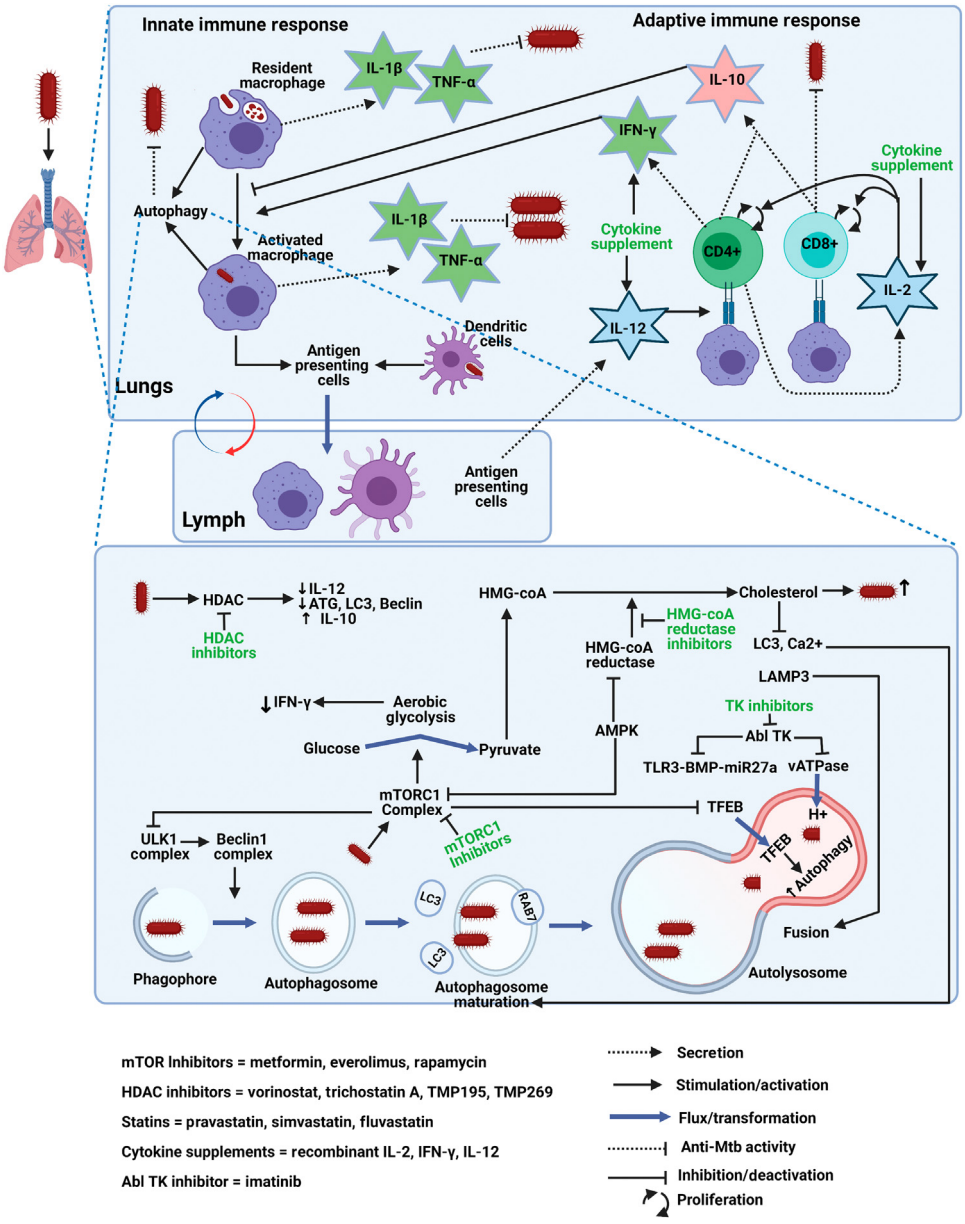

Figure 1. Host–pathogen interactions as basis for host-directed therapy strategies for the treatment of *Mycobacterium tuberculosis* (Mtb) infections. Initiation of the host innate immune response occurs shortly after inhalation of aerosols containing Mtb bacteria and Mtb implantation in macrophages. Both resident and activated macrophages stimulate the release of proinflammatory cytokines, such as tumour necrosis factor (TNF)-α and interleukin (IL)-1β, following phagocytosis and autophagy. Antigen-presenting cells (macrophages and dendritic cells) that drain into local lymph nodes activate $CD4^+$ and $CD8^+$ T-cell-mediated adaptive immune responses. Antigen-presenting cells also stimulate the release of IL-12, which helps recruit additional $CD4^+$ T cells. $CD4^+$ T cells secrete interferon (IFN)-γ that stimulates macrophage activation, IL-2, TNF-α, and IL-10 that helps balance the proinflammatory response by deactivation of macrophages. $CD8^+$ cells have cytotoxic activities. $CD4^+$ T-cell-secreted IL-2 drives further proliferation of $CD4^+$ as well as $CD8^+$ T cells. Autophagic pathways start with parting of a section from endoplasmic reticulum, the phagophore, followed by the elongation of phagophore with engulfment of Mtb, autophagosome formation and maturation, and fusion of the autophagosome with lysosomes. Mtb activates mammalian target of rapamycin complex

(Figure legend continued at the bottom of the next page.)

a key role in determining its effectiveness as HDT. Overall, these results highlight the potential of targeting the HMG-CoA reductase pathway as autophagy induction strategy.

Regulation of host epigenetics

Infection with Mtb is associated with alterations of some gene functions important for the ensuring immune response. Two key pathways known to be involved in Mtb-induced host epigenetic alterations are histone deacetylase (HDAC)1 pathway and TLR3–BMP–miR27a pathway; both of which can be pharmacologically exploited [23,24].

HDAC inhibitors

Infection with Mtb leads to upregulation of HDAC1, which leads to suppression of *IL-12B* gene expression and suppression of T cell immunity (Figure 1). Additionally, HDAC1 is known to modulate autophagy-associated genes [23]. HDAC inhibitors, such as trichostatin A, TMP195, and TMP269, reduced bacterial growth in macrophage cell cultures. Vorinostat, an HDAC inhibitor, promotes immune response in macrophage cell cultures [25]. In zebrafish embryos infected with *Mycobacterium marinum* (Mm), HDAC inhibition significantly reduces microbial burden [23]. HDAC inhibition significantly inhibits Mtb growth and shows increased production of key cytokines in mice [26]. These results highlight the potential of exploiting HDAC inhibition as HDT strategy.

Abl tyrosine kinase (ATK) inhibitors

Protein ATK is involved in entry and survival of Mtb within macrophages through the TLR3–BMP–miR27a pathway. ATK also inhibits expression of vATPase pump-relevant genes, and thus inhibits acidification of autolysosomes (Figure 1). Pharmacological inhibition of ATK using imatinib improves containment of Mtb within macrophages, induces autophagy, and decreases bacterial load in human macrophage cell cultures and in mice [6,24]. Imatinib also leads to decreased bacterial load in macrophage culture and in mice infected with rifampin-resistant Mm [27]. A clinical study assessing effects of imatinib alone and in combination with conventional anti-TB drugs in drug-resistant and HIV coinfected TB patients is ongoing [28]. These data suggest that imatinib may prove effective as HDT towards Mtb.

Modulation of cytokine response

The kinetics of the key cytokines, such as interferon (IFN)-γ, tumour necrosis (TNF)-α, interleukin (IL)-1β, IL-10, IL-4, IL-12, and IL-2, during Mtb infections have been well studied in humans and in mice. IFN-γ is one of the most important players to the host immune response and its main role is activation of macrophages (Figure 1). Both activated and resident macrophages produce proinflammatory cytokines TNF-α and IL-1β that possess microbicidal properties against Mtb; however, activated macrophage-mediated production is more efficient [29]. Excessive production of proinflammatory cytokines, however, can lead to tissue damage *in vivo* [30]. Anti-inflammatory cytokines IL-10 and IL-4 are also induced upon macrophage phagocytosis and balance proinflammatory cytokines by macrophage deactivation [30]. Excessive production of anti-inflammatory cytokines may result in limiting the immune-mediated microbicidal activities [31]. Thus, the fine balance between the pro- and anti-inflammatory cytokines may determine the overall outcome of the Mtb infection.

(mTORC)1 and thus inhibits autophagy, while mTORC1 activates aerobic glycolysis. Intracellular cholesterol inhibits LC3, Ca^{2+}, and LAMP3, and thus inhibits autophagy-mediated Mtb killing. Mtb activates the histone deacetylase (HDAC) pathway and thus downregulates various genes responsible for innate and adaptive immune response. Potential host-directed therapy strategies are presented in green text.

Adjunctive treatment with IFN-γ has been evaluated in various clinical studies; however, different patient conditions, routes of administration, and dosing regimens resulted in varying outcomes [31]. Adjunctive treatment with aerosolized IFN-γ showed benefits in reducing cavitary lesions and induced negative sputum conversion in TB patients in clinical studies [32]. Thus, modulation of cytokine response may be a useful HDT strategy.

Enhancing T-cell mediated host response

The innate immune reaction plays an important role in the initiation of adaptive immune response by antigen presentation and cytokines production. A few weeks after the initial infection, antigen-presenting cells (APCs) that drain into regional lymph nodes initiate adaptive T-lymphocyte-mediated immune response. Upon antigen presentation, the APCs via major histocompatibility molecules (MHC)-I and II prime $CD8^+$ and $CD4^+$ T cells to initiate an adaptive immune response. Both activated $CD4^+$ and $CD8^+$ T cells secrete IFN-γ, IL-2, IL-17A, and IL-10. Mature dendritic cells secrete IL-12p70, which helps increase recruitment of additional $CD4^+$ T cells. IL-2 plays a role in further proliferation of T cells. $CD8^+$ cells have direct microbicidal capabilities through perforin, granzymes, and granulysin, or induce apoptosis through Fas/Fas ligand interaction. Adjunctive cytokine supplementation with IL-12 and IL-2 have been evaluated in clinical studies but did not result in significant benefits. However, recombinant human IL-2 supplementation showed significant improvements in negative sputum culture conversion rates and in enhanced X-ray resolution in drug-resistant TB patients. [33] Therefore, the use of recombinant IL-2 supplementation as HDT strategy for TB should be further evaluated.

Design of HDTs using QSP modelling

The overall outcome of Mtb disease and treatment is reliant on the integrated results of the molecular and cellular events, and their reflection at tissue, organ, and host level dynamics occurring at different time scales. As such, it can be challenging to predict patient responses to different HDT strategies. Species differences in immune response characteristics make it more challenging to translate the results from preclinical studies to clinical scenarios. Additionally, determination of the effects of treatments and disease progression in specific patient populations, can be challenging, that is, in patients with weakened immune response or other conditions, or patients with specific genotypes known to affect certain pharmacology. QSP modelling can address these hurdles through quantitative integration of host–pathogen interaction mechanisms with **pharmacokinetics (**PK) and **pharmacodynamics** (PD) aspects of HDTs, making it a relevant tool to guide drug discovery and development of HDTs. Development of QSP models for HDTs against TB is the requirement for large amount of mechanistic quantitative data to parametrise the model, which may concern biological system-specific data relating to immunodynamics and pathogen dynamics, as well as drug-specific model related to pharmacokinetics and drug–target interactions. Importantly, once defined, a QSP framework for specific HDT mechanisms is developed, it can be applied as a platform model towards different investigational therapeutic agents. Selection of appropriate experimental approaches are important to provide quantitative understanding about components of drug–host–pathogen interactions. Here, we discuss key experimental models that can be of relevance for characterization of HDTs using QSP modelling. Then, we discuss three main components of the QSP framework to evaluate HDTs for Mtb infection: (i) drug PK models; (ii) host immune response models; and (iii) pathogen dynamic models (Figure 2). Lastly, we discuss applications of these models (Figure 3).

Experimental approaches to facilitate parameterisation of the QSP models

Human-derived macrophage and peripheral blood mononuclear cell cultures are extensively used to screen for the antibiotics but also identify compounds with HDT potential [14,34,35]. The *in vitro* hollow fibre infection model (HFIM) is commonly used to study the direct effects of

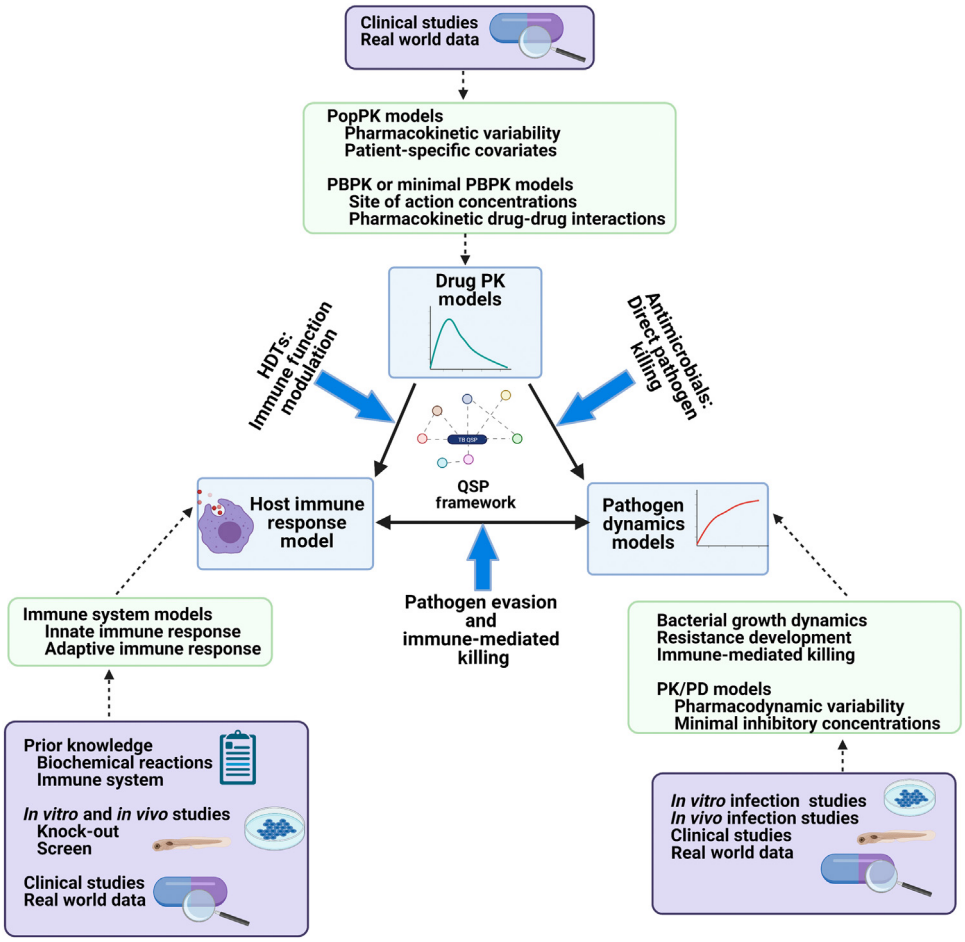

Figure 2. Components of the conceptual quantitative systems pharmacology framework to assess host-directed therapies (HDTs) for tuberculosis. A quantitative systems pharmacology (QSP) framework for HDTs should contain a combination of model components for pharmacokinetics (PK) of the drugs, host immune response, and pathogen dynamics, including their interactions. Classical antibiotics and HDTs act by modulating pathogen dynamics and host immune response, respectively. Immune-mediated pathogen killing is dependent on interplay between the host immune response and pathogen evasion mechanisms, that is, host–pathogen interactions. Key considerations for each model components are listed in the green box. Types of studies and data that can be used to inform each model components are presented in the purple box. Abbreviations: PBPK, physiologically based PK.

antibiotics agents on Mtb, and readily allows to include cocultures with macrophages. In HFIM, Mtb is cultured in a closed chemostat system with continuous flow of medium, while it allows simulation of concentration–time profiles of underlying PK/PD relationships of antibiotics and HDTs [36]. Several advanced cell culture systems, such as 3D cell cultures, organoids [37], and lung-on-chip [38], have been increasingly used to study host–pathogen interactions. While these approaches are attractive for purposes of quantitative characterisation of key mechanisms and phenotypic response profiles to be implemented in QSP models, these systems remain a simplified system that does not include all aspects related to the host immune response.

Adult zebrafish have gained increasing attention as it possess an innate immune system that is highly similar to that of mammals [39,40]. Zebrafish embryos are of interest due to their optical transparency and thus allowing the use of advanced imaging methods. Infection of zebrafish

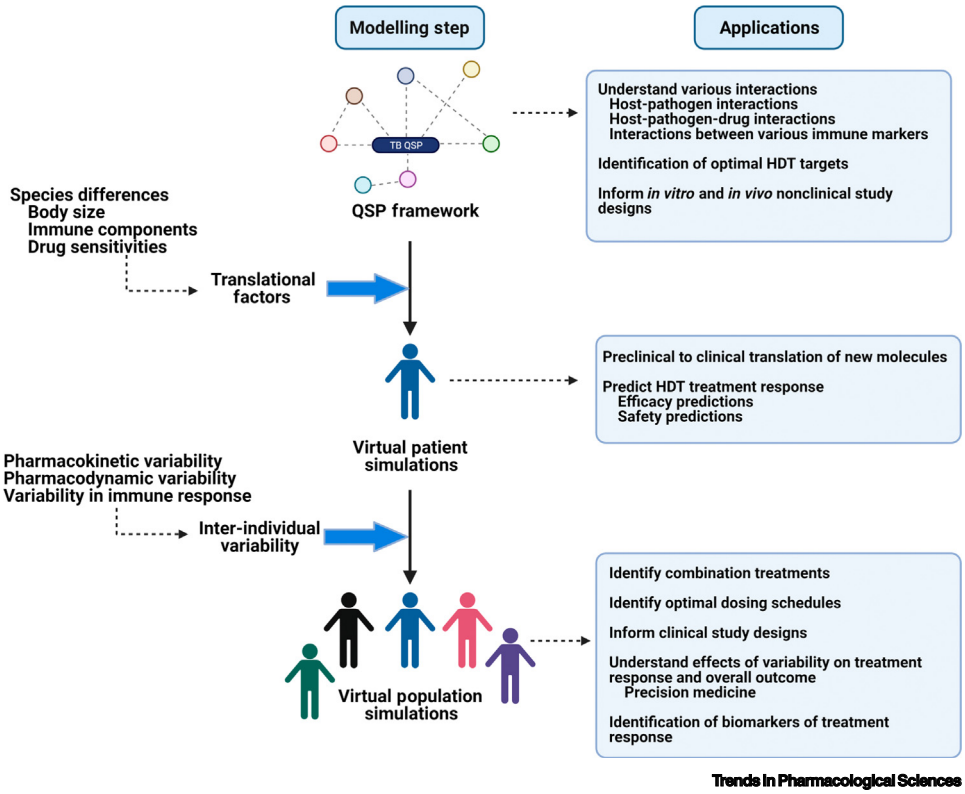

Figure 3. Applications of the conceptual quantitative systems pharmacology framework to assess host-directed therapies (HDTs) for tuberculosis (TB). Quantitative systems pharmacology (QSP) models can guide TB HDT drug discovery and development at various phases depending on the model attributes. For example, a model developed based on experimental *in vitro* and/or *in vivo* data can be useful to study various host–pathogen interactions, to screen for optimal HDT targets, and to guide *in vitro* and/or *in vivo* data experimental designs. Upon addition of various translational factors and inter-individual variability components, the models can be useful to design optimal clinical studies, to identify optimal combination strategies, and to individualise treatments.

with various mycobacteria leads to formation of granuloma structures that are highly similar to those observed in human TB patients; therefore, it has been a successful model to study the progression of TB and the effects of drug treatment [41]. Pharmacological screening of drugs to treat mycobacterial infection at a high throughput level is also possible [42]. Knockdown and overexpression experiments in zebrafish combined with translational QSP modelling would especially provide insights into contribution of certain component to overall immune response and anti-TB effects [43]. Mice, rabbits, and guinea pigs, are commonly used as infection models for Mtb [39]. Even though these models incorporate a full immune system, differences between the human immune response remain and lead to translational challenges [11]. Nonhuman primates (NHPs) have been widely used in immunology and vaccine research. NHPs infected with Mtb are of interest to generate HDT-relevant data due to their similarities to humans in basic physiology, immunology, and disease pathology. However, the use of these models has been limited in TB treatment research due to the requirements of scientific and financial resources as well as safety issues due to the highly infectious and contagious nature of Mtb [44].

Overall, data collected from a combination of various experimental models, such as *in vitro*, zebrafish, and mice, can be used to parameterise QSP models. QSP models can link the results from various experimental infection models, enabling predictions in humans.

Components of the QSP modelling framework

A QSP framework for HDTs should contain a combination of model components for PK of the drugs, host immune response, and pathogen dynamics, including their interactions (Figure 2). Depending on the type of HDT drug studied, QSP models may be parameterised and adapted in specific ways, for example, to capture the drug-specific parameters to induce specific immune system effects.

Pharmacokinetics

Consideration of drug concentration–effect relationships, and therefore PK, is of essential value for design of HDT strategies. Physiologically based PK (PBPK) models describe the concentration profiles in specific tissues of interest and are informed by both drug- and system-specific parameters. PBPK models are of relevance to scale PK between preclinical species and humans in a mechanistic fashion. For TB, PBPK models describing lung exposure are of specific relevance. In the clinical phase, quantifying interpatient variability in PK is important. Here, population PK models are of relevance, which capture interindividual variation in underlying parameters that can be explained by specific patient-specific covariates [45]. It is furthermore helpful that because many HDTs involve repurposed drugs, often PK models are available already to characterize their PK [46,47].

Immunodynamics

Models describing the key immune response components, such as dynamics of macrophage counts, cytokines, and $CD4^+$ and $CD8^+$ lymphocytes are essential for QSP models to study HDTs. Systems biology models describing the host–Mtb interactions within the lungs [48] have been previously developed, and later linked with lymphatics [49] and blood circulations [50]. The states included in these models were resting, activated, and infected macrophages, cytokines, such as IFN-γ, IL-10, and IL-12, dendritic cells, $CD4^+$ lymphocytes, and intra- and extracellular Mtb. The key feature of this model was the contributions of various immune components on intra- and extracellular Mtb. The above-developed model was later expanded to include $CD8^+$ cell dynamics in lungs [51]. The parameters in these models were identified from published human-derived or NHP experiments or model fitting to experimental data. These models can be expanded to include key drug targets involved in Mtb HDTs and their downstream effects on functional immune response changes and the quantitative interaction with Mtb.

There are currently no mathematical models available in the literature describing HDT-relevant pathways, such as autophagy in Mtb infections; however, components and parameter estimates from single cell systems biology models [52] can be adapted and extended using experimental data. For example, an HDT model containing key biological features of autophagy [52], including HDAC1-related components (Figure 1), may be developed. The model parameters can be informed using prior data available in the literature [52] and data from *in vitro* experiments [23]. The model may describe dynamics of the phagocytic cells and zebrafish infection with Mm load overtime in HDAC1-inhibitor-exposed macrophage cell cultures as compared to controls to estimate the parameters relevant to the effect of HDAC1. The simulations from the models may be compared with the experimental outcomes; preferably from different experimental conditions than the original experiments used for parameter estimation. This allows validation of the model structure and parameter estimates. In the above example, the simulations may be validated against data from zebrafish exposed to HDAC1 inhibitors (at various HDAC1 levels) experiments [23]. If multiple targets are affected by certain drugs, that is, ATK inhibitors (Figure 1), all relevant mechanisms must be captured in such models.

Pathogen dynamics

Models for the dynamics of pathogens include the effect of antibiotic drug on the growth and elimination of Mtb and emergence of treatment resistance. *In vitro* and *in vivo* infection studies

have enabled our understanding of parameters of Mtb growth rates [12], bactericidal and bacteriostatic effects of conventional anti-TB drugs [36], and resistance rates of bacteria [12]. The incorporation of immune cell effects on pathogen killing is a key required step to study the effects of HDTs on Mtb treatment. Published host–Mtb interaction models [49] can be updated to include contributions of key HDT components on pathogen killing, as well as pathogen evasion mechanisms. For example, an autophagy model may contain the quantitative relationship between bacterial load, mTOR, and autophagy. This will allow evaluations and predictions of various mTOR inhibitors on Mtb clearance by autophagy.

Applications of the QSP modelling framework

QSP modelling has successfully influenced decision making at different stages, starting from discovery to late phase in various therapeutic areas [53], and offered potential for the challenges faced in translation and design of HDT strategies against Mtb [66] (Figure 3).

Target identification, drug discovery, and drug repurposing

QSP models integrate various host–pathogen interactions and drug PK/PD components; therefore, they can readily provide assessment of target engagement upon stimulation or inhibition of certain targets at various doses and affinities. This allows evaluations of the iterative process of hypotheses generation, designing new experiments, hypotheses validation, and/or generation of new hypotheses. This approach can be applied to evaluate known HDT targets and molecules, to discover new HDT targets, and to discover new HDT molecules. With advances in technologies, applications of combining quantitative modelling and machine learning approaches are being evaluated to screen new virtual drug compounds with optimal characteristics [54]. For example, different ADME properties for a set of virtual compounds were used in a PBPK model combined with tumour dynamics model to simulate tumour size. Machine learning algorithms were then applied to the simulated dataset to identify the combination of ideal drug properties to provide desired outcome. This information may then be applied for lead prioritisation [54]. Similar approaches can be applied to repurpose or reposition already marketed drugs using large scale drug–target interactions data [55]. Advanced target screening techniques, that is, CRISPR-Cas9, can be also considered in combination with QSP models for HDT drug discovery and development in future.

Translational predictions

With increased complexity and innovation in design of new drugs within the last two decades, mechanistic models are increasingly being applied to inform translation of the results across different experimental conditions and species. The systematic incorporation of system-specific parameters not only for various species, but also incorporation of differences between *in vitro* systems and *in vivo* models, is crucial to enable translation towards clinical HDT treatment designs [39]. In some cases, that is, for scaling from HFIM to humans, such scaling is well studied [36], while further studies are needed for the host's immune response components [56]. Consolidating immune-relevant differences between preclinical models and humans [56] may be challenging and resource intensive, as there may be varying strains of models used across different experiments depending on the objectives of the experiments. The shown evolutionary conservation of the metabolic responses to mycobacterial infection in human patients, mice, and zebrafish shows that basic disease symptoms such as wasting syndrome are not dependent on species or varying strains [57]. Gene expression analysis data across species may be used to inform parameters of expressions of genes responsible for certain immune functions [58]. Such expression data studies can be used to predict metabolism using whole-genome metabolic network theoretical modelling approach in various organisms [59]. Factors such as severity of infection and sensitivity of drugs to bacterial strains (i.e., Mtb vs Mm) may also be applied within the QSP framework.

Variability and precision medicine

The presentation and severity of TB is variable among patients, and thus treatment responses, especially to HDTs, are variable. Many factors such as age, sex, genotypes, and comorbid conditions play a role in determining the outcome of the disease and treatment. PopPK models have evaluated these factors' impact on variability in PK/PD of antibiotics [60], and can be included in QSP simulations. For example, known differences in PK and immune-response components for HIV coinfected TB patients may be incorporated in the framework, enabling extrapolation of results from studies in TB patients to HIV–TB patients [61]. In addition, considering immune-response relevant endotypes is important [62,63]. Technological advances within the last century enabled generation of large-scale omics data. These data may enable us to better understand the interindividual variations associated with the parameters of the QSP models. For example, parameters, together with interindividual variations, describing the expression of baseline state of immune response components within lymph nodes and blood were estimated using data from a flow cytometry analysis of blood leukocytes and genome-wide DNA genotyping from humans [64]. Gene expression analysis of omics datasets from TB patients enabled stratification of the patients into two groups. One of the two groups was characterised by increased gene activity score for inflammatory response and decreased gene activity score for metabolism-relevant pathways, and patients in this group showed slower time to negative TB culture conversion and poor clinical outcome [62,63]. Similarly, gene expression data can be used to include variability in the QSP models and inform outcome of certain HDT treatment.

Selection of optimal dosing regimens and combination therapies

QSP models are well-suited to efficiently evaluate combination therapies and dosing schedules, which is important to combination treatment strategies of HDTs and classical antibiotics against Mtb. In the field of immuno-oncology, such QSP models have been widely applied to design optimal combination treatments of immune-targeting agents [65]. In the TB disease space, a QSP modelling approach for conventional antibiotic Mtb therapy has recently been applied to predict patient outcome with intensive dosing regimen and to explore shorter treatment duration scenarios [12].

Concluding remarks and future perspectives

HDTs offer a unique treatment strategy to combat Mtb infections but are challenged by complex and multiscale interactions between drug, host, and pathogen. Several key mechanisms are of interest to be exploited as HDTs but are facing challenges in translation towards clinically effective treatment strategies. The combined use of innovative experimental infection models with QSP modelling approaches can address these translational challenges and accelerate the design of novel HDT (combination) treatment strategies towards patients. QSP models supporting HDT design include model components describing biological system specific host-specific immunodynamics, pathogen dynamics, and drug-specific models for PK and PK/PD for compounds of interest. Design of QSP models for HDTs relies on the availability of detailed mechanistic knowledge of relevant immunological and pharmacological aspects related to drug–host–pathogen interactions of Mtb infection, with significant knowledge gaps still present. Future work should focus on filling these knowledge gaps, which will require close and prospective coordination with such investigational efforts ensuring the correct data will be collected (see Outstanding questions).

Outstanding questions

How can we best leverage advanced quantitative methods, such as QSP modelling, bioinformatics, and artificial intelligence, including machine learning, in TB research, drug discovery, and development?

Can we identify opportunities for collaboration amongst researchers to enable collection and sharing of relevant data for development of QSP models to guide design of HDTs for treatment of TB?

Can we apply quantitative approaches to guide design of experiments and clinical studies to collect the large body of data required to validate QSP models to further guide and personalize treatment of TB patients?

Can we utilize QSP models combined with patient-level data, including multiomics data, to understand factors affecting heterogeneity of response to HDTs amongst TB patients?

Declaration of interest

No interests are declared.

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