Correction

MICROBIOLOGY

The authors note that Jia-Yao Hong should be added to the author list between Xueliang Ge and Suparna Sanyal. Jia-Yao Hong should be credited with performing research. The corrected author line, affiliation line, and author contributions appear below. The online version has been corrected.

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Selective translation by alternative bacterial ribosomes

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Alternative ribosome subunit proteins are prevalent in the genomes of diverse bacterial species, but their functional significance is controversial. Attempts to study microbial ribosomal heterogeneity have mostly relied on comparing wild-type strains with mutants in which subunits have been deleted, but this approach does not allow direct comparison of alternate ribosome isoforms isolated from identical cellular contexts. Here, by simultaneously purifying canonical and alternative RpsR ribosomes from Mycobacterium smegmatis, we show that alternative ribosomes have distinct translational features compared with their canonical counterparts. Both alternative and canonical ribosomes actively take part in protein synthesis, although they translate a subset of genes with differential efficiency as measured by ribosome profiling. We also show that alternative ribosomes have a relative defect in initiation complex formation. Furthermore, a strain of M. smegmatis in which the alternative ribosome protein operon is deleted grows poorly in iron-depleted medium, uncovering a role for alternative ribosomes in iron homeostasis. Our work confirms the distinct and nonredundant contribution of alternative bacterial ribosomes for adaptation to hostile environments.

Ribosomes are the macromolecular machines that translate the genetic code into functional proteins (1–3). Shortly after their discovery and role in gene translation, the “one gene, one messenger RNA (mRNA), one ribosome” hypothesis was proposed (4), but was quickly disproven (5). This led, in turn, to the “homogeneity hypothesis” for ribosomes: that all ribosomes were identical macromolecules, that would translate all mRNAs with equal efficiency (6). However, observations that ribosome composition varied according to environmental conditions and other variables immediately challenged the homogeneity hypothesis (7). But, until recently, the functional significance of ribosomal heterogeneity has not been well understood.

In eukaryotic systems, there is increasing evidence for the role and importance of ribosomal heterogeneity in fundamental physiology, development, and disease, in systems from budding yeast to organelles and animals (8–11). In particular, studies have suggested, not entirely without controversy (12, 13), that specialized ribosomes are important for vitamin B12 transport and cell cycle components (14), hematopoiesis (15), and development (16). Mutations in ribosomal proteins, or haploinsufficiency of their coded genes, have been implicated in a number of disorders such as the ribosomopathies (9, 17). Our understanding of ribosomal heterogeneity in bacteria is less advanced (18). High-fidelity mass spectrometry of intact 70S ribosomes from Escherichia coli revealed considerable heterogeneity, such as the presence or absence of the stationary-phase-induced ribosomal-associated protein, SRA (19). Other studies implicating specialized bacterial ribosomes (20, 21) have recently been questioned (22–25). Nonetheless, it is intriguing to speculate that alternative bacterial ribosomes, generated in response to environmental stresses, would result in altered translation, which, in turn, might allow adaptation to the stressful environment (18, 26, 27).

Alternative ribosomes could be generated via changes in the stoichiometry of canonical ribosomal components, association of accessory ribosomal proteins, modification of ribosomal RNA (rRNA), or incorporation of alternative ribosomal subunits, coded by paralogous or homologous genes (reviewed in refs. 9, 28, and 29). Most eukaryotic organisms code for paralogues of ribosomal subunit genes, and around half of sequenced bacterial genomes from one study included at least one ribosomal protein parologue (30). One well-characterized group of paralogous ribosomal proteins are those that lack cysteine-rich motifs (C−) compared with canonical cysteine-containing homologs (C+). C− paralogues have been described in many bacteria, including mycobacteria (31–33). In mycobacteria, the conserved alternative C− ribosomal subunits are coded in a single operon regulated by a zinc uptake regulator (zur), which represses expression in the presence of zinc ions (34), and has led to the suggestion that the function for C+/C− ribosomal subunit paralogues is to allow for dynamic storage of zinc (35–37). Furthermore, although these alternative mycobacterial ribosomal proteins (AltRPs) have recently been demonstrated to incorporate into assembled ribosomes, it has been suggested that they form nontranslating hibernating ribosome complexes due to exclusive

Significance

Many organisms, including bacteria, code for multiple paralogues of some ribosomal protein subunits. The relative contribution of these alternative subunits to ribosome function and protein synthesis is unknown and controversial. Many studies on alternative ribosomes have been confounded by isolation of alternative and canonical ribosomes from different strains or growth conditions, potentially confounding results. Here, we show that one form of alternative ribosome from Mycobacterium smegmatis has a distinct translational profile compared with canonical ribosomes purified from an identical cellular context. We also identify a role for alternative ribosomes in iron homeostasis. Given the prevalence of alternative ribosomal genes in diverse organisms, our study suggests that alternative ribosomes may represent a further layer of regulation of gene translation.


The authors declare no competing interest.

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Data deposition: Ribosome profiling and RNAseq data have been deposited in the Gene Expression Omnibus (GEO) database, https://www.ncbi.nlm.nih.gov/geo (accession no. GSE127827).

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association of a hibernation factor with alternative ribosomes (38). Here, we demonstrate, using a fully reconstituted mycobacterial translation system, that ribosomes containing the alternative subunit RpsR2 (AltRpsR) actively translate. Furthermore, the translational landscapes as measured by ribosome profiling of these alternative mycobacterial ribosomes are distinct from those generated by canonical ribosomes purified from the same cell and are characterized by a 5′ positional polarity shift. Alternative ribosome proteins were also necessary for optimal growth in iron-depleted medium, suggesting that alternative bacterial ribosomes may provide a further layer of regulation during nutrient stress.

**Results**

**Alternative Mycobacterial Ribosomes Engage in Gene Translation.** Mycobacteria encode for several alternative C–ribosomal proteins, four of which are conserved throughout the genus and are encoded within one operon (32, 38) (Fig. 1A and B). We wished to biochemically characterize alternative ribosome (AltRibo) function by purifying ribosomes containing alternative or canonical subunit proteins. We chose to C-terminally tag RpsR2 (AltRpsR) with 3xFLAG, since, of the four alternative ribosome genes within the operon, the C terminus of RpsR showed the greatest sequence variation, and we reasoned that it therefore was most likely to tolerate tagging.

To investigate AltRibo and canonical (CanRibo) RpsR ribosome function within the same cellular context, we constructed a strain of *Mycobacterium smegmatis* in which both RpsR subunits had affinity tags inserted at their C terminus, at their native loci on the mycobacterial chromosome (Fig. 1B and see Materials and Methods). In keeping with prior studies (33, 39), growth of mycobacteria in relatively zinc-depleted Sauton’s medium up-regulated AltRpSR expression, and supplementation with zinc restored CanRpSR expression (SI Appendix, Fig. S1A). To investigate whether AltRibo and CanRibo pull-down would be able to isolate intact ribosomes, we subjected immunoprecipitated ribosomes to semiquantitative mass spectrometry with labeling by tandem mass tags (TMT; SI Appendix, Fig. S2A). Of note is that our purification strategy was able to isolate ribosomes including all ribosomal subunits. AltRibs were four-fold enriched for AltRpSR (RpS18), but not the other alternative ribosomal subunits to a similar degree (SI Appendix, Fig. S2 and Dataset S1). AltRibs also had alternative ARpR proteins, for example, S19 (SI Appendix, Fig. S2); therefore, the alternative ribosomes studied by our tagging strategy under these growth conditions represent RpsR AltRibs.

We grew the dual-tagged *M. smegmatis* strain in both zinc-replete and relatively zinc-depleted conditions, purified ribosomes, and subjected them to subunit profiling. Under both conditions, translating ribosomes (polysome fraction) could clearly be identified (Fig. 1C). Immunoblotting against AltRpSR-FLAG and CanRpSR-HA confirmed that zinc depletion up-regulated AltRpSR expression. Importantly, a substantial proportion of polysomes isolated from growth in zinc-depleted medium were AltRibs (Fig. 1C), suggesting that AltRibs are resident on translating polysomes and supporting their active role in gene translation. We further subjected affinity purified AltRibs and CanRibs to biochemical analysis in a mycobacterial cell-free translation system (39). AltRibs were able to synthesize dipeptides at an efficiency similar to CanRibs (Fig. 1D), confirming that AltRibs are capable of protein synthesis.

We also constructed a strain in which the alternative subunit operon was knocked out, ΔARP. This strain grew poorly with medium in which zinc was depleted by N,N,N′-tetrakis (2-pyridinylmethyl)-1,2-ethanediamine (TPEN) (SI Appendix, Fig. S3), confirming prior results. We wondered whether this might be because, under conditions of zinc depletion, CanRibs are less proficient at protein synthesis. We performed subunit profiling on both wild-type and ΔARP *M. smegmatis*, scraped both from agar plates grown on standard medium (7H10-agar) and plates supplemented with TPEN at a concentration of TPEN that did not interfere with bacterial growth (SI Appendix, Fig. S4). Although the polysome fraction was preserved in both strains when isolated from standard growth conditions, the polysome fraction of ΔARP was substantially smaller under zinc depletion (Fig. 1E), suggesting that canonical ribosomes may translate less effectively under zinc depletion, and that alternative RpsR ribosomes are likely to be the major translating fraction under those conditions.

**Alternative Mycobacterial Ribosomes Have Distinct Translational Profiles Compared with Canonical Ribosomes.** The dual-RpsR-tagged strain (strain A) permitted us to interrogate selective ribosome translation profiles from the same cellular population, which would eliminate potential differences due to mRNA abundance or other confounding factors (40, 41). We grew the strains in relatively zinc-replete conditions, which allowed cultures to grow to greater density for ribosome isolation prior to ribosome profiling (40, 42–44). Under these conditions, the majority of ribosomes were CanRibs. To exclude the formal possibility that observed differences were due to the use of the affinity tags, we generated a second dual-tagged strain in which the affinity tags were swapped (strain B, Fig. 2A). Both strains were similarly regulated by zinc (32, 38) (SI Appendix, Fig. S1), suggesting they had comparable physiology.

Position analysis of aligned reads revealed a clear three-nucleotide periodicity (SI Appendix, Fig. S5), confirming that reads were derived from translating ribosomes for both AltRibs and CanRibs, and showed a high degree of reproducibility between replicates (SI Appendix, Table S1). Comparison of translational profiles confirmed that CanRibo-derived reads were highly correlated with total ribosome input, consistent with the fact that the majority of ribosomes under the tested condition were CanRibs (SI Appendix, Fig. S6). However, reads generated from AltRibs were less well correlated, suggesting that translational profiles from AltRibs were distinct from CanRibs (Fig. 2B). Regardless of affinity tag, CanRibo- and AltRibo-derived reads were highly correlated with themselves when comparing translational efficiency profiles generated by strain A and strain B (Fig. 2C), following correction for mRNA expression (SI Appendix, Table S1). These data, together, strongly support that AltRibs and CanRibs generate distinct translational profiles for other strains as well.

Our data suggested that alternative ribosomes had intrinsic differences in gene translation compared with canonical ribosomes. We performed differential expression analysis on AltRibo- and CanRibo-generated ribosome profile datasets, and compared these with the total ribosome input. Pull-down efficiency (but not purity) of HA-tagged subunits was less efficient than FLAG-tagged subunits. Although this was not an issue in strain A, where the highly abundant CanRibs were HA tagged, it meant that the number of reads from the HA-tagged AltRibs from strain B were lower, and, as such, fewer genes were differentially translated (up or down) in AltRibs isolated from strain B. As expected, there were few differences between CanRibs and total ribosomes. By contrast, there were a large number of genes that were translated with either decreased or increased preference by AltRibs compared with total ribosome input (Fig. 2D and E and Dataset S2). Of note is that there was significantly greater enrichment in underrepresented translated genes in AltRibs isolated from strains A and B (SI Appendix, Fig. S7). Gene ontology analysis of the overrepresented and underrepresented translated genes revealed overlap between strain A and strain B in membrane proteins and growth-related proteins for underrepresented genes (Fig. 2F), but no overlap for enriched genes (SI Appendix, Fig. S7B).

**Alternative Ribosomes Have Positional Polarized Read Distribution and a Relative Initiation Defect.** Our analysis of differences in translational profiles between canonical and alternative mycobacterial
Ribosomes revealed that, for translation of certain genes, there were clear differences in the distribution of sequencing reads along the gene length between the two samples, for example, for translation of Msmeg_0363 (Fig. 3A). To characterize these differences on a genome-wide basis, we calculated the polarity score to determine the distribution of aligned reads for each coding gene (45). Polarity scores between $-1$ and 0 represent read accumulation at the 5' end of the coding region, and scores between 0 and +1 represent read accumulation at the 3' end of the coding region (see Materials and Methods). Comparing the polarity score of AltRibos with CanRibos and total ribosome input from both strain A and strain B, there was a clear positional polarity shift toward a 5' read accumulation in alternative ribosomes (Fig. 3B).

Translation elongation does not proceed at a uniform pace (46–48). We investigated whether alternative and canonical ribosomes differed in codon occupancy. AltRibos from either strain A or strain B showed similar, although not identical, codon occupancy patterns across all 61 sense codons (Fig. 3C and SI Appendix, Fig. S8A). Comparing CanRibos with AltRibos with total ribosome input across all coding genes, there were significant differences in codon occupancy between the two ribosome isoforms in both strain A and strain B (Fig. 3D and SI Appendix, Fig. S8B). From our analysis of all 61 sense codons in both strains, 12 showed relatively high occupancy in AltRibos compared with total ribosomes, and 12 showed relatively low occupancy (SI Appendix, Fig. S8C). We wished to determine whether altered codon occupancy might be associated with the observed
Fig. 2. Alternative ribosomes have distinct translational profiles. (A) Cartoon outlining work flow for performing selective ribosome profiling in the two RpsR-tagged strains—strain A and strain B (see Materials and Methods). (B) Scatter plot showing selective ribosome profiles compared with total ribosome input in strain A and strain B. Axes represent RPKM. Blue and red dots represent down- and up-regulated reads, respectively. R2 represents Pearson correlation. (C) Correlation of translation efficiency of total ribosome, selective CanRibo, and selective AltRibo inputs in strain A compared with strain B. R2 represents Pearson correlation. (D and E) Normalized ribosome profile read density for (D) CanRibos and (E) AltRibos compared with total ribosome input in strain A and strain B. Significantly up-regulated (log2 FC > 0.5, P value < 0.05) and down-regulated (log2 FC < −0.5, P value < 0.05) genes are represented by red and blue dots, respectively. (F) Gene ontology analysis (using DavidTools) of the top three categories of down AltRibo-enriched translated genes.
Fig. 3. Alternative ribosomes have 5′ read accumulation and a relative initiation defect compared with canonical ribosomes. (A) Normalized reads of each ribosome input for the gene Msmeg_0363 were plotted along gene length using IGV software (see Materials and Methods). Reads from AltRibos show a clear 5′ accumulation compared with reads generated from CanRibos or total ribosomal input. (B) Shifts in positional polarity scores for the entire genome generated from selective AltRibo and CanRibo reads from strains (Upper) A and (Lower) B. A negative score indicates 5′ read accumulation, and a positive score indicates a 3′ read accumulation. (C) The relative A-site codon occupancy for all 61 sense codons for AltRibos and CanRibos in strain A compared with total ribosome input. (D) Cumulative probability and violin (Inset) plots for correlation of each gene between codon occupancy for AltRibos and CanRibos compared with total ribosome input from strain A. ***P < 0.001 by Student’s t test. (E) The relative codon frequencies of the 5′ 50 codons and 3′ 50 codons for each ORF were analyzed. Comparing AltRibo (Left) high-occupancy codons and (Right) low-occupancy codons with nonsignificantly enriched codons, there was significant enrichment of high-occupancy codons at the beginning of ORFs, and a trend toward enrichment of low-occupancy codons at the end of ORFs, by χ² test. (F) The extent of initiation complex formation by AltRibos compared with CanRibos measured by retention of 3H-fMet count on a nitrocellulose filter. (G) The kinetics and extent of binding of the initiator tRNA to the mRNA programmed 70S ribosome (AltRibo vs. CanRibo) followed with boron-dipyrromethene (BODIPY) fluorescence.
polarity differences between AltRibos and CanRibos. We considered the first and last 50 codons of all coding genes and compared the relative abundance of the 12 high- and 12 low-occupancy codons in these regions. For the 12 high-occupancy codons, 10 were relatively enriched at the 5′ end of coding regions, and for the 12 low-occupancy codons, 8 were relatively enriched at the 3′ end of coding regions (Fig. 3E). Furthermore, although purified AltRibos formed 70S initiation complexes, they appeared to do so at slightly lower efficiency compared with CanRibos (Fig. 3F), suggesting another potential mechanism for the observed 5′ polarity shift. The lower efficiency in 70S initiation complex formation could be due to impaired binding of the initiator transfer RNA (tRNA) as demonstrated by BODIPY-Met-tRNA\textsuperscript{Met} binding to the ribosome monitored by increase in BODIPY fluorescence (Fig. 3G).

Our in vivo and in vitro data suggested that, although AltRibos and CanRibos both partake in protein synthesis, they are not identical in translation. Both our observed positional polarity shift from ribosome profiling and our biochemical data suggested that AltRibos may have a relative initiation defect. Given the potential role of AltRibos for protein synthesis under zinc-depleted conditions, which may be a marker of generalized environmental stress, could it be that AltRibos are “slow and accurate” compared with CanRibos? To address relative translation rates, we made a modified Nlu luciferase reporter under control of a tetracycline promoter, in which the C terminus was tagged to make the translated protein unstable (ref. 49 and SI Appendix, Fig. S9A, and see Materials and Methods). This would ensure that measured Nlu activity represented recently synthesized proteins following addition of the ATc inducer, and not due to accumulation of the luciferase prior to induction by ATc due to leaky expression from the promoter. Measurement of Nlu activity after a 5-min pulse under conditions of normal zinc (CanRibon dominant) and zinc depletion with TPEN (AltRibon dominant) did not reveal any differences (SI Appendix, Fig. S9B), suggesting that protein synthesis rates under conditions that favor either CanRibos or AltRibos do not measurably differ. Addition of chloramphenicol as a protein synthesis inhibitor to examine Nlu synthesized only during the pulse and not subsequently also confirmed the same result. We also looked for correlations of codon usage frequency and AltRibo and CanRibo translatomes and did not find any consistent patterns that might suggest that AltRibo codon occupancy is associated with rare codons or vice versa (SI Appendix, Figs. S10 and S11).

RpsR (S18) has been implicated in accuracy of translational decoding due to a potential role in constraining mRNA exit from the ribosome (50). We measured relative translational error rates in high/low zinc conditions using three different reporters that measure ribosomal decoding errors (51). Again, there were no significantly different rates of translational error (SI Appendix, Fig. S12), suggesting that AltRibos are neither more nor less accurate than CanRibos in decoding mRNA, and can equally well translate a model protein.

To gain further potential insights into AltRibo function, we examined the relative enrichment of “ribosome-associated” proteins (41) that were pulled down with either the AltRibos or CanRibos in our semiquantitative mass spectrometry analysis (Dataset S1). There were several proteins that were enriched with either AltRibos or CanRibos (Fig. 4A). Of note is that two of the top three AltRibo-enriched proteins were type VII secretion-associated proteins. Furthermore, we only isolated two Esx-3-associated proteins (EccB3 and EccC3), both of which were relatively AltRibo enriched (Fig. 4A). Since Esx-3 has been implicated in iron homeostasis in mycobacteria (54), and, furthermore, is, similarly to ARPs, regulated by the zur regulon (55), we wondered whether AltRibos might play a role under iron depletion conditions. We therefore compared growth of wild-type \textit{M. smegmatis}, the \text{AltAR} strain, and \text{AltAR} complemented with the AltRop operon in medium that had iron removed by chelex 100 (54). In iron-chelated medium, \text{AltAR} had a major growth defect. Since chelex 100 is a relatively nonspecific metal chelator, we supplemented medium with either zinc or iron. Zinc supplementation led to only partial rescue, but the growth defect could only be fully complemented by replacement of either the operon or iron (Fig. 4B), suggesting a specific iron-limiting phenotype for mycobacteria lacking the alternative ribosome operon.

**Discussion**

Together, our studies demonstrate that alternative mycobacterial ribosomes incorporating the C–paralogue AltRpsR are not only competent for translation but that these alternative ribosomes have distinct translational landscapes compared with their canonical counterparts. The ribosome is an RNA machine (2), and recent studies have identified functional importance for rRNA heterogeneity in bacterial ribosomes (26, 27, 56). The role of rProtein heterogeneity is more controversial, but multiple studies have shown that alterations, for example, by mutation, in ribosomal subunit proteins may also have profound impacts on aspects of translation function (14, 41, 57, 58). Furthermore, since RpsR forms part of the 30S “core” that interacts directly with 16S rRNA (59), it is possible that ribosomes composed of alternate RpsR isoforms may influence diverse aspects of ribosome function.

We leveraged the power of ribosome profiling and affinity purification of alternative ribosomes to show that alternative RpsR mycobacterial ribosomes have altered codon occupancy compared with ribosomes containing the canonical RpsR paralogue, as well as a relative 5′ positional polarity shift in translation of open reading frames (ORFs). It should be noted that, due to our tagging and purification strategy, we were primarily comparing RpsR canonical and alternative ribosomes. Due to their differential expression, we would expect that, in
high and low zinc environments, alternative and canonical ribosomes would contain mostly the entire canonical or alternative subunit proteins. In environments where expression of all subunits is sustained (such as our experimental conditions), multiple combinations of “alternative” ribosomes could coexist, and our data are unable to resolve between these. Ribosomal profiling of specialized ribosomes has previously demonstrated specific functions of heterogeneous ribosome populations in stem cells and for the translation of mitochondrial proteins in eukaryotic cells (14–17). In bacteria, ribosome profiling of trigger factor associated with ribosomes demonstrated the requirement of trigger factor particularly for the translation of outer membrane proteins in E. coli (41), but ribosome profiling had not been employed for ribosomes incorporating ribosomal protein paralogs.

There have been relatively few studies of bacterial ribosomal heterogeneity when compared with eukaryotic systems (18). However, there is evidence that ribosomal heterogeneity may be just as pervasive in bacteria as eukaryotes (26, 27, 56). Mycobacteria, for example, have very distinct translational features compared with the model E. coli system (44, 60, 61). Recent structural information about the mycobacterial ribosome identified new ribosomal protein subunits, but these new subunits, bl37 and bs22, were not present in all ribosomes identified by cryoelectron microscopy (39, 62, 63).

Many diverse bacterial species code for C− ribosomal subunit paralogs (30), but their distinct translational functions, if any, have not been fully characterized. A recent examination of the mycobacterial C− paralogs that are the subject of this study suggested that C− ribosomes are hibernating and do not actively engage in gene translation under zinc depletion due to exclusive C− ribosome interaction with the hibernation factor MPY (38, 64). Those findings are in contradistinction with our own. By both biochemical analysis and ribosome profiling, our data support a role for translating AltRibos, even under conditions of zinc depletion. It is possible that use of supraphysiological (1 mM) zinc in culture medium—50 times higher than the concentrations in human plasma (65)—led to lack of binding of MPY to canonical (C+) ribosomes under those conditions (38). However, our isolation of ribosomes from standard growth medium showed lack of enrichment of MPY with AltRibos compared with CanRibos (Fig. 4). We also demonstrated that canonical ribosomes less polyosomal fraction under zinc depletion (Fig. 1E). Together with previous studies of M. smegmatis grown under conditions where C− ribosomes would not have been predominant (66, 67), these data suggest that MPY is not exclusively associated with C− ribosomes.

Structural data showed association of aminoacylated tRNA with C− ribosomes (33), supporting a role for C− ribosomes in protein synthesis. However, our data suggest that alternative ribosomes and canonical ribosomes are not only competent for protein synthesis, but they have differences potentially in both translation initiation and codon occupancy. Both of these differences may contribute to the relative 5′ positional polarity shift of reads in alternative ribosomes as well as the specific enrichment only of down-regulated synthesized proteins by AltRibos. However, we cannot exclude that the positional polarity itself led to the codon occupancy differences observed in the beginning and end of genes (Fig. 3E). Multiple mechanisms have been proposed for observed differences in codon occupancy and elongation (68). Decoding of modified tRNA bases (47) and differential affinity of specific ribosome isoforms for aminoacyl tRNAs (46) also contribute to altered rates of gene translation. Of note is that RpsS18 (of which AltRpsR and CanRpsR are the two mycobacterial isoforms) is part of an mRNA “nest,” which contributes to preinitiation binding of mRNA to the 30S subunit (69), and it is tempting, therefore, to speculate that differences in RpsR protein sequence may contribute the observed differences in initiation complex formation.

We have also uncovered a role for the alternative ribosome operon in iron homeostasis: Mycobacteria lacking this operon have substantially attenuated growth under iron limitation compared with wild-type M. smegmatis. This was not entirely due to nonspecific chelation of zinc by chelex-100. Supplementation of zinc led to only partial rescue of the growth defect, unlike the full complementation seen with iron supplementation alone. While the precise molecular mechanisms by which AltRpsR contributes to iron homeostasis is unknown, we were intrigued by the observation that pull-down of AltRibos enriched for interactions with esx-3, as well as siderophore synthesis-associated proteins (Fig. 4/4). The recent finding that M. smegmatis ΔARP had a pronounced colony morphology phenotype (70) suggest that ARPs may be implicated in the maintenance of the mycobacterial membrane and secretion apparatus. Our study confirms not only that alternative mycobacterial ribosomes actively participate in protein synthesis but also that RpsR alternative ribosomes have distinct translational features, and alternative bacterial ribosomes contribute to environmental adaptation.

Materials and Methods

Bacterial Strains and Culture. Wild-type M. smegmatis mc2−155 (71) and derived strains were grown in either Middlebrook 7H9 media supplemented with 0.2% glycerol, 0.05% Tween-80, 10% albumin-dextrate-salt with appropriate antibiotics, or Sauton’s medium (0.05% KH₂PO₄, 0.05% MgSO₄·7H₂O, 0.2% citric acid, 0.005% ferric ammonium citrate, 6% glycerol, 0.4% asparagine, 0.05% Tween, pH 7.4) (32). Zinc sulfate at indicated concentrations was added to Sauton’s medium as per specific protocols. For the iron depletion experiments, we modified a previous method (54). Briefly, Sauton’s medium was prepared as above with the exception of the magnesium sulfate. After preparation, 10 g of chellex 100 resin was added to 1 L of medium, thoroughly mixed, and left for 24 h. The medium was sterile filtered to remove the chelating agent beads, and 1 g of sterile MgSO₄·7H₂O was added to the medium. Zinc sulfate and iron chloride were also supplemented at the indicated concentrations as appropriate for the experimental condition. If not otherwise noted, bacteria were grown and maintained at 37 °C with shaking.

M. smegmatis AltRPs Knock-Out Strain and Complemented Strain Construction. In normal conditions (High zinc), the AltRPs operon is not required for growth. A double cross-over strategy was used to construct an unmarked AltRPs knockout strain as previously described (72). Sequences 1,000 base pairs (bp) upstream and downstream of the operon were cloned and ligated into the P2NIL suicide vector. The lacZ and sacB genes were cloned from pGOAL17 and ligated to P2NIL containing upstream and downstream 1,000-bp regions to generate the AltRPs deletion construct. Two micrograms of plasmid transformed to wild-type M. smegmatis competent cells by electroporation and selected on lysogeny broth (LB) plates supplemented with 25 μg/mL kanamycin and 50 μg/mL X-gal. Blue colonies were screened for single cross-over recombinants and further verified by Southern blot. White recombinants were further plated on LB plates containing X-gal and 2% sucrose with 10-fold serial dilutions. White colonies were screened for double cross-over strains by PCR verification. A correct knockout strain was further verified by Southern blot and used in subsequent experiments.

For complementation of the knockout strain, the upstream 500 bp of the coding region for the AltRPs operon (presumably incorporating the promoter region) along with the whole AltRPs operon was cloned with C-terminal 3xFlag tag to AltRpsR and ligated to pML1342 as a complementation plasmid. The plasmid was transformed to ΔAltRPs competent cells and plated on LB plates with 50 μg/mL hygromycin. Recombinants were further verified by Western blot in Sauton’s medium supplemented with different concentrations of zinc to check the expression from the operon.

Generating Endogenous AltRpsR/CanRpsR with Different Affinity Tags Strains. Upstream 500 bp (US500) and downstream 500 bp (DS500) of AltRpsR/CanRpsR, stop codons were cloned. Different affinity tag sequences (3xFlag/3xHA) fused with different antibiotic expression cassette (Hygromycin/Zeocin) were generated by overlap PCR (3xFlag-Zeo oligo cassette was kindly provided by Jun-Hao Zhu, Harvard University). The upstream, tag, antibiotic, and downstream cassettes were fused by Gibson assembly and cloned into pUC19 vector. The pUC19 plasmid containing four different recombineering oligo cassettes (AltRpsR-3xFlag-Zeo, AltRpsS-3xHA-Hgy, CanRpsR-3xHA-Hgy, and CanRpsR-3xFlag-Zeo) was generated. M. smegmatis containing the
plasmid pNltET-Sadi-kan (73) was grown to optical density at 600 nm (OD$_{600nm}$) of 0.2, and 10 μM isovaleronitril was added to induce the expresion of RecET, after inducing for 6 h, competent cells were prepared by three washes in 10% glycerol. Oligos for recombineering were amplified from pUC19 series plasmid, and 2 μg of DNA was transferred to the competent cells. Bacteria were plated on LB plates supplemented with either 50 μg/mL Hygromycin or 20 μg/mL Zeocin. Desired colonies were genotyped by PCR and further verified by Western blot to test the expression of AltRpsR/CanRpsR by blotting with either Flag or HA antibody respectively.

**Western Blot to Test Zinc-Switch Phenotype.** Strain A and strain B were cultured in TH9 medium to stationary phase (OD$_{600nm}$ ≈ 3) and subcultured 1:500 to Sauton's medium (zinc free) supplemented with different concentrations of zinc sulfate. When bacteria reached stationary phase, bacteria were washed and resuspended in TE buffer. The bacterial suspension was disrupted by bead beating and lysate centrifuged at 17,950 × g, 4 °C for 5 min. Protein concentration was quantified by Bradford assay (Bio-Rad), and the same amount of protein was loaded onto 5%/12% sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS/PAGE) gel. Proteins were further transferred onto poly(vinylidene difluoride) membrane (Bio-Rad). The membrane was blocked in 4% skim milk at room temperature (RT) for 1 h. Primary antibody was diluted 1:2,000, and the blot was incubated at 4 °C overnight. The membrane was then washed with tris-buffered saline-Tween 20 (TBS-T) at RT and secondary antibody, diluted 1:5,000 rate, and incubated at RT for 1 h. After washing with TBS-T, the image was developed by ECL Western Blotting Substrate (Pierce).

**Subunit Profiling of M. smegmatis.** For liquid culture, M. smegmatis strain was grown on Middlebrook TH9 medium till OD$_{600nm}$ = 1 and collected by centrifuge at 4,500 × g, 4 °C for 20 min. For plates, wild-type M. smegmatis strain and ΔALT strains were plated on 7H10 plate or 7H10 plate supplied with 10 μM TPEN, and bacteria were collected by scraping. The bacterial pellet was washed and resuspended with polysome buffer (50 mM Tris-acetate pH = 7.2, 12 mM MgCl$_2$, 50 mM NH$_4$Cl). Bacteria were pulverized by beads beating or French Press, and the lysate was centrifuged at 18,800 × g, 4 °C for 45 min. Cleared lysate was further loaded to a linear sucrose gradient with one gradient fraction centrifuged at 39,000 rpm, 4 °C for 5 h. Gradients were fractionated with continuous A$_{260}$ measurement, and fractions were collected for downstream analysis.

**Relative Translation Rate Assay.** The reporter used in this assay is depicted in SI Appendix, Fig. S9A. Of note is that the lysine and threonine codon in the Niuc sequence were codon-optimized to be neutral with regards to codon occupancy by AltRibo or CanRibo generated from prior ribosome profiling data, to minimize the bias in the assay. The codon-optimized Niuc was cloned to pMC15 vector with a C terminus tag to target Niuc from protease degradation (74). This would limit expression from the promoter in the absence of inducer to below detection limits, and therefore only newly synthesized protein upon addition of inducer would be measured by Niuc activity. Bacteria containing the reporter was grown in Sauton’s medium to stationary phase (OD$_{600nm}$ = 3) and diluted to OD$_{600nm}$ = 0.2 into Sauton’s medium supplied with either 10 μM zinc sulfate or 0.5 μM TPEN, and ATC was added to the culture at a final concentration of 50 ng/mL. Five minutes after induction, bacteria were pelleted, washed twice, and resuspended in fresh medium as before but without ATC, and ± 200 μg/mL chloramphenicol as a protein synthesis inhibitor. Bacterial aliquots were collected every 10 min and fast frozen in liquid nitrogen. After samples from all time points were collected, luminescence was measured. For each condition, three biological replicates were included.

**Ribosomal Decoding Assay.** The procedure of dual luciferase-based mis-translation assay was carried out as previously described (51, 53). Briefly, the bacterial strains containing the reporter plasmid were grown to late stationary phase (OD$_{600nm}$ > 3) and diluted to OD$_{600nm}$ = 0.2 into Sauton’s medium supplemented with either 10 μM zinc sulfate or 0.5 μM TPEN, following acetamide induction for 6 h. After induction, bacterial pellets were collected, and supernatant was discarded. Bacteria were disrupted by passive lysis buffer provided by dual luciferase kit (Promega), and Firefly and Renilla luminescence was measured by luminometer with 1,000 ms as integration time. For each experiment, three biological replicates were included.

**Selective Ribosome Profiling with Affinity-Purified Tagged AltRibosomes.** Bacterial cultures of dual-tagged strain A or strain B were grown until OD$_{600nm}$ = 1 and treated with 100 μg/mL chloramphenicol for 3 min to arrest elongating ribosome before harvesting bacteria. Bacterial pellets were collected by centrifuging at 4,500 × g, 4 °C for 10 min. The pellet was washed and resuspended with ice-cold polysome buffer with minor recipe (12 mM Tris-acetate pH 7.2, 12 mM MgCl$_2$, 100 μg/mL chloramphenicol). The suspended bacterial suspension was dropped into liquid nitrogen and smashed into powder. The powder was smashed several times with repeated chilling with liquid nitrogen and was further pulverized with beads beating four to five times with chilling in liquid nitrogen between each step. After centrifugation at 18,500 × g for 45 min, the cleared lysate was transferred to a new tube supplied with 70 μL MNase to digest ribosome-unprotected mRNA. The predigested lysate was layered over a 1-M sucrose cushion and centrifuged at 30,000 rpm, 4 °C for 20 h in Beckman 70Ti rotor. After ultracentrifugation, the ribosome pellet was washed and dissolved in polysome buffer. The dissolved ribosome solution was further digested with RNase at 4 °C for 1 h. The digested ribosome fraction was incubated with either Flag resin or HA resin at 4 °C overnight. After washing of the bound resin, the resin was eluted with 3×Flag/3×HA peptide to isolate the AltRibo (eluate), and the remaining flow-through was confirmed as consisting almost entirely of CanRibos.

The procedure for building deep sequencing libraries was followed as previously described (43), with minor changes. The detailed protocol is described below. Ribosome-protected mRNA fragments were extracted by miRNeasy kit according to the manufacturer’s instructions and size-selected for 26- to 34-nm fragment by marker oligo through 15% TBE-UREA gel (8 M urea, 20% acrylamide, 37.5% methyleneacrylamide). Polyacrylamide gel electrophoresis. The gel lane was sliced and smashed into pieces and soaked in 400 μL of RNA gel extraction buffer (300 mM sodium acetate pH 5.5, 1 mM EDTA (ethylenediaminetetraacetate acid), and 0.25% SDS) and rotated at RT overnight. RNA was precipitated with 1.5 μL of GlycoBlue and 500 μL of isopropanol. The RNA was dephosphorylated with 1 μL of T4 PNK at 37 °C for 1 h. RNA was chromatin digested by isopropanol precipitation. Samples were washed and resuspended in 0.5 μL of Universal miRNA cloning linker and 1.0 μL of T4 RNA ligase (truncated) at RT overnight. The ligation product was purified by isopropanol precipitation and visualized by 15% TBE-UREA PAGE. After slicing the corresponding ligated mRNA fragment, the samples were then subjected to reverse transcription with superscriptase III and RT-Primer. After incubating the reaction at 48 °C, 30 min, the RNA template was further hydrolyzed with 2 μL of 10 M RTR at 98 °C for 20 min. The RNA product was precipitated with isopropanol and size-selected with 15% TBE-UREA PAGE. The corresponding region was sliced and soaked in 400 μL of DNA gel extraction (300 mM NaCl, 10 mM Tris pH = 8, and 1 mM EDTA) and rotated at RT overnight. The complementary DNA (cDNA) was purified by isopropanol precipitation and circularized with 1 μL of CircLigase and incubated at 60 °C for 1 h. The circularized cDNA template was incubated with 1 μL of 10 mM Biotinylated RNA subtraction oligo pool mix. The Oligo sequence was adopted from another study (44), with additional oligos newly designed according to our preliminary ribosome profiling data (SI Appendix, Table S2). The mixture was denatured for 90 s at 100 °C and then annealed at 0.1 °C to 37 °C. This was then incubated at 37 °C for 15 min. Thirty microliter of streptavidin C1 DynaBeads was added to the mixture and incubated for 15 min at 37 °C with mixing at 1,000 rpm. Then the mixture was placed on a magnetic rack to isolate streptavidin-DynaBeads. The supernatant was transferred into Sauton’s medium supplemented with 20 μL of 0.5 μM zinc sulfate or 0.5 μM TPEN, and 1 mM EDTA, and rotated at 4 °C for 1 h. The RNA product was purified by isopropanol precipitation. The subsequent cDNA template was used for library amplification with Phusion high-fidelity DNA polymerase for 12 to 14 cycles. PCR products were purified from 8% TBE PAGE gel. The corresponding bands were sliced and soaked in DNA gel extraction buffer and rotated at RT overnight. The PCR products were purified by isopropanol precipitation, and the concentration and quality were measured with Agilent 2100 Bioanalyzer. Libraries were sequenced on the Illumina X Ten sequencer.

**Semi-Quantitative Mass Spectrometry.** Strain A was grown in Sauton’s medium supplemented with 10 μM zinc sulfate to OD$_{600nm}$ = 1, and bacterial pellets were collected by centrifugation at 4,500 × g for 20 min, 4 °C. For semi-quantitative mass spectrometry, three biological replicates were collected and mixed together for further analysis. Total ribosome, CanRibo, and AltRibo were collected by using the same purification strategy described above for ribosome profiling. Western blot performed on samples confirmed the purity of each ribosome fraction. The purified ribosomes representing total ribosomes, AltRibs, and CanRibs were then subjected to mass spectrometry by TMTs as previously described (75) using a Thermo Scientific Q Exactive HF-X Hybrid Quadrupole-Orbitrap Mass Spectrometer.

**Large-Scale Tagged Ribosome Purification for Biochemical Analysis.** Bacterial cultures (−30 L) were grown to around OD$_{600nm}$ ≈ 1, and bacterial pellets were collected by centrifugation at 4,500 × g for 20 min, 4 °C. Pellet was washed and resuspended in polysome buffer. Bacteria were disrupted by
French Press and centrifuged at 18,500 × g, 4 °C for 1 h to collect supernatant. MNase was added to the cleared lysate at a concentration of 70 U/ml and digested at 4 °C overnight. The digested lysate was loaded onto 1-M sucrose cushions and centrifuged at 30,000 rpm, 4 °C for 20 h. After centrifugation, the supernatant was discarded, and the ribosome pellet was washed with polysome buffer and dissolved in polysome buffer with gentle shaking at 4 °C. The crude ribosome suspension was further digested with MNase at 4 °C overnight. After secondary digestion, the ribosome preparation was dialyzed against Hepes:Polymix buffer (76, 77). The ribosome preparation was incubated with anti-Flag M2 beads at 4 °C overnight. After binding with M2 beads, the flow-through was collected as CanRibo and AltRibo was collected by eluting with Flag peptide. Each fraction, comprising total Ribo, CanRibo (flow-through), and AltRibo (Eluate), was probed by Western blotting for quality check and purity prior to further analysis.

In Vitro 70S Initiation Complex Formation. Initiation complex was formed by incubating 70S ribosome variants as described above (0.2 μM), [3H]Met-tRNA\textsuperscript{Met} (0.5 μM), XR7mRNA (AUG-UAA) (76) (0.5 μM), initiation factors (0.5 μM) and guanosine triphosphate (GTP) (1 mM) at 37 °C for 15 min in Hepes:Polymix buffer (76). The reactions were thereafter filtered through BA-85 nitrocellulose membranes and washed with 10 ml of ice-cold Hepes:Polymix buffer (pH 7.5). The radioactive information on the filter was measured in a Beckman LC6500 scintillation counter.

In Vitro Initiator tRNA Binding. BODIPY-labeled Met-tRNA\textsuperscript{Met} (0.1 μM) was rapidly mixed in stopped flow with 70S ribosomes (1 μM) preincubated with XR7mRNA (AUG-UAA) (0.5 μM). BODIPY fluorescence was excited at 575 nm, and the change in fluorescence signal was monitored in real time after passing through a 590-nm cutoff filter. The time course data were obtained by averaging three to five individual traces and fitted with a single exponential model.

In Vitro Dipeptide Assay. For Met-Leu dipeptide formation, an initiation complex was formed with recombinant 70S ribosome variants (1 μM) at 37 °C which contained M. smegmatis EF-Tu (20 μM), EF-Ts (20 μM), tRNALeu (100 μM), Leu amino acid (0.5 mM), Leu-tRNA synthetase (1 unit per μM), Hepes:Polymix buffer (76) (1 mM) preincubated with EF-Tu (20 μM), EF-Ts (20 μM), tRNALeu (100 μM) and guanosine triphosphate (GTP) (1 mM) at 37 °C. Both initiation complex and elongation mixture were collected from the same population of bacteria, to identify differential translated genes, we used edgeR on the corresponding ribosome profiling fragments (RPFs) were included to study the frequencies of all codons. For each coding gene, its codon density was calculated by normalizing the observed RPF frequencies by the total frequencies of codons. Later, we included genes with at least 100 RPFs as input and obtained an averaged codon density for each codon. Here we denoted $T_{\text{codon}}$, as the averaged codon occupancy of codon, for AltRibo or CanRibo population, while $R_{\text{codon}}$, is the averaged codon occupancy of codon, for reference population, in this case, the total ribosomes. To better clarify the difference between AltRibo and CanRibo population, we further defined codon occupancy shift as follows:

$$\text{codon occupancy shift}_{\text{codon}} = \frac{T_{\text{codon}} - R_{\text{codon}}}{R_{\text{codon}}}.$$  

Significantly different codon usage was detected by comparing the codon density of all studied aORFs under test conditions (AltRibo/CanRibo) against the corresponding density under the reference condition (total ribosome input) ($t$ test $P$ value < 0.05 and shift < -0.05).

Additionally, for each individual aORF, we correlated its codon density from AltRibo/CanRibo population with that from total ribosome population (Pearson correlation was used in this study).

Differential Codon Abundance. In this study, we used the concept of codon abundance to measure the occurrence of specific codons in the 50 codons within the 5’ or 3’ of the coding region. The calculation of codon abundance followed a previous study (81). To better demonstrate the difference, the final results were presented in the following form:

$$\text{Slope}_{\text{codon}} = \frac{\text{codon abundance}_{\text{codon}, 3’} - \text{codon abundance}_{\text{codon}, 5’}}{\text{codon abundance}_{\text{total}, 3’} - \text{codon abundance}_{\text{total}, 5’}}.$$  

Slope$_{\text{codon}}$ represents the slope of codon, in which codon abundance$_{\text{codon}, 3’}$ represents the codon abundance of codon, in the 3’ region, while codon abundance$_{\text{total}, 3’}$ represents the codon abundance of codon, in the 5’ region.

Differential Translation Analysis. Since AltRibo, CanRibo, and total ribosomes were collected from the same population of bacteria, to identify differentially translated genes, we used edgeR on the corresponding ribosome profiling datasets (82). During analysis, replicates were included. Differentially translated genes were identified by log2 fold change (FC) > 0.5 (up-regulated) or log2 FC < -0.5 (down-regulated) and $P$ value < 0.05. In this study, the datasets of total ribosome were treated as the control and compared against AltRibo or CanRibo to identify differentially translated genes.

Statistical Analysis. Appropriate statistical tests are detailed within each protocol and in the figure legends.

Data Availability. Ribosome profiling and RNAseq data presented in this study are available with GEO accession number GSE127827.


