



New drug candidates and therapeutic targets for tuberculosis therapy

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Despite advances in chemotherapy and the BCG (*Bacillus Calmette–Guérin*) vaccine, tuberculosis remains a significant infectious disease. Although it can be cured, the therapy takes at least 6–9 months, and the laborious and lengthy treatment brings with it dangers of noncompliance, significant toxicity and drug resistance. The increasing emergence of drug resistance and the problem of mycobacterial persistence highlight the need to develop novel TB drugs that are active against drug resistant bacteria but, more importantly, kill persistent bacteria and shorten the length of treatment. Recent new and exciting developments in tuberculosis drug discovery show good promise of a possible revolution in the chemotherapy of tuberculosis.

Mycobacterium tuberculosis, the causative agent of tuberculosis (TB), is a tenacious and remarkably successful pathogen that has latently infected a third of the world population. Each year there are eight million new TB cases and two million deaths (<http://w3.who.sea.org/tb/dots.htm>). The increasing emergence of drug resistant TB, and HIV infection, which compromises host defense and allows latent infection to reactivate or render individuals more susceptible to TB, pose further challenges for effective control of the disease [1,2]. Although TB can be cured with chemotherapy, the treatment is exceedingly lengthy and takes 6–9 months [3]. Apart from significant toxicity, the lengthy therapy also creates poor patient compliance, which is a frequent cause for selection of drug resistant and often deadly multidrug resistant TB (MDR-TB) bacteria. Currently, TB chemotherapy is made up of a cocktail of first-line drugs (Figure 1), isoniazid (INH), rifampin (RIF), pyrazinamide (PZA) and ethambutol (EMB), given for six months [3]. If the treatment fails as a result of bacterial drug resistance, or intolerance to one or more drugs, second-line drugs are used, such as para-aminosalicylate (PAS), kanamycin, fluoroquinolones, capreomycin, ethionamide and cycloserine, that are generally either less effective or more toxic with serious side effects [3]. Treatment is made quite difficult by the presence of metabolically silent, persistent or dormant bacteria within host lesions, which are not susceptible to the

antimycobacterial drugs that usually kill growing bacteria but not persistent bacteria [4]. During the interaction between mycobacteria and host cells, a cyclic reinfection of host macrophages by tubercle bacillus can occur, allowing for the prolonged survival and persistence of the bacilli [5]. Thus, it is almost impossible to achieve complete sterilization of lesions. It is this unique ability of the bacilli to withstand chemotherapeutic and host immune attack and to survive for decades before reactivation that makes tuberculosis so difficult to treat and eradicate. Due to the heterogeneous bacterial populations in the tuberculous lesions and perhaps also to insufficient host immunity, treatment with a combination of drugs must be given for extended periods of time to prevent reactivation of disease by persisting bacilli. Much research effort focuses on understanding the biology of persistence and developing therapies that kill persistent bacilli more efficiently [4].

The increasing problem of MDR-TB has focused attention on developing new drugs that are not only active against drug resistant TB, but also shorten the lengthy therapy [5–7]. There is urgent need and significant interest in developing new TB drugs [5–7]; however, no new class of TB drugs has been developed in the past 40 years. In developing new TB drugs, it is crucial to think about which targets in the tubercle bacillus are good drug targets. Several recent reviews on this topic are already available [7–11]. This review will provide a brief update on the most recent developments in current TB drug discovery efforts.

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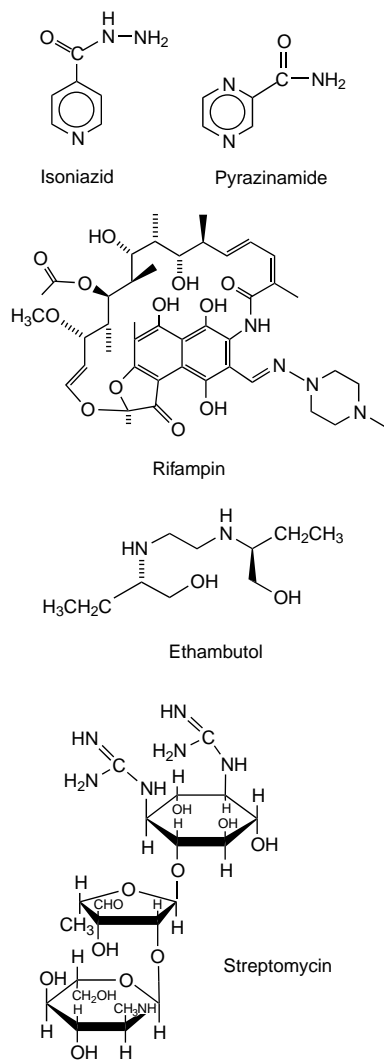


FIGURE 1
Structures of frontline TB drugs.

Promising new drug candidates

Some promising TB drug candidates are described in the following paragraphs. Their structures are shown in Figure 2.

Diarylquinoline

The recent discovery of diarylquinoline as a promising TB drug that can shorten therapy [12] has caused a lot of excitement. Andries *et al.* [12] identified diarylquinoline compounds that are highly active against mycobacteria in an *in vitro* drug screen using fast-growing *Mycobacterium smegmatis*. Modification of the diarylquinolines led to the identification of diarylquinoline R207910 (J compound) as the most active agent, with minimum inhibitory concentration (MIC) of 0.003 $\mu\text{g/ml}$ for *M. smegmatis* and 0.030 $\mu\text{g/ml}$ *M. tuberculosis*. J compound is much less active against other bacterial species, such as *Escherichia coli* and *Staphylococcus aureus* (MIC >32 $\mu\text{g/ml}$). *M. tuberculosis* and *M. smegmatis* could develop resistance to diarylquinoline at a frequency of 1×10^{-7} to 1×10^{-8} . Diarylquinoline resistant *M. smegmatis* and *M. tuberculosis* strains were found to harbor mutations in the subunit c encoded by *atpE*

(D32V for *M. smegmatis* and A63P for *M. tuberculosis*) in the FO moiety of mycobacterial F1FO proton ATP synthase, which is a key enzyme for ATP synthesis and membrane-potential generation. Complementation studies confirmed that the mutations in *atpE* are responsible for resistance to diarylquinoline. The target for diarylquinoline was proposed to be the mycobacterial F1FO proton ATP synthase [12], which is a new drug target in mycobacteria. Indeed, the J compound is also active against MDR-TB strains. Based on transposon mutagenesis analysis, F1FO ATP synthase seems to be an essential enzyme in *M. tuberculosis* [13], although the enzyme is not essential for *E. coli* because mutants of F1FO were viable but grew at a reduced rate and were attenuated for virulence in mice [14]. The J compound was more active than INH and RIF in the mouse model [12] and could shorten TB therapy from four months to two months in mice with established infection [12]. Of particular interest is the synergy between diarylquinoline and PZA, which seems to be the most effective drug combination in sterilizing infected spleens and lungs [12]. This finding is consistent with the previous observation that *N,N*-dicyclohexylcarbodiimide (DCCD) – which also inhibits the same c chain of the FO moiety of F1FO ATPase as diarylquinoline – has synergy with PZA against *M. tuberculosis* [15]. Thus, the observed synergy of diarylquinoline with PZA [12] could be explained in the same way as the synergy of DCCD with PZA [15]. The J compound had excellent early and late bactericidal activity, good pharmacokinetic and pharmacodynamic properties with a long half life, absence of significant toxicity in mouse and preliminary human safety testing, raising the hope that diarylquinoline might be used for shortening TB therapy in humans [12]. However, there are several unusual features of the J compound that require further explanation. First, antimycobacterial drugs usually do not show the same degree of activity against fast and slow growing mycobacteria. Drugs like INH, RIF, and PZA are more active against slow growing *M. tuberculosis* but less active against fast growers like *M. smegmatis*, which has higher efflux activity and is better able to maintain its energy status compared with *M. tuberculosis* [16,17]. However, in this case, diarylquinolines are even more active against fast growing *M. smegmatis* than against *M. tuberculosis* [12], which is quite unusual. Second, the high early and late bactericidal activity in mice is unusual because other TB drugs show either early or late sterilizing activity but not both. Third, the selective activity of diarylquinolines against the mycobacterial enzyme F1FO ATPase (present in all mycobacteria, but also in host cell mitochondria) without apparent toxicity is quite remarkable. Fourth, mycobacteria would be expected to have alternative means, such as the electron transport chain, to produce energy or ATP without F1FO ATPase, and thus the inhibition of F1FO ATPase by diarylquinoline would not be lethal unless the J compound also interferes with other drug targets in the mycobacteria. The J compound is currently under clinical testing. It remains to be seen whether diarylquinoline can be used as a new TB drug for more effective treatment of TB in humans.

New fluoroquinolones

Fluoroquinolones are broad-spectrum antibiotics currently used as second-line drugs in tuberculosis therapy or as stand-ins for drugs made unfeasible by drug resistance. The new C-8-methoxy-FQ moxifloxacin (MXF) and gatifloxacin (GATI) have a longer half life and are more active against *M. tuberculosis* than ofloxacin and

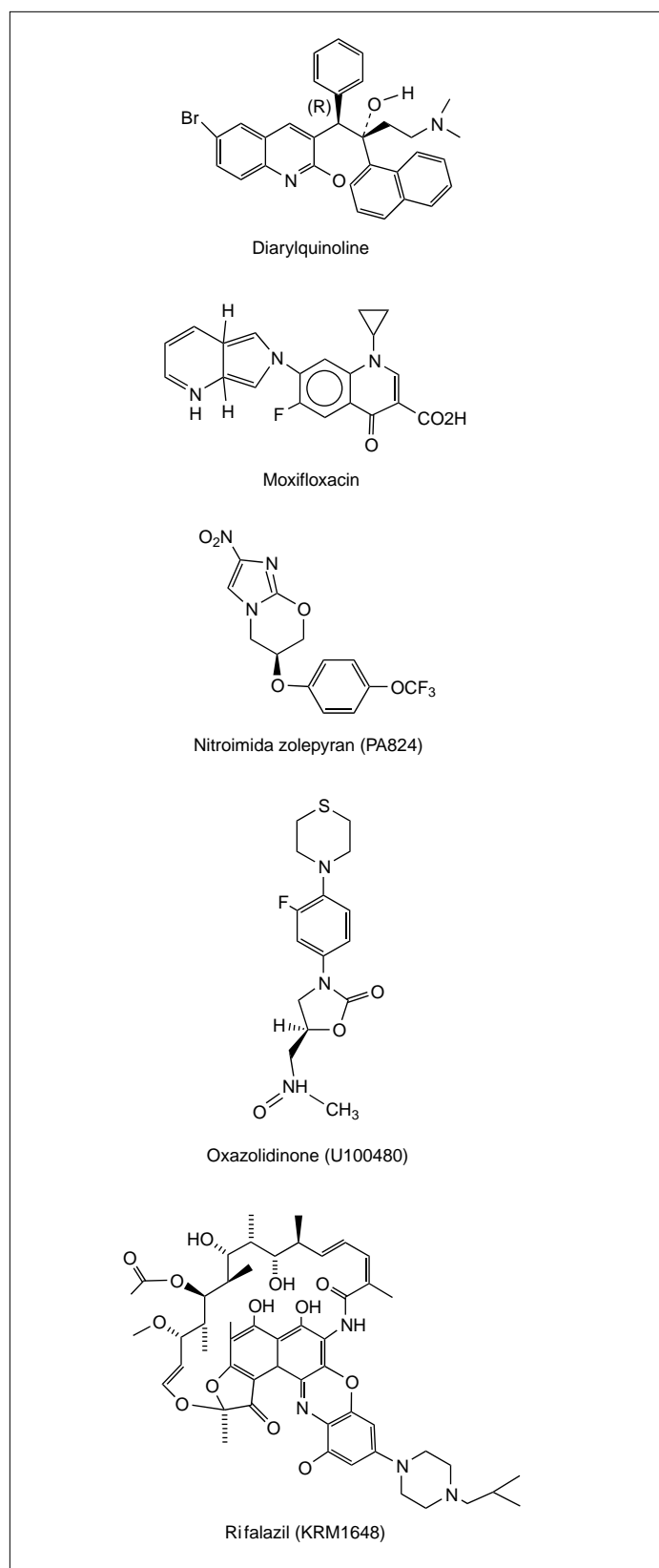


FIGURE 2
Structures of some promising TB drug candidates.

ciprofloxacin [18–20]. MXF has been shown to kill a subpopulation of tubercle bacilli not killed by RIF [21]. In a mouse model, MXF was as active against *M. tuberculosis* as INH [18–20]. MXF in

combination with RIF and PZA killed tubercle bacilli in mice more effectively than the standard regimen of INH+RIF+PZA [22] and could achieve stable cure in 4 months with no relapse [23]. These promising studies raise the hope that MXF might replace INH+RIF+PZA to shorten TB therapy in humans. MXF has early bactericidal activity against tubercle bacilli comparable to INH and was shown to be well tolerated in a preliminary human study [24]. Combination therapy with MXF seems to be as effective as current standard drug combinations [25]. MXF and GATI are currently being evaluated in clinical trials in combination with RIF and PZA (R. Chaisson, personal communication). Both agents could have the potential to be used as first-line drugs for improved treatment of TB.

Rifamycin derivatives

Rifamycin derivatives, such as rifapentine, rifabutin and rifalazil (RLZ, also known as KRM1648 or benzoxazinorifamycin), have been synthesized to improve antimycobacterial activity and prolong half life. Rifapentine was approved by the FDA in 1998 for the treatment of TB. Rifapentine appears to be safe and well-tolerated at once-weekly dosing and is currently being evaluated in Phase III efficacy trials for treatment of latent tuberculosis [26]. RLZ is a new semisynthetic rifamycin derivative with a long half life, which is highly active against a range of intracellular bacteria including *M. tuberculosis*, *Mycobacterium avium*, *Chlamydia trachomatis*, *Chlamydia pneumoniae*, and *Helicobacter pylori* [27]. RLZ is more active than RIF or rifabutin against *M. tuberculosis* in mice both *in vitro* and *in vivo* [28]. RIF-resistant strains confer cross-resistance to all rifamycins, including RLZ [29], limiting the use of RLZ in the treatment of RIF-resistant TB. A preliminary safety study in humans showed that although RLZ at doses of 10 mg and 25 mg was safe, a dose of >100 mg produced flu-like symptoms and a transient dose-dependent decrease in white blood cell and platelet counts, and did not show better efficacy than RIF [30]. However, no information is available for clinical trial of RLZ for the treatment of mycobacterial infections.

Oxazolidinones

Oxazolidinones, discovered at DuPont in the 1970s and later sold to Pharmacia Upjohn, are a new class of compounds that are active against a variety of Gram-positive bacteria, including *M. tuberculosis*. Oxazolidinones inhibit protein synthesis at an early stage by binding to 23S rRNA of the 50S ribosomal subunit [31]. Oxazolidinones had significant activity against *M. tuberculosis* with an MIC of 2–4 $\mu\text{g/ml}$ and were also active against tubercle bacilli in mice [32–34]. Sbardella *et al.* [35] recently demonstrated the antimycobacterial activity of 3-(1H-pyrrol-1-yl)-2-oxazolidinone. Two novel oxazolidinones, RBx7644 and RBx8700, were active against MDR-TB and tubercle bacilli inside macrophages [36]. Linezolid is the first oxazolidinone to be developed and approved by the FDA to treat single- or multiple-resistant Gram-positive bacterial infections [31]. In two recent clinical studies, most MDR-TB patients were successfully treated with linezolid in combination with other drugs [37,38], but prolonged use of linezolid in the treatment of MDR-TB frequently caused significant toxicity, including anemia and peripheral neuropathy [37,38]. Although oxazolidinones have promising potential for the treatment of MDR-TB, more extensive clinical studies are needed to evaluate their efficacy and toxicity, as well as the degree of resistance development by mycobacteria.

TABLE 1

Current tuberculosis drugs and their targets

Drugs	MIC ($\mu\text{g/ml}$)	Mechanisms of action	Targets	Genes involved in resistance ^a
Isoniazid	0.01–0.20	Inhibition of cell wall mycolic acid synthesis	Enoyl acyl carrier protein reductase (InhA)	<i>katG, inhA</i>
Rifampin	0.05–0.50	Inhibition of RNA synthesis	RNA polymerase, β subunit	<i>rpoB</i>
Pyrazinamide	20–100 (pH 5.5 or 6.0)	Depletion of membrane energy	Membrane energy metabolism	<i>pncA</i>
Ethambutol	1–5	Inhibition of cell wall arabinogalactan synthesis	Arabinosyl transferase	<i>embCAB</i>
Streptomycin	2–8	Inhibition of protein synthesis	Ribosomal S12 protein and 16S rRNA	<i>rpsL, rrs</i>
Kanamycin	1–8	Inhibition of protein synthesis	16S rRNA	<i>rrs</i>
Capreomycin	4	Inhibition of protein synthesis	16S rRNA, 50S ribosome, rRNA methyltransferase (TlyA)	<i>rrs, tlyA^b</i>
Fluoroquinolones	0.2–4.0	Inhibition of DNA synthesis	DNA gyrase	<i>gyrA, gyrB</i>
Ethionamide	0.6–2.5	Inhibition of mycolic acid synthesis	Acyl carrier protein reductase (InhA)	<i>inhA, etaA/ethA</i>
PAS	1–8	Inhibition of folate pathway and mycobactin synthesis?	thymidylate synthase (ThyA)?	<i>thyA^c</i>

^aKatG, PncA, EtaA/EthA are enzymes involved in the activation of the prodrugs isoniazid, pyrazinamide and ethionamide, respectively.

^bData from Ref. [74].

^cData from Ref. [75].

Nitroimidazopyran PA824

A particularly promising candidate for TB treatment is nitroimidazopyran PA824, derived from 5-nitroimidazoles. PA824 is highly active with MIC as low as 0.015–0.250 $\mu\text{g/ml}$ against *M. tuberculosis* and MDR-TB [39]. PA824 is a prodrug that requires activation by a bacterial F420-dependent glucose-6-phosphate dehydrogenase (Fgd) and nitroreductase to activate components that then inhibit bacterial mycolic acid and protein synthesis [39]. However, the active moiety of activated PA824 remains to be identified. In complementation experiments in F420-negative mutants resistant to the drug, Fgd could restore drug sensitivity in *M. tuberculosis* and *Mycobacterium bovis* [40]. In animal models, PA824 was active against nongrowing bacilli even in microaerophilic conditions (which might have some sterilizing action for nongrowing persistent bacilli in the anaerobic environment of granulomas) and its activity is comparable to INH, RIF and moxifloxacin [39,41,42]. PA824 had bactericidal activity in the mouse model in the initial two months of treatment and also in the continuation phase of treatment, which indicates significant activity against nongrowing persistent bacilli *in vivo* [43]. Additional studies are needed to evaluate PA824 in terms of its ability to shorten TB therapy in combination with other drugs without significant relapse, drug resistance or toxicity. PA824 is currently being evaluated in clinical trials by the Global Alliance for TB Drug Development.

Other drug candidates

Drugs used for treatment of other diseases, such as antifungal azoles [44,45], phenothiazines (chlorpromazine and thioridazine) [46] and riminophenazine derivatives like clofazimine [47,48], have good antituberculosis activity and could be candidates for further evaluation for the treatment of TB [7]. The ethambutol (EMB) analog SQ109, a novel 1,2-diamine [49], has good activity against *M. tuberculosis* with MIC of 0.5 $\mu\text{g/ml}$ versus its parent EMB with MIC of 5.0 $\mu\text{g/ml}$ [50]. SQ109 is also more active against *M. tuberculosis* in macrophages and in mice than EMB, but is less active than

INH [50]. It is likely that the new EMB analogs have a different mechanism of action to EMB, which inhibits biosynthesis of the cell wall arabinogalactan. SQ109 has promising *in vitro* and *in vivo* antituberculosis activity [51] but data from clinical studies are not yet available. The peptide deformylase inhibitor BB3497 is active against *M. tuberculosis* with MIC of 0.06–2.00 $\mu\text{g/ml}$ [52] and could have potential as a new drug for the treatment of TB. Pyrrole LL3538 is a potential TB drug in preclinical development by Lupin [53].

Novel drug targets

Desirable targets should be involved in vital aspects of bacterial growth, metabolism and viability, whose inactivation will lead to bacterial death or inability to persist. The availability of the *M. tuberculosis* genome sequence [54] and mycobacterial genetic tools, such as transposon mutagenesis, gene knockout and gene transfer, greatly facilitate target identification. Moreover, targets involved in the pathogenesis of the disease process should also be considered for drug development. For example, liquefaction from solid necrotic lesion to cavity formation is a key step in the spread of infection to other individuals [55–57]. If the liquefaction and cavity formation could be interrupted, the bacilli in the lesion would not be coughed up and spread to others. Thus, inhibition of host liquefaction process represents a novel approach to the design of new drugs that stop the transmission of the disease [55–57].

It is increasingly acknowledged that new drugs should not only be active against drug resistant TB, but should also kill persisters and shorten the lengthy TB treatment, which underlies the problem of drug resistance due to poor compliance to the length of therapy [7,8]. Current TB drugs inhibit particular targets in DNA synthesis, RNA synthesis, cell wall synthesis and energy metabolism pathways (Table 1) [7]. Enzymes in these metabolic pathways that are not inhibited by current TB drugs could also be good targets. Mycobacterial two-component systems, sigma factors and virulence factors have also been proposed as targets for TB drug

development [7] and will not be detailed here. Novel drug targets for which new drugs can be developed are discussed below.

Essential genes

Transposon mutagenesis and signature-tagged mutagenesis have been used to identify genes essential for *M. tuberculosis* growth *in vitro* [57,58] and survival *in vivo* [59,60]. In a recent study, 614 genes, about one-sixth of the total number of genes in *M. tuberculosis*, were found to be essential for *in vitro* growth [58], whereas 194 genes were demonstrated to be essential for *in vivo* survival in mice [59]. The genes that are essential for survival *in vitro* and *in vivo* are grouped into the following categories [57–60]: lipid metabolism; carbohydrate and amino acid transport and metabolism; inorganic ion transport and metabolism; nucleotide transport and metabolism; energy production and conversion; secretion; cell envelope biogenesis; cell division; DNA replication; recombination and repair; transcription and translation; post-translational modification; chaperones; coenzyme metabolism; and signal transduction. However, the function of a significant number of essential genes is unknown [57–60]. Besides systematic analysis of essential genes by transposon mutagenesis, targeted knockout of specific genes is also a valuable approach to identifying essential genes, in other words, those whose disruption leads to nonviability of the bacilli. These essential mycobacterial genes should be good targets for TB drug development.

Persistence targets

Mycobacterial persistence refers to the ability of tubercle bacillus to survive in the face of chemotherapy and/or immunity [61]. The nature of the persistent bacteria is unclear but might consist of stationary phase bacteria, post-chemotherapy residual survivors and/or dormant bacteria that do not form colonies upon plating [4]. The presence of such persistent bacteria is considered to be the major reason for lengthy therapy [5–8]. A lot of research activity is currently aimed at understanding the biology of persistence of the tubercle bacillus and developing new drugs that target the persisters [5–8]. Gene products involved in mycobacterial persistence, such as isocitrate lyase (ICL) [62], PcaA (methyl transferase involved in the modification of mycolic acid) [63], RelA (ppGpp synthase) [64], and DosR (controlling a 48-gene regulon involved in mycobacterial survival under hypoxic conditions) [65], have been identified and could be good targets for the development of drugs that target persistent bacilli.

Toxin–antitoxin modules

Studies – primarily in *E. coli* – have identified toxin and antitoxin pairs (called TA modules), such as MazEF, HigAB, ParDE, Phd/Doc, RelBE, VapBC, that are involved in bacterial cell death and persistence [66]. Inappropriate or uncontrolled expression of the toxin or a decrease in the expression of antitoxin can cause bacterial cell death. In *E. coli*, some antibiotics (e.g. rifampin, chloramphenicol and spectinomycin) that inhibit transcription and translation, respectively, and also sulfa drugs that cause thymine starvation, kill bacteria by inducing the toxin MazF [67]. It is interesting to note that the *M. tuberculosis* genome has recently been found to contain at least 38 TA modules including three *relBE* and nine *mazEF* loci [66]. The TA modules are attractive targets in *M. tuberculosis* for designing drugs that either induce the production of the toxin or inhibit the expression of the antitoxin.

Energy production pathways

All bacteria require energy to remain viable. Although the energy production pathways in *M. tuberculosis* are not well characterized, their importance as drug targets is demonstrated by the recent finding that PZA (a frontline TB drug that is more active against nongrowing persistent bacilli than growing bacilli and shortens TB therapy) acts by disrupting membrane potential and depleting energy in *M. tuberculosis* [15]. This study implies that energy production or maintenance is important for the viability of persistent nongrowing tubercle bacilli *in vivo*. The recent discovery of the highly effective TB drug diarylquinoline also highlights the importance of energy production pathways for mycobacteria. It is likely that energy production pathways, such as the electron transport chain, glycolytic pathways (like the Embden–Meyerhof pathway) and fermentation pathways, could be good targets for TB drug development.

Novel approaches in drug discovery

Besides the choice of drug targets, there are many different approaches one should consider and use in TB drug development. One is the way drug screens are designed. Current TB drugs were mostly discovered based on their activity against growing bacilli *in vitro*, with the exception of PZA. However, activity against nongrowing persisters is correlated with good sterilizing activity that is responsible for shortening therapy *in vivo*, as shown by PZA and RIF. Thus, novel drug screens that mimic *in vivo* conditions in lesions (i.e. acidic pH and hypoxia) [7] and act against old stationary-phase nongrowing bacilli [8] could be important for identifying drugs that kill persisters and thereby shortening TB treatment. In addition, drug combination screens could be performed to identify drugs that have synergistic effects. For example, it would be of interest to identify agents that synergize with PZA or RIF and improve the activity of these TB drugs. Along this line of combination screen is the recent interest in the use of systems biology approach for drug discovery [68,69]. Instead of the conventional reductionist approach of finding a single drug that hits a single target, the systems biology approach proposes using multiple compounds that hit multiple targets in different pathways to achieve the desired outcome. A systems biology approach can be used for identifying novel drug combinations against TB. Another approach is to make use of the growing knowledge of the unique physiological characteristics of the tubercle bacillus for drug design or screening, for example, the deficient efflux for pyrazinonic acid and other weak acids [7]. Microarray technology can have a role in identifying potential drug targets such as those relevant to persistence of mycobacteria.

Conclusion

Drug resistant TB and the HIV pandemic present major challenges for the effective control of TB. The TB drugs currently in use were developed 40 years ago and there is a great need for a new generation of TB drugs. Current research involves testing new or reformulated drugs, combinations of different drugs to shorten therapy, supplementation and enhancement of existing drugs, development of novel slow-release drug delivery systems that could reduce the frequency and amount of drug necessary during treatment [70], and research into molecular targets. The goal is to find better and more effective drugs that reduce time of treatment, reduce toxicity associated with drugs and provide backup measures in case of drug

resistance. The approaches include: chemical modification of existing drugs (such as rifampin, fluoroquinolones and macrolides) [53]; the identification of drug targets (such as persistence genes) using microarray analysis and molecular biology tools; structure-based drug design and *in vitro* and *in vivo* screening to identify new drugs; evaluation of novel drug combinations; and the order of drugs given in treatment. There are currently a number of drug candidates that are being investigated in the laboratory and in clinical trials that show high antituberculosis potential [52], the most promising are diarylquinoline [12] and PA824 [39] because of their high activity against *M. tuberculosis* and the potential to shorten therapy. Besides chemotherapy, immunotherapeutic approaches such as DNA vaccines [71,72] and cytokines used in combination with chemotherapy also offer some promising prospect for improved treatment of TB [73].

In searching for novel drug targets, more research must go into understanding the biology of persistence, the factors involved in tissue liquefaction and cavity formation, and the host immune mechanisms that control latent infection. The outcome of such

research will not only provide improved understanding of the disease, but also new relevant biology-based targets for drug intervention. This is a battle that might not be easily won, but given persistent effort and sustained support, it is quite likely that the current endeavors will bear fruit and lead to more effective treatment. After years of neglect, the field of TB drug discovery is finally gaining momentum thanks to the persistence of many dedicated individuals and the establishment of The Global Alliance for TB Drug Development (www.tballiance.org) and the support of The Gates Foundation. The race to develop new and more effective TB drugs is on. With several promising drug candidates in the pipeline [53], there is a fair amount of excitement and even optimism in the field. It is hoped that new more effective TB drugs will be discovered in the not-too-distant future that could shorten the therapy from six months to a few weeks and improve control of TB worldwide.

Acknowledgements

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