Accurate target identification for *Mycobacterium tuberculosis* endoribonuclease toxins requires expression in their native host

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The *Mycobacterium tuberculosis* genome harbors an unusually high number of toxin-antitoxin (TA) systems. These TA systems have been implicated in establishing the nonreplicating persistent state of this pathogen during latent tuberculosis infection. More than half of the *M. tuberculosis* TA systems belong to the VapBC (virulence associated protein) family. In this work, we first identified the RNA targets for the *M. tuberculosis* VapC-mt11 (VapC11, Rv1561) toxin *in vitro* to learn more about the general function of this family of toxins. Recombinant VapC-mt11 cleaved 15 of the 45 *M. tuberculosis* tRNAs at a single site within their anticodon stem loop (ASL) to generate tRNA halves. Cleavage was dependent on the presence of a GG consensus sequence immediately before the cut site and a structurally intact ASL. However, in striking contrast to the broad enzyme activity exhibited *in vitro*, we used a specialized RNA-seq method to demonstrate that tRNA cleavage was highly specific *in vivo*. Expression of VapC-mt11 in *M. tuberculosis* resulted in cleavage of only two tRNA isoacceptors containing the GG consensus sequence, tRNAGln32-CUG and tRNALeu3-CAG. Therefore, our results indicate that although *in vitro* studies are useful for identification of the class of RNA cleaved and consensus sequences required for accurate substrate recognition by endoribonuclease toxins, definitive RNA target identification requires toxin expression in their native host. The restricted *in vivo* specificity of VapC-mt11 suggests that it may be enlisted to surgically manipulate pathogen physiology in response to stress.

The bacterial pathogen that causes tuberculosis, *M. tuberculosis*, is able to evade the immune system and persist within its host for extended periods of time as a latent infection. Elucidation of the molecular mechanisms that underlie the latent state of *M. tuberculosis* is essential for developing more effective therapeutics for latent tuberculosis infection.

The *M. tuberculosis* genome harbors ~90 TA systems of which 50 belong to the VapBC family¹–⁵. All VapC toxins contain a conserved catalytic PIPT N-terminus (PIN) domain¹,²; an intact PIN domain is essential for VapC toxicity and nuclease activity⁶. However, the stresses that trigger VapC toxin activities during infection are not known. In fact, the precise physiological roles of these 50 VapC toxins in *M. tuberculosis* infection and virulence are not well understood, although proposed to reduce protein synthesis⁷. It is also a conundrum why this pathogen harbors so many VapBC TA systems if collectively their only role is to simply reduce translation. To begin to tackle these broad and complex questions, we and others have been systematically studying their enzymatic activity as a first step toward understanding how they may influence the course of tuberculosis infections and reduce the efficacy of antituberculars.

RNA cleavage by members of the *M. tuberculosis* VapC-family of toxins has been reported using one of two general approaches. The first *in vitro* approach involves incubation of recombinant toxin with synthetic tRNAs⁸,⁹, synthetic RNAs¹⁰–¹³, or total RNA isolated from *M. tuberculosis*⁸. The second approach involves ectopic expression

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of the toxin in alternate rapidly growing hosts that do not require biosafety containment (*Escherichia coli* and *M. smegmatis*)[13,14]. Both of these approaches appeared to be reliable because only one or a few RNA targets were identified within the total RNA pool. Therefore, they are routinely employed to identify and characterize *M. tuberculosis* VapC toxin targets.

The enzymatic activities of 13 of the 50 *M. tuberculosis* VapC toxins have been studied to varying degrees[6-14]. Two of these 13 VapC toxins specifically target 23S rRNA at the sarcin–ricin loop[14]. The proposed RNA targets for the other 11 *M. tuberculosis* VapC toxins studied previously by Winther et al.[7]—including VapC-mt11 (aka VapC11, Rv1561)—that is the focus of our study presented here—are derived from an RNA–VapC interaction screen using an *M. smegmatis* host.

We performed a thorough characterization of the enzymatic properties of the *M. tuberculosis* VapC-mt11 TA toxin *in vitro* and *in vivo* as well as its effect on protein synthesis and mycobacterial growth. We demonstrate that the *M. tuberculosis* VapC-mt11 toxin exhibits highly precise target specificity only when expressed in its natural *M. tuberculosis* host, in striking contrast to its much broader spectrum tRNAse activity *in vitro*. These results also differ from those of Winther et al.[7] and serve as a useful guide for the benefits and limitations of the array of approaches implemented by those studying endoribonuclease TA toxins.

**Results**

**VapC-mt11 expression causes growth arrest in both *M. smegmatis* and *M. tuberculosis*.** *M. tuberculosis* H37Rv and *M. smegmatis* mc^1^55 cells were transformed with a VapC-mt11-containing anhydrotetracycline (ATc) inducible vector (pMC1s15). For *M. smegmatis*, VapC-mt11 expression resulted in growth arrest 2 h post-induction, which was sustained through the length of the growth profile (Fig. 1A). Likewise, VapC-mt11 expression arrested growth in *M. tuberculosis*. In contrast to the uninduced control, the OD_560 for cells expressing VapC-mt11 remained near zero for the duration (10 days) of the growth profile (Fig. 1B). In concordance with the growth profile, the average CFU/ml recovered when *M. tuberculosis* cells were plated in the presence of ATc inducer was 50 CFU/ml compared to 12,000 CFU/ml from the uninduced control (Fig. 1C). These results were consistent with the strong growth inhibition we observed when VapC-mt11 was expressed in *E. coli* cells[6].

**VapC-mt11 inhibits translation.** *An in vitro* translation system was used to determine if the strong growth arrest phenotype characteristic of VapC-mt11 was a consequence of defective protein synthesis. Preincubation of the *in vitro* translation mix with VapC-mt11 before DHFR DNA template addition resulted in complete inhibition of synthesis relative to the control lane, which was not treated with recombinant VapC-mt11 (Fig. 2A). This translation defect was confirmed upon VapC-mt11 expression in *M. smegmatis* (Fig. 2B). Cells were radioactively labeled at intervals after VapC-mt11 induction to monitor new protein synthesis. Nearly complete shutdown of protein synthesis was observed 2 h after induction (the point where growth inhibition commences Fig. 1A) followed by sustained and complete inhibition of protein synthesis after 4 h of toxin induction. Therefore, the strong growth arrest phenotype characteristic of VapC-mt11 expression appears to be a consequence of complete translation inhibition in mycobacteria.

**VapC-mt11 is a tRNase that targets multiple synthetic *M. tuberculosis* tRNAs.** Since there is precedent for VapC recognition of both tRNA and rRNA targets that is highly structure-dependent[8,14], we assayed VapC-mt11 cleavage activity with each of these two intrinsically folded classes of RNAs. We first analyzed 23S and 16S rRNA from *E. coli* cells expressing VapC-mt11 and did not observe a decrease in the overall abundance of these rRNAs or the presence of any degradation products (data not shown). This suggested that VapC-mt11 likely targets tRNAs. Next, to determine which tRNAs were preferred substrates of VapC-mt11, each of the 45 tRNAs present in *M. tuberculosis* were synthesized *in vitro* and incubated with recombinant VapC-mt11 (Fig. 3). To our surprise, VapC-mt11 cleaved 15 tRNAs, one third of the 45 *M. tuberculosis* tRNAs. However, among these 15, ten were cleaved efficiently (eight to completion, two ~90% cleaved; shown in red) while five exhibited only weak cleavage (blue, Fig. 3) The extent of cleavage did not change when assay times were increased (data not shown).

**VapC-mt11 tRNA recognition and cleavage is not modification dependent.** To determine if posttranscriptional modifications present on tRNAs influenced cleavage, we used northern analysis to assess the cleavage efficiency of VapC-mt11 for all 15 tRNAs synthesized *in vitro* (Fig. 3) versus *in vivo* in *M. tuberculosis* cells (Figs 4 and 5). Generally, tRNA cleavage efficiency trends were in agreement. The *in vivo* counterparts for eight of the ten *in vitro* tRNAs that were cleaved to ~90–100% completion (Fig. 3, red) were also completely cleaved (Fig. 4). The two exceptions, tRNA^Leu^ and tRNA^Ser^, were ~50% cleaved by VapC-mt11 when derived from Mtb cells (Fig. 5 c, respectively). Four of the five very weakly cleaved *in vitro* synthesized tRNAs (blue tRNAs in Fig. 3) exhibited marginal or no detectable cleavage by northern analysis (Fig. 5). The exception was *in vivo* synthesized tRNA^Ket^, which was fully cleaved by VapC-mt11 (Fig. 5 b). Since cleavage efficiency was generally comparable between synthetic tRNA and its counterpart from *M. tuberculosis* cells, VapC-mt11 target recognition and cleavage did not appear to require tRNA modifications.

**VapC-mt11 generates tRNA halves upon cleavage after a GG sequence in the anticodon loop.** We used primer extension analysis to map the VapC-mt11 cleavage sites for nine tRNAs that were efficiently cleaved *in vitro* (Fig. 6A), all but one of these (tRNA^Ket^) were also 100% cleaved *in vivo*. In each case, three trends were observed. First, the primary cleavage site always occurred after a GG sequence (GG↓). Since we observed cleavage at GG↓[A, GG↓U and GG↓G] sequences among these nine tRNAs, the base following cleavage site does not appear to contribute to target specificity. Yet, several GG-containing mRNAs were not cleaved by VapC-mt11. For example, *E. coli* OmpF and OmpC mRNAs contain 67 and 65 GG motifs, respectively, but were not cleaved by VapC-mt11 (data not shown). Likewise, as mentioned earlier, *E. coli* 23S and 16S rRNAs were not also cleaved,
and they contain hundreds of GG motifs. Therefore, the presence of a GG RNA consensus sequence alone cannot serve as the sole determinant for tRNA target recognition. Second, all nine cleavage sites occurred at the same position in the anticodon loop, 3′ of the ribonucleotide that followed the anticodon. Third, VapC-mt11 always targeted the anticodon loop. This is consistent with our earlier observation for another VapC family member and a subsequent paper demonstrating that several M. tuberculosis VapC toxins target tRNAs for cleavage at their anticodon loop7,8. Therefore, VapC-mt11, and all M. tuberculosis VapC toxins known to cleave tRNA, result in the generation of tRNA halves (Fig. 6B).

VapC-mt11 cleavage is both sequence- and structure-dependent. To pinpoint the determinants that contribute to toxin recognition and cleavage by VapC-mt11, we created a variety of mutants using one of the efficiently cleaved tRNAs, tRNAPro14, as the test tRNA template (Fig. 7A). First, we interrogated the importance of the conserved GG sequence 5′ of the cleavage site. Mutation of the second G of the GG consensus to an A (GG → GA) resulted in the shifting of the cleavage site one nt 5′ from the major cleavage site (which also corresponded to the position of the minor cleavage site in wild-type tRNAPro14, Fig. 7B). Next, we mutated the first G of the GG consensus to an A (GG → AG). In this case, we observed very inefficient cleavage, with only a small percentage of the tRNAPro14 template cut by VapC-mt11 (Fig. 7C).

Since we observed cleavage at GG↓A, GG↓U and GG↓G sequences among the 10 preferred tRNA targets (Fig. 6A), the base following the GG consensus sequence did not appear to contribute to target specificity. In agreement with this prediction, cleavage was not affected when we mutated the base 3′ of the GG consensus in tRNAPro14 (Fig. 7C).

Next, we individually mutated each of the two bases 5′ of the GG cleavage consensus, which in each case alters the anticodon sequence (GGG↓G → AGG↓G, Fig. 7E; GGGG↓G → AGGG↓G, Fig. 7F). Neither mutation altered the cleavage of tRNAPro14 by VapC-mt11. Therefore, the only sequence determinants for cleavage of tRNAPro14 by VapC-mt11 were the two GG residues directly 5′ of the cleavage site.

VapC-mt11 cleavage is both sequence- and structure-dependent. The importance of a GG sequence for VapC-mt11 cleavage is underscored when both consensus GG residues were simultaneously mutated to AA (GG→AA, Fig. 8A). In this case, we observed a two base 5′ shift in the cleavage site to the only other GG

Figure 1. Growth inhibition by VapC-mt11. (A) M. smegmatis mc2155 harboring the anhydrotetracycline (ATc) inducible vector pMC1s with VapC-mt11 was grown at 37 °C in 7H9 + TW80 + AND supplemented with 25 ug/mL kanamycin. Cultures were split and one culture was induced by the addition of 200 ng/mL ATc. Time points for uninduced (♦) and induced (■) samples were collected up to 6 h. Growth curve shown is representative of the trend documented in three independent experiments. (B) M. tuberculosis H37Rv transformed with pMC1s-VapCmt11 were grown at 37 °C in 7H9-TW80-ADN medium containing 30% spent medium and supplemented with 25 ug/mL kanamycin. Cultures were separated into uninduced (▲) and induced (●). Induced cultures were supplemented with 200 ng/ml ATc and additional ATc was added every 48 h to maintain the ATc concentration between 100 and 250 ng/ml. Data points represent the average of three independent experiments; error bars represent the S.D. (C) Plate efficiency assay for M. tuberculosis H37Rv cells harboring pMC1s-VapC-mt11 between uninduced (gray) and induced (red). Transformants were plated on 7H9 + TW80 + AND agar with 25 ug/mL kanamycin with or without 500 ng/mL of ATc and incubated for 3 weeks at 37 °C. Error bars represent the S.D. for biological and technical replicates.
sequence remaining in the anticodon loop, suggesting that \emph{in vitro} VapC-mt11 will seek out a GG in proximity when the native sequence is no longer in place.

Since we established that the presence of the GG sequence alone could not account for the specificity of VapC-mt11 for tRNAs, we first altered the structure of the anticodon stem loop (ASL) by abolishing stem formation (Fig. 8B). This relatively severe structural change resulted in an equally dramatic shift in the cleavage site. This open ASL mutant primarily shifted the cleavage site from the GG in the anticodon loop to a GG sequence in the D-loop of tRNA\textsubscript{Pro14} (Fig. 8B, green arrow); only marginal cleavage at the native GG site was detected (Fig. 8B, small yellow arrow).

Finally, when we combined the open ASL mutation (Fig. 8B) with the consensus GG→AA mutation (Fig. 8A), we observed a complete shift of the cleavage site to GG\textsc{\textprime} in the D-loop (Fig. 8C). Apparently, a GG sequence in the loop of an intact stem-loop (much like the original site harbored in the loop of the ASL) was a preferred alternate substrate over other spatially distinct GG motifs present in tRNA\textsubscript{Pro14}. More specifically, a second GG located in a single-stranded region between the ASL and T\textsc{\textprime}C loop of tRNA\textsubscript{Pro14} was not cut in this mutant. Alternatively, the selection of a new cleavage site in this mutant may simply be dictated by toxin accessibility as the D-loop would be predicted to be more surface exposed than the other GG site tucked between two stem loops.

In summary, VapC-mt11 requires the GG consensus sequence to be in the proper structural context within the anticodon loop for tRNA cleavage \emph{in vitro}.

\textbf{VapC-mt11 cleaves only two GG consensus-containing tRNA targets when expressed in its natural \textit{M. tuberculosis} host.} We sought to understand why our \emph{in vitro} cleavage experiments using either synthetic tRNAs or those isolated from \textit{M. tuberculosis} (with modifications) identified numerous VapC-mt11 cleaved tRNAs compared to three identified by Gerdes and colleagues in a screen for \textit{M. tuberculosis} VapC RNA targets expressed in another mycobacteria, \textit{M. smegmatis}.

We expressed VapC-mt11 in \textit{M. tuberculosis} and performed a specialized RNA-seq method, \textit{S'} RNA-seq, developed in our laboratory to identify RNA targets of endoribonuclease toxins\textsuperscript{16}. \textit{S'} RNA-seq methodology enables global analysis of specific populations of RNA transcripts based on the modification at their \textit{S'} end\textsuperscript{16}. VapC family members as well as other RNases have a hydroxyl group (\textit{S'}-OH) at their \textit{S'} ends\textsuperscript{8,17}. Therefore, we analyzed only those transcripts carrying a \textit{S'}-OH in VapC-mt11 expressing \textit{M. tuberculosis} cells compared to an uninduced control. The resulting dataset revealed both the RNA target and the position of toxin cleavage within these RNAs. Only two tRNAs were identified as VapC-mt11 targets, tRNA\textsubscript{Glu2}-\textsc{CUG} and tRNA\textsubscript{Leu1}-\textsc{CAG} (Fig. 9A). Both of these tRNAs were among the ten that were cleaved to completion \emph{in vitro} (Fig. 3). In concordance with the requirements for substrate recognition and specificity we documented \emph{in vitro}, both tRNA\textsubscript{Glu2}-\textsc{CUG} and tRNA\textsubscript{Leu1}-\textsc{CAG}, were cleaved within their ASL and immediately after the GG consensus sequence to generate stable tRNA halves (Fig. 9B). Finally, \textit{S'} RNA-seq did not identify any other class of RNA—mRNA, rRNA or other small stable non-coding RNA—that was directly cleaved by VapC-mt11.

\textbf{Discussion} Here we showed that a single toxin is capable of recognizing and cleaving nine \textit{M. tuberculosis} tRNAs, one-fifth of the 45 distinct tRNA species present in this pathogen \emph{in vitro} (Figs 3 and 4). The broad scope of targets identified \emph{in vitro} seemed consistent with the growth and translation phenotypes observed. Expression of VapC-mt11 dramatically impaired \textit{M. tuberculosis} growth (Fig. 1B) and precluded recovery of viable cells (Fig. 1C). Growth in \textit{M. smegmatis} was also arrested ~2h postinduction and beyond (Fig. 1A), concomitant with a virtually complete shutdown of new protein synthesis (Fig. 2A).
A common feature among these tRNA targets was sequence- (GG↓) and context-specific (anticodon loop of an intact ASL) cleavage. In fact, the requirement for proper structural context is emerging as a general feature of tRNA-cleaving *M. tuberculosis* toxins. However, RNA target selection by VapC-mt11 in *M. tuberculosis* is dictated by more than the enzymatic properties of this toxin.

Figure 3. VapC-mt11 cleaves one third of *M. tuberculosis* tRNAs in vitro. tRNAs and their cleavage products visualized by SYBR Gold staining. 2 pmol of each of the 45 in vitro synthesized *M. tuberculosis* tRNAs was incubated with (+) or without (−) 10 pmol of recombinant VapC-mt11 for 3 h at 37 °C to ensure detection of both strong and weak tRNA cleavage reactions. Full length tRNAs that were cleaved to completion or near completion by VapC-mt11 shown in red; these tRNAs were also cleaved to the same extent shown when incubated for only 15 min at 37 °C. Weak VapC-mt11 tRNA targets shown in blue. tRNA numbering and anticodon sequences of each numbered tRNA from the Lowe lab genomic tRNA database http://gtrnadb.ucsc.edu. All uncropped images shown in Supplementary Information Fig. 2.
In its natural host VapC-mt11 was far more discriminating, cleaving only tRNA\textsubscript{Gln32-CUG} and tRNA\textsubscript{Leu3-CAG}. This much higher level of target discrimination \textit{in vivo} may be due to stress-specific modifications on the tRNAs or the binding of an accessory factor that alters enzyme specificity. However, evidence only exists to support the former explanation. Although we did not detect any difference in cleavage for synthetic tRNA\textsubscript{Gln32-CUG} and tRNA\textsubscript{Leu3-CAG} versus those derived from unstressed \textit{M. tuberculosis} cells, newly added or newly removed post-transcriptional modifications to the tRNA that prevent cleavage of the other seven tRNAs \textit{in vivo} might occur only after a specific stress and/or upon expression of the toxin. Although modifications on \textit{M. tuberculosis}...
Figure 6. VapC-mt11 cleaves tRNAs within the ASL. (A) Primer extension analysis of in vitro synthesized *M. tuberculosis* tRNA$^{Arg27}$, tRNA$^{Pro14}$, tRNA$^{Pro23}$, tRNA$^{Pro35}$, tRNA$^{Leu3}$, tRNA$^{Leu13}$, tRNA$^{Leu15}$, tRNA$^{Gln32}$, and tRNA$^{Gln41}$ treated with (+) or without (−) recombinant VapC-mt11. G, A, T, and C correspond to DNA-sequencing ladders using the same oligonucleotide as in the primer extension reactions for each tRNA. RNA sequence shown below the gels and major cleavage sites are indicated by the red arrow; alternate weak cleavage sites are indicated by yellow arrow for the three proline tRNAs. Major cleavage products in the gels are depicted by the red arrow head (right). The ASL sequence is illustrated above each tRNA sequencing gel, the anticodon (grey shading) and major cleavage position indicated by red arrow. Bands visible in (−) lanes of tRNA$^{Arg27}$, tRNA$^{Leu3}$, and tRNA$^{Gln32}$ correspond to secondary structure. (B) Diagram of tRNA halves produced by VapC-mt11. tRNA numbering and anticodon sequences of each numbered tRNA from the Lowe lab genomic tRNA database http://gtrnadb.ucsc.edu. All uncropped images shown in Supplementary Information Fig. 5 (tRNA$^{Arg27}$, tRNA$^{Pro14}$, tRNA$^{Pro23}$, and tRNA$^{Pro35}$) and Supplementary Information Fig. 6 (tRNA$^{Leu3}$, tRNA$^{Leu13}$, tRNA$^{Leu15}$, tRNA$^{Gln32}$, and tRNA$^{Gln41}$).
Figure 7. VapC-mt11 requires a GG sequence within the proper context. In vitro synthesized *M. tuberculosis* tRNAPro14 mutants were incubated with increasing amounts of recombinant VapC-mt11 (ratios of toxin:tRNA were 0:1, 5:1, 10:1, 15:1) for 3 h at 37 °C. Sizes for full-length and cleavage products (left). Cleavage assays with in vitro synthesized wild-type tRNAPro14 (A), tRNAPro14 point mutation (G → A) of each G residue of the consensus GG sequence (blue shaded circles) mutants (B,C), tRNAPro14 mutant with point mutation 3′ of cut site (D) and tRNAPro14 mutants with point mutations within the anticodon sequence (E,F). Secondary structure of *M. tuberculosis* tRNAPro14 wild-type or mutants shown above gels. Anticodon sequence (shaded grey), base pairing represented as black dots (●), mutated bases (red), consensus sequence (shaded blue circles), wild-type cleavage site (red arrow), alternate cleavage site (green arrow), weak cleavage at wild-type cleavage site (small yellow arrow). All uncropped images shown in Supplementary Information Fig. 7.
Figure 8. Sequence and structure influence the VapC-mt11 cleavage site. Cleavage assays of (A) tRNA\(^{Pro14}\) mutant with a GG consensus sequence replacement by AA, (B) an open stem loop mutant, and a (C) GG → AA and open stem loop mutant. Full length and cleavage product sizes shown on the left. The small 19 nucleotide cleavage product ran off the gel in (C). Secondary structures of the \textit{in vitro} synthesized mutants of tRNA\(^{Pro14}\) are depicted above cleavage reaction gels. Anticodon stem loop (ASL), anticodon sequence (shaded grey), base pairing represented as black dots (●), mutated bases (red), consensus sequence (blue shaded circles), weak cleavage at wild-type cleavage site (small yellow arrow), and alternate cleavage site (green arrow). Primer extension of these mutants shown below. G, A, T, and C correspond to DNA-sequencing ladders using the same oligonucleotide as in the primer extension reactions for each tRNA. Alternate cleavage sites are indicated by the green arrow head to the right of the primer extension gel images. RNA sequence corresponding to the alternate cleavage sites (green arrow) within the (A) ASL or (B,C) D-loop are shown below each primer extension gel image, mutations indicated by underlined red text. All uncropped images shown in Supplementary Information Fig. 8.
tRNAs have not been characterized in any detail, the ASL of tRNAs is generally a modification hotspot that influences tRNA structure and thermostability. If the changes we observed in specificity are indeed attributable to modifications, the VapC-mt11 target recognition seen in vivo cannot be accurately recapitulated in vitro until the exact location and nature of the chemical changes on the entire M. tuberculosis tRNA population is elucidated.

The toxin components of Type II TA systems are characteristically activated in response to stress. In M. tuberculosis, certain TA toxin transcripts are upregulated when cells are exposed to stresses relevant to latent tuberculosis infection—nutrient limitation, hypoxia, macrophage infection, or antibiotic treatment. However, there is no definitively confirmed stress trigger for any TA toxin linking upregulation of toxin mRNA to increased enzymatic activity of the toxin protein. By analogy, TA toxin expression may underlie the observation that hypoxia regulates tRNA modifications in the M. tuberculosis relative M. bovis BCG.

There are five Leu tRNAs in M. tuberculosis to service the six Leu codons. tRNA^{Leu1-CAG} (depleted by VapC-mt11) services the most abundant of the six Leu codons, CUG. The Leu CUG codon is also one of the three most frequently represented codons in the M. tuberculosis transcriptome (50.4/1000 codons; equal to Gly GGC but less than Ala GCC at 59.8/1000 codons). The other four Leu tRNAs, are spared but may not be able to fully compensate for loss of tRNA^{Leu1-CAG}.

There are two Gln tRNAs in M. tuberculosis to service the two Gln codons, CAG and CAA. tRNA^{Gln32-CUG} (depleted by VapC-mt11) services the CAG codon (22.8/1000 codons). If the 5′ anticodon C for tRNA^{Gln32-CUG} is modified, it may also service the CAA Gln codon (8.1/1000 codons). The second Gln tRNA (spared by VapC-mt11) services both Gln CAG and CAA codons.

Gerdes and colleagues identified RNA targets for several M. tuberculosis VapC toxins using a genome-scale toxin-tRNA interaction screen in the rapidly growing, nonpathogenic M. smegmatis. This screen identified three VapC-mt11-interacting M. smegmatis tRNAs—two isoacceptors of leucine, and one of glutamine. These three M. smegmatis tRNAs are designated tRNA^{Leu1-CAG}, tRNA^{Leu13-CAG}, and tRNA^{Gln10-CUG} and are orthologs of M. tuberculosis tRNA^{Leu1-CAG}, tRNA^{Leu15-CAG}, and tRNA^{Gln12-CUG}, respectively. Of the three M. smegmatis tRNAs, only tRNA^{Leu13-CAG} was significantly cleaved in vivo upon ectopic expression of VapC-mt11 in this surrogate host. Thus, only tRNA^{Leu13-CAG} in both M. smegmatis and M. tuberculosis was subjected to more detailed study. More specifically, (1) the sites of VapC-mt11 cleavage of M. smegmatis tRNA^{Leu13-CAG} in vivo were identified by primer extension and (2) relatively efficient in vitro cleavage of M. tuberculosis tRNA^{Leu13-CAG} was demonstrated. Therefore, their data focused on tRNA^{Leu13-CAG} as the likely preferred RNA target for M. tuberculosis VapC-mt11. Our 5′ RNA-seq approach has three advantages over this interaction screen as well as in vitro cleavage assays similar to those presented in Figs 3 and 4. First, by focusing on only 5′-OH transcripts we are identifying transcripts that have been explicitly altered by the enzymatic activity of the toxin, not simply a cross-linkable RNA-protein interaction. Second, this method enables both the detection of the RNA target(s) as well as the exact position of cleavage without needing to perform laborious primer extension experiments. Third, enzyme activity occurs under physiological conditions (i.e., an M. tuberculosis host) to best approximate toxin activity during infection.

Recently, Deep et al. reported a high resolution x-ray crystal structure of VapBc-mt11 along with physiological studies of VapC-mt11. VapC-mt11 overexpression in M. tuberculosis followed by RNA-seq led to an altered transcriptome that mirrored those of M. tuberculosis cells undergoing the enduring hypoxic response as well as cells in a nonreplicating persistent state. Yet paradoxically, deletion of the vapBC11 locus resulted in decreased
recovery of viable cells only upon exposure to oxidative stress. Other stress conditions tested—including nonreplicating persistence, hypoxia using the Wayne model, nitrosative stress, nutritional stress, macrophage infection, and antibiotic treatment—did not alter cell recovery. Finally, although not essential for cell survival, the vapBC11 locus is required for establishment of an M. tuberculosis infection in the guinea pig model.

In summary, our results reveal that analysis of toxin cleavage targets is most accurate in the in vitro setting in which the toxin is active, i.e. within the M. tuberculosis cell. Although in vitro cleavage methods are useful for identification of consensus sequences and structural features required for toxin cleavage, they have inherent limitations that may preclude accurate identification of the true toxin targets in vivo. Likewise, while ectopic toxin expression in alternate hosts followed by 5′ RNA-seq can provide useful clues to RNA targets or general RNA class favored by the toxin, the results will likely differ from that performed in the true host because of the inherent variability between transcriptomes and the presence and position of RNA modifications. Finally, expression of toxins in their natural host not only identifies the precise RNA target(s), it provides more physiologically relevant clues about the impact of toxin activity on discrete pathways and biological processes.

**Methods**

**Strains, Plasmids and Reagents.** The E. coli strain BL21(DE3) (F-ompT hsdS\(_B\)(rK-mK) dcm gal (DE3) tonA) (Novagen) was used for all protein expression. E. coli K-12 Mach1 T1 cells (ΔrecA1398 endA1 tonA \(\Phi80\Delta lacM15 \Delta lacX74 hsrd\(_T\) (r\(_m\) \_m\(_e\)) \_r\(_m\)); Invitrogen) were used for all cloning experiments. M. smegmatis mc\(_c\)155 and M. tuberculosis H37Rv strains were both used for growth profiles. Experiments involving the virulent H37Rv strains of M. tuberculosis were conducted in a BSL-3 laboratory following institutionally approved protocols. M. tuberculosis H37Rv was also used for the plating efficiency assay to determine recovery of viable bacteria upon VapC-mt11 expression. M. smegmatis mc\(_c\)155 was used for metabolic labeling. The vapC-mt11 (Rv1561); “mt” refers to M. tuberculosis) gene was cloned using M. tuberculosis H37Rv genomic DNA. The DNA sequences of PCR fragments were cloned into plasmids for automated DNA sequence analysis. The VapC-mt11 coding region was cloned into the pET28a expression vector (EMD Millipore) and the arabinose inducible pBAD33 plasmid (ATCC) after the addition of 5′ Ndel and 3′ BamHI restriction enzyme sites by PCR. For expression in Mycobacteria, the VapC-mt11 coding region with PCR generated 5′ Clal and 3′ Sall restriction sites was cloned into the corresponding sites in the anhydrotetracycline (ATc) inducible vector pMC1\(_C\)15.

**Growth Assays in Mycobacteria.** M. smegmatis mc\(_c\)155 was transformed by electroporation with 0.5–1 μg of pMC1s-vapC-mt11 DNA. Cultures were inoculated with single colonies, grown at 37 °C in 7H9-TW80-AND medium containing 25 μg/ml kanamycin and induced at an OD\(_{600}\) of 0.4 by addition of 200 ng/ml ATC. Cells were collected from uninduced and induced samples at intervals up to 6 h. M. tuberculosis H37Rv was transformed by electroporation with 0.5 μg of pMC1s-vapC-mt11 DNA. Cultures were inoculated with single colonies, grown at 37 °C in 7H9-TW80-AND medium containing 30% spent medium and 25 μg/ml kanamycin. Upon inoculation, cultures were induced by 200 ng/ml ATC; additional ATC was added every other day to maintain the initial ATC concentration. Three independent experiments were performed and error bars used to represent the S.D. For plating efficiency assays, M. tuberculosis H37Rv VapC-mt11 clones were plated on 7H9-TW80-ADN agar plates containing 25 μg/ml kanamycin and with or without 500 ng/ml ATC. Colonies were counted 3-weeks after incubation at 37 °C.

**Purification of Recombinant VapC-mt11.** E. coli BL21(DE3) cells transformed with the pET28a-vapC-mt11 were grown in M9 minimal medium supplemented with 0.1% glycerol and 50 μg/ml kanamycin at 37 °C to exponential phase. Induction of the protein was achieved by adding 1 mM isopropyl 1-thio-D-galactopyranoside (IPTG). After 4 h, cells were harvested by centrifugation and resuspended in lysis buffer (50 mM NaH\(_2\)PO\(_4\) (pH 8.0), 500 mM NaCl, 20 mM imidazole, 10 mM 2-mercaptoethanol, 1 mM PMSF, 1 mg/ml lysozyme). Cell pellets were then lysed by sonication and lysates applied to a nickel-nitrilotriacetic acid (Ni-NTA) resin (Qiagen) to purify the protein as described previously.

**In vitro Transcription of M. tuberculosis tRNAs.** M. tuberculosis wild-type and mutant tRNAs were synthesized in vitro using synthetic DNA oligonucleotides containing the T7 RNA polymerase promoter and the 5′ end sequence of the tRNA of interest along with a second oligonucleotide with the 5′ end sequence of the tRNA. Oligonucleotides were designed with a region of overlap to serve as a template for PCR with Taq DNA polymerase to create a tDNA. The tDNA was gel extracted from a 2% agarose gel using the QIAquick Gel Extraction Kit (Qiagen). 200 ng of the tDNA was used to transcribe the tRNAs of interest using the RiboMAX Large Scale RNA Production System (Promega) as recommended by the manufacturer. The tRNA transcription reaction was transcribed at 90°C polycrylamide, 7 M urea gel and visualized by ethidium bromide staining. The product corresponding to the correct size was excised from the gel and incubated for 18 h at 37 °C in elution buffer (1 mM EDTA, 0.5 M ammonium acetate, 10 mM magnesium acetate, 0.1% SDS). The elutions were ethanol precipitated and resuspended in nuclease-free water.

**In vitro tRNA Cleavage Assay.** The 45 in vitro transcribed M. tuberculosis tRNAs (2 pmol) were initially incubated with or without VapC-mt11 (10 pmol) for 3 h at 37 °C in 10 mM HEPES pH 7.5, 15 mM KCl, 3 mM MgCl\(_2\), 10% glycerol. Mutants were also incubated with increasing amounts of the toxin (0, 10, 20 and 30 pmol) for 3 h at 37 °C. Samples were analyzed in 7 M Urea, 9% polycrylamide gel and visualized by SYBR Gold (Invitrogen) staining.

**In vitro M. tuberculosis tRNA Primer Extension.** 2 pmol of the in vitro transcribed M. tuberculosis wild-type or mutant tRNAs were incubated with 10 pmol VapC-mt11 toxin or without toxin for 1 h at 37 °C. To detect cleavage
products, the following oligonucleotides were 5’ labeled with [\(^{32}\)P] ATP (Perkin Elmer Life Sciences) using T4 polynucleotide kinase (NEB): tRNA\(^{\text{ Ala11}}\) (5’ GGA GCT AAG GGG ACT CGA ACC C 3’), tRNA\(^{\text{ Arg40}}\) (5’ GCC CTC TTC GGC GAC AGG C 3’), tRNA\(^{\text{ Ser26}}\) (5’ GGA GGA TGG GGG ATT TGA ACC C 3’), tRNA\(^{\text{ Ser24}}\) (5’ GGC GGC GGA GGG ATT TGA ACC CTC 3’), tRNA\(^{\text{ Ser24}}\) (5’ GGC GCT GAC AGG ATT TGA ACC ACC C 3’), tRNA\(^{\text{ Ser14}}\) (5’ GCC GGT GAC AGG ATT TGA ACC TG 3’), tRNA\(^{\text{ Pro35}}\) (5’ CGG GGT GAC AGG ATT TGA ACC TG 3’), tRNA\(^{\text{ Ser14}}\) (5’ GGA GGA TGG GGG ATT TGA ACC C 3’), tRNA\(^{\text{ Ser26}}\) (5’ GGA GGA TGG GGG ATT TGA ACC CTC 3’), tRNA\(^{\text{ Ser28}}\) (5’ GGA GGA TGG GGG ATT TGA ACC CTC 3’), tRNA\(^{\text{ Ser28}}\) (5’ GCC CCT TCA GAG ACC ACC C 3’), tRNA\(^{\text{ Ser24}}\) (5’ GCC GGT GAC AGG ATT TGA ACC CTC 3’), tRNA\(^{\text{ Ser24}}\) (5’ GCC GGT GAC AGG ATT TGA ACC CTC 3’), tRNA\(^{\text{ Ser28}}\) (5’ GCC CCT TCA GAG ACC ACC C 3’), tRNA\(^{\text{ Ser28}}\) (5’ GCC CCT TCA GAG ACC ACC C 3’). Hybridization temperatures used precluded cross-reactivity with other tRNAs.

**tRNA Northern Analysis.** In brief, total RNA from *M. tuberculosis H37Rv* was obtained from cells grown to exponential phase using TRIzol Reagent (Invitrogen). RNA was treated with TURBO DNase (Invitrogen). 1.5 μg of total RNA was incubated with 98 pmol of recombinant VapC-mt11 toxin for 3 h at 37 °C. Reactions were subjected to Urea-PAGE separation on a 9% polyacrylamide, 7 M urea gel and visualized by ethidium bromide staining and transferred to nitrocellulose. The following oligonucleotides were 5’ labeled with [\(^{32}\)P] ATP (Perkin Elmer Life Sciences) using T4 polynucleotide kinase (NEB): tRNA\(^{\text{ Ala11}}\) (5’ CCA CAC TGC TGC TGT GGT GCG C 3’), tRNA\(^{\text{ Arg40}}\) (5’ CCA CAC TGC TGC TGT GGT GCG C 3’), tRNA\(^{\text{ Ser14}}\) (5’ CGG GCT GAC AGG ATT TGA ACC C 3’), tRNA\(^{\text{ Ser14}}\) (5’ CGG GCT GAC AGG ATT TGA ACC C 3’), tRNA\(^{\text{ Ser26}}\) (5’ GGA GGA TGG GGG ATT TGA ACC C 3’), tRNA\(^{\text{ Ser28}}\) (5’ GCC GGT GAC AGG ATT TGA ACC CTC 3’), tRNA\(^{\text{ Ser28}}\) (5’ GCC GGT GAC AGG ATT TGA ACC CTC 3’), tRNA\(^{\text{ Ser28}}\) (5’ GCC GGT GAC AGG ATT TGA ACC CTC 3’). The DNA sequencing ladder was produced using the Sequenase version 2.0 DNA sequencing kit (USB) according to the manufacturer’s instructions. Loading buffer (95% formamide, 0.05% bromophenol blue and 0.05% xylene cyanol) was added to each sample followed by 15% urea PAGE and autoradiography.

**In vitro Translation Inhibition.** To test whether the VapC-mt11 strong toxic phenotype was due to translation inhibition, we added recombinant VapC-mt11 to the PUREexpress Kit (New England Biolabs) at a concentration of 200 pmol. Production of the DHFR protein (~20 kDa) was assessed via \(^{35}\)S Express Protein Labeling Mix (Perkin Elmer Life Sciences) incorporation. An equal volume of 2X Laemmli buffer (125 mM Tris (pH 6.8), 20% glycerol, 4% SDS, 0.01% bromophenol blue) was added to terminate the translation reaction. Samples were heated to 95 °C for 5 min prior to separation by 17.5% SDS-PAGE followed by autoradiography.

**Metabolic Labeling in *M. smegmatis*.** Transforms were obtained as previously described. Individual colonies were grown at 37 °C in 7119- TW80-AND medium containing 20 μg/ml kanamycin until OD\(_{600}\) 0.3–0.5. The culture was then split into equal portions, and 200 ng/ml anhydrotetracycline (ATc) was added to one portion. 1 ml aliquots were removed at 0, 0.5, 1, 2, 4 and 6 h post-induction and incubated with 37.5 μg of \(^{32}\)P] ATP (Perkin Elmer Life Sciences) incorporation. An equal volume of 2X Laemmli buffer (125 mM Tris (pH 6.8), 20% glycerol, 4% SDS, 0.01% bromophenol blue) was added to terminate the translation reaction. Samples were heated to 95 °C for 5 min prior to separation by 17.5% SDS-PAGE followed by autoradiography.

**5’ RNA-seq.** Total RNA was isolated from *M. tuberculosis H37Rv* harboring the plasmid pMC1s containing vapC-mt11 were grown to an OD\(_{600}\) of 0.4 and split into uninduced and induced cultures (+200 ng/ml anhydrotetracycline). Samples were collected at 0, 1, 2, 4 and 24 h post-induction and pelleted by centrifugation. Preparation of 5’-dependent libraries and data analysis was performed as described in Schifano et al.\(^b\). Briefly, for sequencing of RNAs containing 5’ hydroxyl ends (5’-OH), total RNA samples were digested using 1 U of Terminator 5’ Phosphate-Dependent Exonuclease (Epicentre) to remove RNAs containing 5’-monophosphate (5’-P). After purification using RNA Clean & Concentrator\(^{\text{TM-5}}\) (Zymo Research), 5’-OH ends were phosphorylated using 3 U of T4 PNK (New England Biolabs). The small RNA 5’ adapter (5’-GUUCAGAGUUCGAGUGCAUGCN6-3’) was ligated to the phosphorylated 5’ ends using T4 RNA ligase 1 (New England Biolabs) at 16 °C overnight. Ligated RNAs were separated from free adapters on a 6% Urea-PAGE gel and isolated by gel excision. Subsequently, cDNA was generated using Superscript II (Invitrogen) and was treated with Turbo DNase (Ambion). The cDNA was ligated to Illumina paired-end adapters (5’-CAAGCAGAGACACAGCTATATCTAGGGATCTTTACCCAGCAAGATTG-3’ and 5’-TTTGATCTCTCTTCTCTTCCAAGATTGCTAT-3’). Following adapter ligation and quality control, cDNA was amplified using the Phusion polymerase (NEB). The amplified cDNA was purified using the AMPure XP kit (Agencourt) and was checked for quality using the Agilent 2100 Bioanalyzer. The purified cDNA was then pooled and equally divided into 10 libraries. Library quality was checked using the Agilent 2100 Bioanalyzer and a Bioanalyzer DNA 1000 kit (Agilent Technologies). The RNA-Seq libraries were then sequenced on an Illumina HiSeq 2500 using a paired-end run of 100 bp. After trimming the adapter sequences from the resulting FASTQ files, the sequences were trimmed to 20 nt (discarding shorter sequences) and aligned to the *M. tuberculosis H37Rv* genome (Genbank accession: AL123456) using Bowtie 1.2.0, not allowing mismatches. For each nucleotide in the genome, we calculated the number of variants in all samples and the number of reads mapping to each nucleotide.
reads that started at that position (i.e. the number of RNA molecules that had their 5' OH end starting at each nucleotide). Read counts were normalized to sequencing depth and expressed as “reads per million of mapped reads” (rpm). The ratio of counts between induced and uninduced was calculated. Positions that had 0 counts in the uninduced library were adjusted to a pseudo-count of 0.5. We only considered reads that had at least 5 rpm for mRNAs and 50 rpm for tRNAs in the induced sample and a ratio of at least 10. Among the three tRNAs that met these criteria—tRNA\textsubscript{Glu32-CUG}, tRNA\textsubscript{Leu3-CAG} and tRNA\textsubscript{Glu4-UUC}—only two were counted as legitimate primary VapC-mt11 targets (tRNA\textsubscript{Glu32-CUG} and tRNA\textsubscript{Leu3-CAG}) because they had a GG cleavage consensus sequence immediately before the cleavage site. tRNA numbering based on the Lowe lab genomic tRNA database http://grtnadb.ucsc.edu\textsuperscript{13}. The sequencing datasets generated in this study were deposited in the NCBI Sequence Read Archive (Submission ID: PRJNA509278).

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Author Contributions
M.C. conducted the majority of the experiments and created the Figures 1–8, and wrote most of the paper. J.Z. performed in vivo M. tuberculosis experiments and created part of Figure 1. J.W.C. trained M.C. R.N.H. and J.Z. designed and interpreted the in vivo M. tuberculosis experiments. V.C.B. performed the 5′ RNA-seq experiments and created Figure 9. N.A.W, M.C. and V.C.B. interpreted the experiments and wrote the manuscript; R.N.H., J.Z. and J.W.C. reviewed the manuscript prior to submission.

Additional Information
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