Antimicrobial resistance (AMR) threats are typically represented by bacteria capable of extensive horizontal gene transfer (HGT). One clear exception is Mycobacterium tuberculosis (Mtb). It is an obligate human pathogen with limited genetic diversity and a low mutation rate which lacks any evidence for HGT. Such features should, in principle, reduce its ability to rapidly evolve AMR. We identify key features in its biology and epidemiology that allow it to overcome its low adaptive potential. We focus in particular on its innate resistance to drugs, its unusual life cycle, including an often extensive latent phase, and its ability to shelter from exposure to antimicrobial drugs within cavities it induces in the lungs.

So Special
The rapid increase of antimicrobial resistance (AMR; see Glossary) in bacteria is driven by the widespread use, abuse, and misuse of antibiotics, and constitutes one of the most challenging healthcare problems globally. With the notable exception of Mtb, the agent of tuberculosis (TB), all other bacterial species listed as current AMR threats by the Centers for Disease Control (http://www.cdc.gov/drugresistance/pdf/ar-threats-2013-508.pdf) frequently exchange genetic material and frequently acquire novel mutations through the gain of new genes by HGT rather than de novo mutations (Figure 1). Mtb has a virtually nonexistent accessory genome, meaning that almost all genes are common to all strains. Evidence suggests that there is little or no recombination occurring in the species. In addition to its strictly clonal reproduction, Mtb is characterized by a low mutation rate and limited genetic diversity, which has led to it being considered as a ‘monomorphic bacterium’ [1]. Mtb also stands out from most other bacteria considered as AMR threats by being an obligate pathogen.

The lack of HGT, combined with a low mutation rate, makes Mtb an a priori unlikely resistance threat. Despite this, drug-resistant tuberculosis (TB) has become a major public health threat, leading to massive costs in human and economic terms.

Highly transmissible multiresistant Mtb strains have emerged following the use of the same antimicrobial compounds for over four decades. We conclude that, compared to other bacterial resistance threats, the strict reliance of Mtb on de novo chromosomal mutations has led to a relatively slow rate of emergence of AMR. However,
the proportion of resistant strains is increasing, and this trend is proving difficult to contain due to various public health failings, the intrinsic resistance of mycobacteria to a range of antibiotics, and life-style properties such as the ability of Mtb to hide in pulmonary cavities and lesions with limited drug penetrance.

**Roots Bloody Roots**

The genus *Mycobacterium* contains well over 100 recognized species and probably an equally large number of species yet to be discovered. The genetic diversity within described species varies significantly, and this discrepancy follows a simple rule: the more attention a group of mycobacteria has received, the more likely it has been split into multiple species. The genus comprises mainly environmental bacteria, but a number of these can cause opportunistic infections in humans (Figure 2). The more host-specialized members exhibit a clonal mode of inheritance, but recombination is frequent in the genus as a whole.

A comparative analysis including 13 mycobacterial species found only sporadic evidence of recombination in core genes within mycobacteria, but genome content analyses suggest that horizontal acquisition of genes is frequent and played an important role in the evolution of this group [4]. The presence of numerous genomic islands dispersed across different mycobacterial...
species is also suggestive of extensive HGT from outside the genus [5]. A meiosis-like conjugational mechanism termed distributed conjugal transfer (DCT), controlled by a chromosomally encoded mating-identity locus, was recently discovered in Mycobacterium smegmatis [6]. This intriguing mechanism enables the transfer of large unlinked stretches of DNA across entire chromosomes. Genomic signatures indicative of DCT have subsequently been identified in Mycobacterium canettii, an environmental mycobacterium closely related to \textit{Mtb}, suggesting that this mode of HGT may play an important role in shaping the evolution of mycobacteria [7].

Mycobacteria are intrinsically resistant to a number of antimicrobial compounds, an observation that is often explained by the presence of an impermeable mycolic-acid-rich cell envelope. In addition, mycobacteria are members of the order Actinomycetales which also includes Streptomycetes species, well known for their ability to produce a wide range of antibiotics. Antibiotic-producing bacteria must have defence mechanisms in place to guard them against their own toxic compounds. The inducible \textit{whiB7} multidrug-resistance system common to all Actinomycetales has been shown to reduce susceptibility to a wide range of antimicrobials, including macrolides, chloramphenicol, tetracycline, and aminoglycosides [8]. In \textit{Mtb}, the regulon includes genes involved in drug efflux (\textit{tap}), a putative macrolide exporter (Rv1473), the ribosomal methyltransferase \textit{erm}, and the aminoglycoside acetyltransferase \textit{eis} [8].

\textit{Mtb} and closely related animal strains, together with the leprosy bacilli, are unusual insofar as they constitute specialized pathogens of humans and other mammals (Figure 2). In contrast to most other mycobacteria, these bacilli readily transmit between mammalian hosts, a hallmark of true pathogens [9]. Despite the general perception that leprosy is a disease of the past, nearly a quarter of a million cases are reported yearly [10]. The ruminant-infecting \textit{Mycobacterium avium} subsp. \textit{paratuberculosis} also deserves to be mentioned as a host-specialized pathogen. However, even though this subspecies can only grow intracellularly, it can survive for long periods in the environment and transmits via the faecal-oral route and possibly also via nematodes and protozoa [11].

**Upsizing and Downsizing**

Genome-level comparison of \textit{Mtb} and \textit{Mycobacterium marinum} revealed that \textit{Mtb} has also undergone a process of genome downsizing on its path from an environmental ancestor to a specialized, mainly intracellular pathogen [12], but on a far more moderate scale than the leprosy bacilli. The general downsizing has, however, also been accompanied by the acquisition of a number of genes, including genes involved in virulence [12]. There is strong evidence that recombination has been important in shaping the early evolution of \textit{Mtb} as it evolved from an ancestor closely related to present-day smooth tubercle bacilli (STB) [13]. A number of strains adapted to various mammalian hosts have evolved from \textit{Mtb}. Together with \textit{Mtb}, these animal strains have been grouped together in the so-called \textit{Mtb} complex (MTBC). The STB \textit{M. canettii} (not yet accepted as a valid species name) is also generally included in the MTBC, but evidence suggests that this species might be mainly environmental [14]. The human- and animal-adapted MTBC strains represent a clonal expansion rooted in the extensively recombining and genetically diverse STB. STB strains can cause TB in immunocompetent individuals, but they are significantly less virulent than \textit{Mtb} and they do not seem to transmit between humans [9,15]. They have only been isolated from sporadic human cases in East Africa, which has led to the suggestion that this region of the world is where the MTBC originated. The evolutionary history of the MTBC seems to be analogous to the clonal expansion of animal-adapted \textit{Mycobacterium avium} strains from a more diverse environmental group (Box 1).

No consensus has been reached to date on whether modern \textit{Mtb} has retained the ability to undergo recombination [16,17], but the sum of evidence suggests that recombination is exceedingly rare. It is plausible that some analyses pointing to relatively high rates of pathogens of humans and animals as well as the highly diverse, probably environmental, \textit{Mycobacterium canettii}.

**Rifampicin (RIF):** an antibiotic used to treat a number of bacterial infections. It constitutes one of the two first-line agents together with isoniazid (INH). It is on the World Health Organization’s List of Essential Medicines, the most important drugs needed in a functional basic public health system.

**Smooth tubercle bacilli (STB):** a group of mycobacteria found in Eastern sub-Saharan Africa and which are considered as the putative ancestors of \textit{Mycobacterium tuberculosis} (\textit{Mtb}). They include, in particular, the species \textit{M. canettii} that can cause TB but does not seem to transmit directly between human hosts.

**Tuberculosis (TB):** a bacterial infection caused by some species of the genus \textit{Mycobacterium}, the main agent being \textit{M. tuberculosis} (\textit{Mtb}). The infection generally resides in the lungs but can spread through the lymph nodes and bloodstream to any organ. Most people who are infected by \textit{Mtb} remain healthy and asymptomatic and do not transmit the bacterium to others.
recombination in *Mtb* had been misled by convergent evolution at a relatively high number of sites, many of which are likely due to multiple independent emergence of resistance mutations following exposure to antimicrobial compounds [18]. Indeed, both convergent parallel evolution and recombination lead to conflicts between loci over the best-supported topology of a phylogenetic tree.

**Distance Equals Rate Times Time**

Comparing mutation rates across bacterial species is challenging. Fluctuation assays [19], despite often being regarded as the gold standard, only allow estimating mutation rates if all
Box 1. You All Look the Same to Me

*Mycobacterium abscessus* is a rapidly growing environmental species but also a relatively common source of soft-tissue infections, disseminated infections in immunocompromised individuals, and pulmonary infection in cystic fibrosis patients. Treating *M. abscessus* infections with antimicrobials is challenging, as the group is intrinsically resistant to most available drugs [71]. The species harbors three subspecies, namely, abscessus, bolletii, and massiliense. The macrolide clarithromycin has been used frequently to treat infections, but the relatively recent discovery that nearly all abscessus and bolletii strains, but not massiliense, can induce resistance to the drug by activation of the erm(41) gene [72], encoding a ribosome methylase [73], highlights critical differences within this species complex and the need for improved taxonomic assignment tools for effective treatment. *Mycobacterium avium* is a species consisting of four main subspecies ranging from environmental to more specialized pathogens. *M. avium* subsp. *hominisuis*, an environmental species causing opportunistic infection in immune-compromised people, is a diverse group undergoing frequent recombination events. By contrast, the subspecies *silvaticum*, *avium*, and *paratuberculosis* represent clonal lineages radiating out of the *hominisuis* group that have adapted to various animal hosts [74] (see Figure 2 in main text).

*Mycobacterium ulcerans* falls somewhere in the middle of the spectrum between environmental and host-specialized mycobacteria. The bacterium can be considered as a semi-specialized pathogen mainly due to the acquisition of the pUMU plasmid by a *Mycobacterium marinum*-like ancestor [75]. The plasmid encodes the genes necessary for the synthesis of mycolactone, a polyketide-derived macrolide that serves both as a toxin, triggering tissue damage, and an immunomodulatory compound inhibiting the host immune response. Analogous to *Mtb* and the leprosy bacilli, *M. ulcerans* has undergone significant gene loss and contains 771 pseudogenes, in stark contrast to *M. marinum*, where only 65 inactivated genes have been identified [75]. This pseudogenization seems to have been partially driven by the expansion of insertion sequence IS2404 that was acquired after the split between *M. marinum* and *M. ulcerans*. Insertion sequences seem to have played important roles also in the host-adaptation of other pathogenic mycobacteria. *M. ulcerans* has been identified in a wide range of environments, including soil, water, frogs, fish, mosquitoes, water bugs, and mammals. However, the finding that mycolactone specifically inhibits T cell-controlling mammalian microRNAs [76], combined with a very close genetic relationship between *M. ulcerans* isolates in humans and opossums in southwest Australia [77], suggests that the bacterium has evolved to accommodate a mammalian niche.

Possible mutations yielding resistance to a given antimicrobial compound are known, which is generally not the case. Even when comparisons are restricted to experiments using the same antimicrobial compound, estimated mutation rates can vary due to variation in the number of mutations that can potentially bring about resistance in different species. Additionally, the same mutation could yield variable levels of resistance in different species

An alternative approach to estimate mutation rates relies on Bayesian phylogenetic analyses of whole-genome sequences from clinical isolates sampled over several years and for which isolation dates are precisely known. Such data are available for all the species illustrated in Figure 1, and mutation estimates from independent studies are highly congruent for *Mtb* [3,20,21]. In this comparison, *Mtb* has the lowest rate of all, with *Salmonella enterica* next on the list. This comparison is by no means perfect, due to the variation in sampling and methodology between studies. However, the approach offers the major advantage that such mutation rate estimates are scaled over unit time in natural conditions (rather than per generation). As such, these phylogenetic mutation rate estimates capture the capacity of different bacteria to adapt to antimicrobials in the wild. The generation time of *Mtb* is indisputably very long compared to that of the vast majority of clinically important bacteria. As a result, despite what seems to be a relatively unremarkable mutation rate per generation compared to, for example, *Escherichia coli* [22,23], *Mtb* evolves at a very slow pace compared to most other AMR threats.

Extrapolation of these short-term mutation rates to more ancient times points to a fairly recent origin for *Mtb* – less than 6000 years ago [24,25] – which is incompatible with scenarios of ancient origin and a joint colonization of the globe by *Mtb* and anatomically modern humans some 40 000–70 000 years ago that have been suggested [26,27]. These age estimates also fit somewhat uncomfortably with direct evidence for ancient MTBC infection from PCR and the detection of lipid biomarkers targeting the unusual and highly stable components of the cell wall [28]. These include the detection of TB in human remains from Syria some 11 000 years ago [29].
and in a bison from Wyoming dated to ~17 000 years ago [30]. Also of note is the detection of DNA harboring the Mtb-specific TbD1-deletion in a woman and child from Israel some 9000 years ago [31]. At this time, it seems fair to accept that the jury is still out on the age of Mtb, and additional ancient DNA genome sequences will be required to obtain better long-term calibration of mutation rates – the oldest Mtb genomes generated to date being only about 250 years old [25].

Coming Back to Life

Mtb has a very unusual life cycle with a long latency period. About 90% of infected people never develop active transmissible TB but stay healthy and asymptomatic [32], possibly because humans have adapted to control TB quite efficiently even though immune activation does not lead to sterilization. About two billion people are estimated to be latently infected with TB [33], constituting a massive challenge for TB eradication efforts. A 10-year follow-up study of TB contacts found that the majority of people that do develop active TB do so within the first 3 years of exposure [32]. However, old age is also known to be a risk factor for active TB [34].

If Mtb has coevolved with humans since the dawn of our species, or at least for millennia, a long latency period could be regarded as an adaptation to the small and isolated populations of our ancestors. This adaptation might have allowed Mtb to transmit between host generations as active TB developed in the elderly and was transmitted to the next generations, without burning through and killing off small and isolated bands of hunter-gatherers and thus extinguishing its population of hosts [35]. A plausible and worrisome scenario is that modern TB strains are evolving towards shorter latency periods. There are now more than seven billion humans on the planet, and potential human TB hosts frequently travel and migrate between countries and continents. As such, accelerated progression to active disease, and hence possible transmission, could be selected for. In this context, it is interesting to note that the Beijing TB lineage which has expanded globally in recent decades seems to be associated with accelerated progression to active TB relative to other TB strains and Mycobacterium africanum [36].

Space Oddity

Globally, 3.3% of new TB cases were estimated to be MDR in 2014 (http://www.who.int/tb/publications/global_report/en/). This relatively low rate might come as a surprise to many, and does conceal significant variation between and within countries and regions. In many western European countries the burden is low, as exemplified by the situation in the UK, where 1.6% of all cases were MDR-TB in 2013 (https://www.gov.uk/government/publications/tuberculosis-in-england-annual-report). This figure, in itself, does not capture the full extent of the problem as 7.1% of strains in the UK are INH resistant in the (Figure 3), which is unusually high for a western European country. Again, this figure for INH resistance only very imperfectly captures the reality on the ground. INH-resistant strains in the UK are found primarily in London and are patchily distributed even at that scale.

TB drug resistance in the UK and in other high-income countries is a serious public health issue incurring a significant financial burden on public health services, even though the rate of resistance is relatively low compared to some other bacteria (Figure 3). The extraordinarily rapid population-level response to antibiotics seen, for example, in Staphylococcus aureus and Enterococcus faecium is striking when compared to Mtb, and probably partly reflects its low mutation rate and lack of recombination and of resistance-determinants on mobile genetic elements (Figure 1). However, Mtb resistance rates in high-income countries are not representative of the frequency of MDR/XDR-TB strains in other parts of the world, and the burden due to AMR in TB resistance is crippling in some hotspots (Box 2 and Figure 4).
**Road to Resistance**

Although intrinsically resistant to many drugs, there is little evidence to suggest that the \textit{Mtb} genome should be especially prone to evolving additional drug resistance (Figure 1). In fact, rates of RIF resistance in \textit{Mycobacterium leprae}, which is not generally regarded as a major resistance threat, seem to mirror the rates found in \textit{Mtb}. The inability to culture \textit{M. leprae}, and thus to perform phenotypic drug susceptibility testing (DST), complicates analyses of resistance in this bacterium. However, available data from India, South-East Asia, and Colombia all indicated about 3% of all cases to be RIF resistant [37–39], a rate that is similar to recent estimates of \textit{Mtb} RIF resistance globally at 3.3% (http://www.who.int/tb/publications/global_report/en/).

The first outbreaks of MDR-TB were largely restricted to HIV coinfected patients and often confined to hospitals [40–42]. This can easily be explained by HIV infection triggering the development to active TB. To make matters worse, HIV and TB medications have been shown

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**Box 2. Terrible Places (for MDR-TB)**

In India, 4.3% of notified tuberculosis (TB) cases were estimated to be multidrug-resistant tuberculosis (MDR-TB) in 2013, but within the country there are significant regional differences in the resistance burden. A survey of four municipal wards in Mumbai revealed rates of MDR-TB close to 30% in the years 2004–2007 [85] (see Figure 4 in main article), and subsequent studies have confirmed very high rates of drug resistance [86,87]. A significant proportion of the MDR isolates are resistant to additional drugs, exemplified by a study from 2013 that found 10.6% of all MDR-TB isolates to qualify for XDR-TB status [86]. Results from first-line diagnostics reported annually in South Africa found 6.6% of all TB cases in South Africa to be rifampicin (RIF)-resistant in 2013/2014 [88]. However, in the province of KwaZulu-Natal, which is home to 30% of all TB cases in the country, and the region with the highest incidence of MDR-TB in the world, 8.9% of TB cases were RIF-resistant in the same period. RIF-resistance is often used as a proxy for MDR, an assumption that is correct in more than 90% of the cases in KwaZulu-Natal [89], but does not hold, for instance, in the UK. These numbers suggest that the WHO estimates from 2013 of rates of around 2.1% for MDR-TB are overly optimistic.

A study conducted in Minsk (Belarus) in 2009–2010 revealing that almost half of all TB cases were MDR raised a few eyebrows [90]. However, these figures were confirmed by a follow-up country-wide study 1 year later that confirmed that 45.5% of all isolates in Belarus are indeed MDR-TB. Possibly, even more shocking was the observation that among MDR-TB isolates, 11.9% were XDR [91].
to negatively interfere with each other. However, strains with extensive resistance profiles have recently been shown to have emerged and transmitted well before the HIV epidemic took off in the 1980s [2,3] and there is currently little evidence to suggest a causal relationship between HIV coinfection and increased emergence or circulation of MDR-TB strains [43].

In former Soviet Eastern Europe states, the massive rates of drug-resistant TB have been attributed to the collapse of health systems following the fall of the Soviet Union [44]. Similar forces might be at play in lower-middle income countries such as India today where anti-TB medication is available to most, but the health system infrastructure is often weak and antimicrobial stewardship is lacking [45]. Another possible explanation for the regional differences in resistance burden could be due to phenotypic differences between strains. If the dominant lineage in a region were more prone than other lineages to develop resistance, this could exacerbate the resistance burden in the region.

The Beijing lineage (Lineage 2) is the dominating lineage in large parts of Asia and eastern Europe and is often associated with drug resistance [46]. Whether members of the lineage are actually more prone to develop resistance-conferring mutations, as recently suggested by Ford and colleagues [22], remains unclear. In their study, Ford et al. relied heavily on laboratory strains [22], and an earlier similar study with slightly larger sample size did not point to a higher rate of acquisition of mutations of Lineage 2 strains [47]. It is possible that the Beijing lineage simply happened to be at the right place at the right time with the collapse of the Soviet Union, leading to the emergence of resistant strains still circulating in large numbers today. The observation that

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**Figure 4. Hotspots of Multidrug-Resistant Tuberculosis (MDR-TB).** Data on MDR-TB incidence was collected from [91] (Belarus), [85] (Mumbai), and [89] (KwaZulu-Natal). Note that the MDR-TB frequencies reported here for Mumbai are significantly higher than those reported nation-wide by the World Health Organization. The reported MDR-TB incidence in KwaZulu-Natal represents rifampicin (RIF)-resistant isolates as identified by TB Xpert [88].
Beijing isolates are associated with accelerated progression to active TB [36] could be part of the explanation for the relatively recent and ongoing global expansion of the lineage.

To summarize, worldwide distribution of MDR-TB is extremely heterogeneous and has undoubt-edly been shaped by past failings in public health infrastructure in various parts of the world. This heterogeneity might have been further exacerbated by an intrinsic propensity of certain lineages to acquire resistance more readily. However, lineage-specific factors are difficult to quantify because Mtb lineages are themselves patchily distributed.

My Body Is a Cage

The first clinical stage of TB infection is termed primary TB and typically involves the production and spread of granulomas systemically and to regional lymph nodes [48]. Within a few weeks, immunity develops and the infection regresses, but is not sterilized [48]. TB is generally more virulent in animals than in humans, and common animal models such as mice, guinea pigs, rabbits, and monkeys all develop aggressive primary TB that is not transmissible and often results in death [49]. Humans are special in that primary TB is generally not associated with serious illness. In humans, however, Mtb enters a latent stage following regression of the primary infection. Upon reactivation of the dormant organisms, or reinfection with new organisms from the environment, softened and fragmented lung tissue is coughed up, leaving cavities that harbor small numbers of bacilli. This early stage of cavity formation can erode arteries to produce heavy bleeding, a classical sign of TB [48]. Upon maturation, cavities develop a thin fibrous wall. The inner surface is covered with fluid caseum with no viable cells. Mtb grows extracellularly on the surface of cavities as a pellicle (biofilm) [50]. Mtb can grow in massive numbers on the surface of cavities where it can be coughed into the environment while the host remains in health except for the coughing [48]. This form of clinical TB is obviously extremely transmissible as billions of bacteria can be produced each day [51].

In addition to the role of cavities in the transmission of TB, they constitute a significant complication for successful antimicrobial therapy as different drugs penetrate cavities with varying efficiency: the fluoroquinolone moxifloxacin seems to penetrate well, whereas the first-line drugs INH, RIF, and pyrazinamide (PZA) are less efficient [52]. The more experimental drug linezolid has been shown to be effective against cavitary TB, albeit often with quite serious side-effects [53]. Mathematical modelling has revealed that using drugs with different penetration profiles leads to spatial monotherapy and rapid evolution of multidrug resistance [54]. It is no surprise then, that cavitary TB is associated with treatment failure [55] and is a major risk factor for acquired resistance to second-line drugs [56,57]. In fact, a recent study from Georgia found that additional resistance emerges in 58% of cavitary MDR-TB cases treated with second-line drugs, but in ‘only’ 16% of such patients not presenting with cavities [56]. Efforts to optimize regimens for progressed cavitary TB minimizing resistance development are warranted.

The emergence of drug-resistant TB is most often attributed to poor patient adherence to drug treatment schemes, a problem that is ameliorated by directly observed treatment (DOT). Patients are typically enrolled on anti-TB therapy for 6–24 months, depending on response and the resistance phenotype of the infection. In light of this, one cannot expect the problem of imperfect patient compliance to go away any time soon. Yet, based on a hollow-fiber model, pharmacokinetic variability alone was estimated to result in acquired multidrug-resistance in about 1% of patients, irrespective of adherence [58]. Many bacteria exhibit increased drug tolerance when growing in biofilms, and this phenomenon has also been observed in Mtb. Bacilli in cavities are also separated from the host’s immune defenses by the wall of the cavity that prevents penetration of viable cells. When allowed to form biofilms in vitro, a small but possibly clinically important subpopulation emerges, which is able to tolerate very high doses of antimicrobials [59]. Mtb biofilm formation was recently shown to depend on keto-mycolic acids,
and, when cocultured with a wild-type strain, even drug-sensitive biofilm-defective mutants were found to become drug tolerant [60]. The biological relevance of biofilm formation within patients remains to be determined, but the biofilm-like growth of Mtb within and on the surface of cavities [50] suggests that this growth mode could be clinically very important.

**Chemical Warfare**
Recent studies utilizing deep-sequencing of patient isolates have revealed a surprising degree of Mtb genetic diversity within patients [61–65]. Resistance mutations have been found to emerge multiple times within a single patient, generally followed by selective sweeps resulting in one clone replacing the whole within-host population [61,64,65]. Large Mtb population sizes and significant genetic diversity upon diagnosis surely play important roles in the emergence of resistance, as a diverse population is more likely to encompass mutants with decreased susceptibility to anti-TB therapeutic drugs. The importance of within-host Mtb population size and genetic diversity in resistance development is a research avenue that deserves further attention.

Even more worrisome than resistance evolving in individual patients is the transmission of resistant strains with little or no apparent fitness cost to the bacterium. The overall robustness of Mtb when challenged with antimicrobials led to standardized drug-treatment schemes including a cocktail of four drugs. Unfortunately, these schemes are not always paired with robust drug-susceptibility testing. It has been argued that standardized treatment schemes for susceptible and MDR-TB in the absence of phenotypic resistance testing has been a direct driver of the evolution of XDR-TB in South Africa [66]. It is well documented that the most commonly transmitted RIF-resistance mutation, rpoB S450L, in combination with secondary compensatory mutations in polymerase subunits is associated with little or no fitness cost [67,68] whereas the picture is less clear for INH-resistance. It has, however, been shown that the most common INH-resistance mutation, namely katG S315T, retains residual catalase–peroxidase activity, is virulent in mice, and importantly, transmits well between people [69,70].

Recent studies have documented that MDR-TB strains have been in circulation for decades [2,3]. The four-drug anti-TB regimen currently in use includes drugs that have all been used continuously against TB for 40–60 years. It may thus come as no surprise that this has selected for highly transmissible MDR-TB strains, and we might perhaps consider ourselves lucky that the problem is not yet worse than it is.

**Concluding Remarks: Know Your Enemy**
Essentially, irrespective of the feature under scrutiny, Mtb stands out from all other bacteria considered as AMR threats. Some of these peculiarities should constitute major chinks in its armor, making it a tractable target for a rare success in stemming the rise of AMRs. In particular, Mtb has a low mutation rate and limited genetic diversity, lacks any mechanism for extensive HGT, and does not benefit from any hiding place outside its human host, such as an environmental or zoonotic reservoir. It remains to be defined what exact form a determined assault against AMR-TB (and TB more generally) should take. However, it is clear that any successful public health strategy will have to be informed by robust fundamental scientific evidence and be multipronged to be successful. We have learned a lot about Mtb and TB, in particular since the advent of fast and affordable sequencing technologies. However, it would be foolish to assume that the current knowledge is sufficient to vanquish Mtb (see Outstanding Questions), as it remains a deadly and surprisingly adaptable foe despite its apparent inherent weaknesses.

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**Outstanding Questions**
Is HIV coinfection a driver of the TB-AMR pandemic?
Do different Mtb lineages have variable propensity to evolve AMR resistance?
How old is TB?
Is Mtb evolving towards shorter latency in human hosts?
How important are lesions, cavities, and biofilms in the emergence of drug resistance in TB?
How should we optimize treatment for cavitary TB?
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