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Quantitative Control for Stoichiometric Protein Synthesis

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Abstract

Bacterial protein synthesis rates have evolved to maintain preferred stoichiometries at striking precision, from the components of protein complexes to constituents of entire pathways. Setting relative protein production rates to be well within a factor of two requires concerted tuning of transcription, RNA turnover, and translation, allowing many potential regulatory strategies to achieve the preferred output. The last decade has seen a greatly expanded capacity for precise interrogation of each step of the central dogma genome-wide. Here, we summarize how these technologies have shaped the current understanding of diverse bacterial regulatory architectures underpinning stoichiometric protein synthesis. We focus on the emerging expanded view of bacterial operons, which encode diverse primary and secondary mRNA structures for tuning protein stoichiometry. Emphasis is placed on how quantitative tuning is achieved. We discuss the challenges and open questions in the application of quantitative, genome-wide methodologies to the problem of precise protein production.

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1. INTRODUCTION

In 1959—two years prior to the proposal of the operon model—Bruce Ames and Barbara Garry (4) showed that the four histidine biosynthesis enzymes in *Salmonella* were always produced at the same ratios, regardless of induction levels. This evidence for coordinated regulation, together with the genomic linkage of the genes encoding these enzymes, was key to François Jacob and Jacques Monod's (83) hypothesis of polycistronic operons. At that time, it was not known that these proteins are produced in differing amounts despite being regulated and transcribed together. Such constant, nonequimolar proportions appeared to be under positive selection, as the same stoichiometry of functionally related proteins, e.g., glycolytic enzymes, was observed in cells from yeasts to mammalian tissues (134). Fast-forward to the turn of the century, when genomic techniques revealed that these constant-proportion groups constitute the foundation of gene regulatory networks, which can be decomposed into modules of coexpressed proteins that allow for a small number of regulators to control a large number of genes (54, 149). In essence, the synthesis rate of a protein is set in two orthogonal dimensions: the overall expression of the module it belongs to and the relative stoichiometry within the module.

Although stoichiometry is often not subject to regulation, perturbations to relative expression can be detrimental. For proteins that assemble into heteromeric complexes, excess subunits that do not have binding partners may misfold or aggregate. Some coregulated proteins play antagonistic roles with each other, making balanced production critical for their functions. For many other groups of proteins, the rationale for their precise stoichiometry remains unknown. Nevertheless, a recent comparative proteomic analysis revealed that most of them maintain the same ratios of

Operon: group of genes originally defined by Jacob and Monod as the genetic unit of coordinated expression

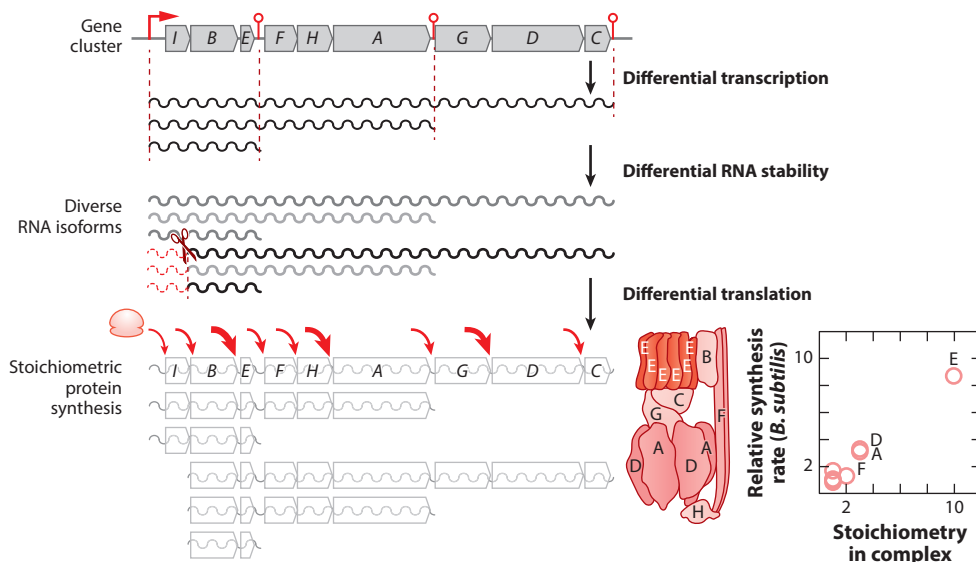


Figure 1

Schematic representation of the *atp* operon from *Bacillus subtilis*. Control in the expression of genes occurs at the steps of differential transcription due to leaky intrinsic terminators, followed by mRNA processing that leads to differential mRNA stability (a minor processing site in *atpB* is omitted for clarity; see **Figure 3**). The genes transcribed in the diverse polycistronic mRNA isoforms are then translated at different rates. All control steps contribute to ATP synthase subunits being produced in proportion to their stoichiometry in the complex (ribosome profiling data from Reference 98).

synthesis rates across large phylogenetic distances, despite dramatic divergences in the molecular mechanisms that determine their relative rates (98). These results suggest that stoichiometric protein synthesis did not happen by chance. Rather, it is intricately optimized according to the quantitative relationship between expression and cell fitness.

Mechanistically, stoichiometric protein synthesis is often implemented at the posttranscriptional level in bacteria (**Figure 1**). Because many functionally related genes are organized into operons, they can be coregulated by transcription. The relative rates of protein synthesis are then set by posttranscriptional processes, such as mRNA processing, differential translation, and other RNA-based regulation. Characterizing these posttranscriptional processes at a quantitative level is thus critical for understanding the control of stoichiometric protein synthesis. It must also be noted that the idealized operon model, in which neighboring genes are exclusively cotranscribed as a single unit of polycistronic mRNA, applies to only a fraction of coregulated genes in bacteria. Neighboring genes are often punctuated by internal promoters, leaky transcription terminators, and RNA-processing sites that are also important for setting the final stoichiometry of protein synthesis. Increasingly, these transcriptional and posttranscriptional events can be better mapped throughout the genome using high-throughput technologies, revealing a diverse set of control strategies.

Here we review recent evidence for why and how bacterial cells establish quantitative control for stoichiometric protein synthesis. We start with genome-wide evidence for the requirement of precise control among coregulated genes. We then revisit the definition of operons by taking into account the diverse mRNA isoforms that one can now routinely map with high resolution using variations of RNA sequencing (RNA-seq) methods. We focus our discussion on recent progress in

mRNA processing: event driven by ribonucleases through which a single transcription unit is diversified to two or more well-defined isoforms of different abundances

mRNA isoform: transcription unit generated by differential transcription and mRNA stability for operons with complex mRNA architectures

Translation

efficiency: rate of protein production per mRNA copy for a given gene; total synthesis rate is given by mRNA abundance multiplied by translation efficiency

Expression

stoichiometry: relative rate of protein production among functionally related genes

using these methods to understand the quantitative determinants of the stoichiometry of protein synthesis rates within operons. The stoichiometry may be further regulated by environmental signals, and Adhya (2) summarized a number of classic examples in a review. After summarizing these operon-based controls, we briefly discuss the challenges that nonproximal genes must face for concerted regulation to maintain relative stoichiometry. Finally, we close by providing a perspective on the remaining challenges that must be overcome to achieve a fully quantitative understanding of protein production in bacteria.

2. PRECISE PROTEIN SYNTHESIS CONTROL: PROPORTIONAL SYNTHESIS AND IN-PATHWAY STOICHIOMETRIES

2.1. Historical Perspective

As early as the 1960s, the study of protein synthesis in phage-infected cells provided clear evidence for differential protein synthesis from polycistronic genes (128). Despite being encoded on the same viral RNA genome, different phage proteins exhibit orders of magnitude of variation in synthesis (127). This allows the phage to produce many more copies of coat proteins than enzymes for replicating the phage. Such early evidence for gene regulatory mechanisms that tune protein synthesis stoichiometries motivated work in subsequent decades to understand the molecular basis for this control, particularly the encoding of translation efficiency (148). Stark examples of tuned protein synthesis stoichiometries continued to emerge as our understanding of bacterial physiology expanded (reviewed in 2). However, it remained unknown whether there is a broad requirement of stoichiometric protein synthesis for most operons.

2.2. Genome-Wide Quantification of Protein Synthesis

It was not until recently that tools became available to quantify the rates of protein synthesis at a genomic scale. The classic approach of metabolic labeling followed by 2D electrophoresis is not suited to simultaneously detecting thousands of proteins whose abundances span orders of magnitude, and it requires a potentially perturbative metabolic labeling step (100). mRNA levels might also be used as a proxy for protein synthesis, but such an approximation misses the greatly varying translation efficiencies observed in bacterial RNAs (102). Recent advances in mass spectrometry techniques allow increasingly accurate absolute quantification of protein synthesis, though high-precision comparisons between different proteins remain difficult (reviewed in 3, 23).

The development of ribosome profiling (see the sidebar titled Ribosome Profiling) circumvented these challenges in globally quantifying protein synthesis. By capturing ribosome-protected mRNA footprints transcriptome-wide, ribosome profiling allows direct, genome-wide characterization of translation (81). When most ribosomes have equivalent average elongation rates and produce complete proteins, ribosome footprint density can be used as a readout of protein synthesis rates from each gene (101, 102). Ribosome profiling can be flexibly applied to diverse organisms, including a number of model and nonmodel bacteria (65, 98, 153).

2.3. Evidence for Precisely Tuned Expression Stoichiometry

The global picture of protein synthesis provided by ribosome profiling has revealed general principles shaping proteome stoichiometry. In *Escherichia coli*, a comprehensive survey of obligate protein complex subunits found that they are synthesized with rates proportional to their required stoichiometry in the complex (102). This proportional synthesis indicates selective pressure against wasteful production of excess subunits, which may be more prone to aggregation and drive proteotoxicity (130). A similar principle also applies to modules for which functional

RIBOSOME PROFILING

Ribosome profiling provides a snapshot of the relative density of ribosomes across the transcriptome with codon-level precision (81, reviewed in 19). If RNA is treated with translation elongation inhibitors, ribosomes can be arrested on the sequence they are decoding. RNA is then treated with an endonuclease, with arrested ribosomes sheltering short fragments of mRNA (termed ribosome footprints or ribosome-protected fragments) from decay. These fragments are then isolated and sequenced. In rapid steady-state growth, most ribosomes complete translation and have similar average elongation rates genome-wide. As a result, ribosome density can be used to infer relative protein synthesis rates, providing a quantitative window into proteomics (101, 102). This technique can also be used to assess relative efficiencies of translation (101) when coupled with traditional mRNA sequencing. Because ribosome profiling provides a relative measurement, additional information, such as total protein content per cell, is required to calibrate translation initiation or protein synthesis rates to an absolute scale.

constraints demand hierarchical expression, such as type II toxin-antitoxin systems or sigma-anti-sigma pairs, for which protein synthesis rates have evolved to ensure adequate amounts of the antagonist protein for robust inhibition of their partner despite active protein degradation (1, 102, 182). Proportional synthesis of protein-complex subunits appears to be widespread beyond *E. coli*, occurring for complexes in model gram-positive bacteria and budding yeast and for large protein complexes such as the ribosome and proteasome in higher eukaryotes (98, 165, 166).

Beyond obligate protein-complex subunits, ribosome profiling has revealed surprising requirements of relative synthesis rates for many multi-enzyme pathways that defy simple rationalization. A comparative analysis of the synthesis of proteins in cellular pathways conserved between diverse bacterial species, including evolutionarily distant *E. coli* and *Bacillus subtilis*, showed quantitatively conserved stoichiometries within cellular pathways such as translation, DNA repair, and numerous metabolic processes (98). The gene regulatory strategies that underpin these synthesis rates dramatically diverge between *E. coli* and *B. subtilis*, with widespread remodeling of operon structures and compensatory changes in translation efficiency preserving in-pathway synthesis stoichiometries (98). The divergence in gene regulatory strategies helped reveal fundamental differences in gene expression machinery between distantly related bacteria, including a lack of functional transcription-translation coupling in *B. subtilis* that prevents ribosome-mediated cotranscriptional regulation (84).

Convergent evolution of enzyme stoichiometries suggests that strongly preferred ratios exist for constituents of many cellular pathways, despite evidence suggesting excess capacity for enzymes (74, 88, 133). The molecular mechanisms underlying this selective pressure have been characterized experimentally for factors within the translation pathway such as the aminoacyl tRNA synthetases (132) and peptide chain release factors (97). The extent of expression conservation over large evolutionary times underscores that relative protein synthesis rates must commonly be tuned to a degree that places strict constraints on precision at every step of the central dogma. New technologies for quantitative interrogation of gene expression can now uncover the mechanistic basis of such stoichiometric synthesis among functionally related proteins.

3. THE OPERON REVISITED: ALTERNATIVE mRNA ISOFORMS IN PROKARYOTES

3.1. Genomic Organization of Functionally Related Genes

In bacteria, proteins that take part in related cellular functions are often encoded in operons, which were originally defined as genetic units of coordinated expression (83). In the canonical

view, coordinated expression is achieved via integral cotranscription of a whole gene cluster into a single polycistronic mRNA, allowing individual regulatory elements to transduce modulating signals on numerous genes at once.

Several hypotheses pertaining to the adaptive value of polycistronic transcripts have been formulated, e.g., cotranscription reduces noise in stochastic gene expression (164), facilitates complex assembly (158), or supports coregulation (83, 136). For any gene of a cotranscribed cluster, production is proportional to the RNA polymerase (RNAP) initiation frequency, with additional downstream control points contributing multiplicatively to production of each member. Hence, with cotranscription, expression changes in a functional module are actuated through control of RNAP initiation, and the orthogonal dimension of relative member stoichiometry is implemented by additional intraoperonic regulatory signals.

Importantly, operons do not always warrant equal production among cotranscribed genes within a polycistronic mRNA, and some production stoichiometries for enzymatic pathways span orders of magnitude. One way to enable such a wide range of differential protein production is diversification of mRNAs arising from a gene cluster. Indeed, in contrast to the original operon hypothesis put forth by Jacob & Monod (83), subsequent studies indicated that often there is not a unique integral mRNA per operon but rather a diverse set of isoforms (e.g., 33, 37, 72, 98, 104, 183). These isoforms not only provide different amounts of templates for translation but also can possess dramatically different translation efficiencies (112). Resolving and quantitating these isoforms genome-wide remained difficult until recently.

3.2. Mapping and Quantifying the Diversity of Primary RNA Isoforms

Variants of RNA-seq methods (recently reviewed in 77) now permit characterization of bacterial transcriptomes with unprecedented precision in both the quantification of mRNA abundance and localization of 5' and 3' mRNA boundaries (see the sidebar titled RNA End-Mapping Techniques). mRNA ends can be mapped at single-nucleotide resolution transcriptome-wide. Transcription start sites and other stable 5' ends have been identified using various methods, such as differential RNA-seq (156), high-throughput 5' RACE (rapid amplification of 5' complementary DNA ends) (116), parallel assessment of ends (49), modified 5' RACE (33), 5'-end sequencing (181), and EMOTE (exact mapping of transcript ends) (89). Stable 3' ends of mRNAs can also be mapped at high throughput (43, 121).

In conjunction with a global readout that reports mRNA abundance, end-mapping can be used to enumerate isoforms and reveal complex transcript architectures. However, unit-by-unit quantification of identified isoforms is difficult, especially for operons with nested transcripts (33, 37).

RNA END-MAPPING TECHNIQUES

Several techniques capture genome-wide 5' and 3' end profiles across the transcriptome (e.g., 33, 37, 43, 49, 72, 85, 89, 98, 104, 116, 121, 156, 183). Though they differ in specifics, most such approaches directly capture RNA ends prior to fragmentation through addition of a reverse transcription or PCR handle by the enzymatic activity of an RNA ligase, polyA polymerase, or terminal transferase. Because these activities capture only native 3' and 5' ends, such methods allow for sensitive detection of transcription start sites, mRNA processing sites, and transcription termination events. Such techniques can also be modified to detect specific functional groups at RNA ends (89, 140). End-mapping techniques are limited in their ability to quantify mRNA abundance and generally need to be paired with more traditional RNA-seq if such information is desired.

END-ENRICHED RNA SEQUENCING

Rend-seq combines the advantages of traditional RNA-seq (quantitative measurement of mRNA abundance) with sensitive detection of RNA termini, allowing precise quantification of mRNA isoforms beyond the limits of traditional RNA-seq (98). End detection is achieved through sequencing of short RNA fragments produced by sparse fragmentation, which naturally biases detection toward RNA termini (as producing a terminal fragment requires only a single fragmentation event instead of the two required for an internal fragment). Rend-seq is agnostic to the moiety at the 5' and 3' ends of an RNA, though additional enzymatic treatments can be used to access this information [e.g., treatment with a 5'-monophosphate-specific exonuclease (48)].

In particular, systematic biases introduced by certain molecular cloning steps can confound abundance assessments. For example, generation of the first strand of complementary DNA (cDNA) from randomly primed reverse transcription leads to a spurious depletion of signal at transcript 3' ends (40), because fewer priming events cover these regions. Such biases preclude abundance measurement of overlapping transcripts. End-enriched RNA-seq (Rend-seq) (98) (see the sidebar titled End-Enriched RNA Sequencing), an all-in-one method that simultaneously maps 5' and 3' ends of transcripts and accurately quantifies mRNA abundance, partly circumvents these limitations. Rend-seq relies on sparse fragmentation of transcripts (162) followed by near-quantitative cloning of short fragments to a cDNA library (81). The resulting signal is increased by a factor of >50 at ends of mRNAs over single base pairs and is largely constant across gene bodies. From the clear demarcations of mRNA boundaries and precise abundance quantitation, individual isoform abundances can be reconstructed (98) (**Figure 2**).

Transcription initiation and termination are major contributors to the observed mRNA isoform diversity of bacterial operons. Internal promoters are estimated to make up nearly 30% of start sites in *E. coli* (37). Transcription termination also plays an underappreciated role in generating diversity in operon transcripts. Programmed partial intrinsic transcription termination between genes, such as the early documented example of a leaky terminator in the σ^{70} operon in *E. coli* (25), occurs at hundreds of locations in the genomes of multiple species (37, 98). These programmed terminators act as tuning *cis*-elements to reduce production of genes downstream and can have activities spanning a wide dynamic range in readthrough, from a small percentage to near complete leakiness. When present in combination, internal promoters and programmed terminators can lead to a complex set of mRNAs covering a gene cluster [e.g., the *asd* operon in *B. subtilis*, with three internal promoters and two internal terminators, leading to a set of nine possible isoforms (**Figure 2**)].

Until recently, RNA-seq methods mostly focused on short-read approaches and did not capture long-range information in mRNAs. Consequently, possible correlations between regulatory elements were difficult to identify at a genomic scale. Techniques have now been developed to quantify full-length mRNAs on a variety of platforms (71, 85, 135, 183). Full-length approaches have already revealed intriguing isoform-specific activity of regulatory elements such as transcription terminators (183). Sequencing depth and size-dependent biases remain important bottlenecks for genome-wide characterization using these techniques.

3.3. Quantitative Determinants of Transcriptional Output

The transcription rate of an operonic gene is determined by the combined activities of upstream promoters and the intervening programmed transcription terminators. Quantitative knowledge

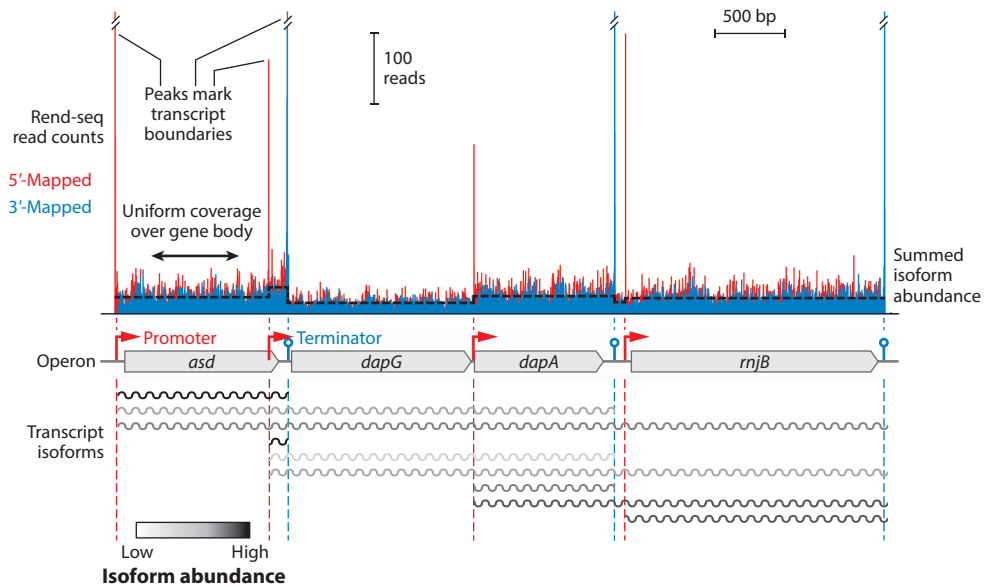


Figure 2

End-enriched RNA-seq (Rend-seq) data (from 98) showing coverage trace for the *asd* operon in *Bacillus subtilis*, which includes four cotranscribed genes. Peaks in 5'-mapped (red) and 3'-mapped (blue) reads mark mRNA boundaries. Four promoters can be seen, as well as three intrinsic terminators. Transcript ends were confirmed not to arise from mRNA processing by orthogonal experiments (not shown). The internal promoters and terminators lead to a complete set of nine possible mRNA isoforms, highlighting the possible complexity of transcription architecture. The read coverage between peaks can be used to infer the abundance of each isoform.

of the determinants of these two regulatory elements is thus at the core of understanding stoichiometric expression control.

Bacterial promoters are specified by sigma factor–recognition sequences, and their activity is influenced by myriad features (reviewed in 115), including the quality of the promoter binding site; the concentration of RNAPs available to transcribe mRNAs; the number, quality, and relative positions of nearby regulatory elements [e.g., transcription factor (TF)-binding sites]; the available concentration and allosteric properties of TFs; the concentration of TF-cognate ligands; the competition between alternative sigma factors; abortive initiation; possible RNAP reinitiation; the supercoiling state of the DNA, etc.

Progress toward empirically identifying quantitative determinants of promoter activity has been driven by sequencing-based, massively parallel reporter assays (reviewed in 91) (see the sidebar titled Massively Parallel Reporter Assays) in synergy with quantitative thermodynamic models of protein–DNA interactions. This biophysical viewpoint condenses promoter complexity to a single property by positing that activity is ultimately proportional to the probability that an RNAP holoenzyme is bound to the promoter region (14). The resulting framework leads to quantitative predictions (20, 64, 176) and reduces the determination of promoter output to the identification of TF-binding sites and measurement of corresponding binding affinities. Dissection of these features is possible: Sequence-to-function relationships for RNAP and TF-binding sites have been measured at scale (8, 92, 174, 179) and binding sites precisely identified across the genome (11, 82, 173). Still, computational predictions remain imperfect (20, 64), in part due to interactions between sequence elements. For example, promoters with consensus –10 and

MASSIVELY PARALLEL REPORTER ASSAYS

The sequence-to-function relationship of compact *cis*-regulatory elements, such as promoters (82, 92, 174) and 5' untranslated regions (27), has been successfully dissected with massively parallel reporter assays (MPRAs) (reviewed in 91). In MPRAs, a library of specified regulatory elements, either array-synthesized or generated by random mutagenesis of a functional element, is inserted in the context of a reporter gene (typically encoding a fluorescent protein), and the cassettes are transferred into cells for quantitative measurement of reporter gene expression. Importantly, experimental design directly connects reporter expression to the identity of a specific regulatory element in the library. For example, cells can be sorted into fluorescence intensity bins by flow cytometry, and the proportion of the regulatory element variants in each bin can then be assayed by DNA sequencing (27, 92). Another common strategy is to include a unique barcode sequence in each reporter mRNA variant. Output is then quantitatively captured by the proportion of the barcode in the RNA pool normalized by its proportion in the DNA pool (e.g., 82, 174). Because *cis*-element function is indirectly read out through steady-state levels (e.g., fluorescence or RNA abundance), care must be taken to ensure variant changes and barcodes impact only the process being studied.

$-35 \sigma^{70}$ recognition sites show hard-to-predict tenfold changes in activity across different surrounding sequences (174), and even binary classification of *de novo* DNA sequences in promoter (some activity) versus nonpromoter (no activity) categories is largely unresolved (173).

With respect to transcription termination, although much is known mechanistically about intrinsic terminators (reviewed in 139), these insights have not permitted quantitative predictions of activity. In particular, properties enabling intrinsic transcription terminators to finely punctuate operons via partial levels of RNAP readthrough are yet to be completely identified despite the simplicity of the distinctive signature of terminators: an RNA hairpin immediately followed by a stretch of multiple U nucleotides. Large numbers of intrinsic terminators' activities have been measured both in libraries using fluorescent reporters (28, 32, 98) and sequencing (79) and in endogenous genomic contexts with RNA-seq-based approaches (85, 98, 121, 183). However, attempts to relate terminators' biophysical properties to termination activity only capture a small fraction of the observed variance (28, 32, 98).

Quantitative prediction of terminator activity is challenging for several reasons. First, the interaction between the nascent RNAs and the RNAP is inherently kinetic (177). Second, *in vivo* RNA secondary structures are difficult to predict (145), especially given upstream RNA structures possibly competing with hairpin formation (28). Third, despite terminology, intrinsic terminators can be influenced by a number of proteins, such as transcription elongation factors (73, 108, 121) and sigma factors, via their possible retention through the elongation cycle (75), and by the ribosome itself, through transcription-translation coupling (103, 144). Importantly, the influence of translation on transcription termination was recently shown to be limited in *B. subtilis* (84), as the RNAP travels faster than ribosomes in that species. This stark difference between *E. coli* and *B. subtilis* exemplifies that regulatory rules for terminators might fundamentally differ across phylogenetic clades. Finally, RNAPs concurrently transcribing a gene could cooperate or otherwise interact (56, 90), which would modulate termination.

4. DIVERSIFYING THE TRANSCRIPTOME THROUGH RNA PROCESSING

4.1. Specifying Differential Expression Through mRNA Processing

Beyond transcriptionally generated boundaries in operonic transcripts, differential RNA stability is a common posttranscriptional mechanism to generate differential protein production from

cotranscribed genes. Such events, referred to here as mRNA processing to avoid confusion with all-or-nothing, decay-initiating cleavage events, have been documented for a number of operons across many bacterial species (reviewed in 143, 170). Proper mRNA processing is required for many critical cellular functions, including cell division, for which differential stabilities following RNase E cleavage in the *E. coli* *ftsQAZ* operon set the proper ratio of cell division proteins FtsA and FtsZ required for nonfilamentous growth (26, 167, 168).

Both exo- and endonucleases can in principle initiate processing of bacterial mRNAs. In one model, an exonuclease engages either the 5' or 3' end of an mRNA, processively acting until it reaches a feature that may obstruct continued degradation. In this model, the strength of the obstructing feature and differential susceptibility of transcript ends to exonucleolytic degradation control the differential abundance of coding regions. Alternatively, processing can be initiated by endonuclease cleavage within an operon, followed by differential decay of the cleavage products by exonucleases. The rate of endonuclease cleavage and exonuclease susceptibility of both ends of each cleavage product impact RNA abundances and hence protein synthesis stoichiometry in this model. The specifics of the RNA decay machinery in any particular bacterium will determine which of these routes is preferentially used and what mRNA features might specify efficient processing. In this review, we focus primarily on how mRNA processing is controlled in *E. coli* and *B. subtilis*, the two species with perhaps the best-characterized mRNA decay pathways.

Processing and decay of bacterial mRNAs are performed by a broad suite of endo- and exonucleases, and though the cohort of enzymes present in any given species can vary significantly (reviewed in 80, 120), a few common principles have emerged. At the core of the *E. coli* and *B. subtilis* mRNA decay pathways are an endonuclease (RNases E and Y, respectively), 3'-5' decay (fulfilled by polynucleotide phosphorylase and a small number of other exonucleases that vary between species), and 5'→3' decay activity. 5'→3' decay is carried out by RNase J1 in *B. subtilis*, while in *E. coli*, repeated cleavage by RNase E followed by 3'-5' exonuclease activity can fill a similar role, as RNase J1 is absent in this organism (reviewed in 36). RNases E and Y form membrane-associated oligomers and recruit a larger mRNA decay complex termed the degradosome, typically comprising exonucleases, RNA helicases, and glycolytic enzymes (reviewed in 169). Both endonucleases are thought to form these larger complexes, though RNase Y degradosomes appear to be less stable in *B. subtilis* than their equivalent species in *E. coli*, and the functional importance of such higher-order assembly in the degradosome remains unclear (169). Additional enzymes, such as RNases III and G, play a more limited role in RNA decay (34, 49, 53, 106, 161), and more comprehensive reviews of the many players in bacterial RNA decay can be found in References 10, 80, 120, and 170.

Though many examples of differential stability within operons have been characterized on a case-by-case basis, recently developed high-resolution RNA-seq techniques allow transcriptome-wide mapping of mRNA processing activity analogous to mapping of initiation and termination (43, 49, 98, 140, 156). By globally inhibiting transcription initiation with rifampicin, RNA-seq can be used to determine the individual half-lives of coding regions within each polycistronic operon (31, 44, 118). In *E. coli*, such an approach, combined with high-resolution mapping of 5' and 3' ends, revealed that dozens of operons have gene stoichiometries tuned by differential RNA stability (44). These differential decay rates appear to be shaped in part by terminal secondary structures and ribosome density along cleavage fragments. Though no global estimate of mRNA half-life based on RNA-seq is currently available in *B. subtilis*, Rend-seq has revealed processing events in tens of operons where endonucleolytic cleavage yields one product that is substantially more stable than the other (48). For example, multiple such cleavage events occur in the *B. subtilis* ATP synthase operon, shown in **Figure 3**. Differential stabilities are thus a common strategy

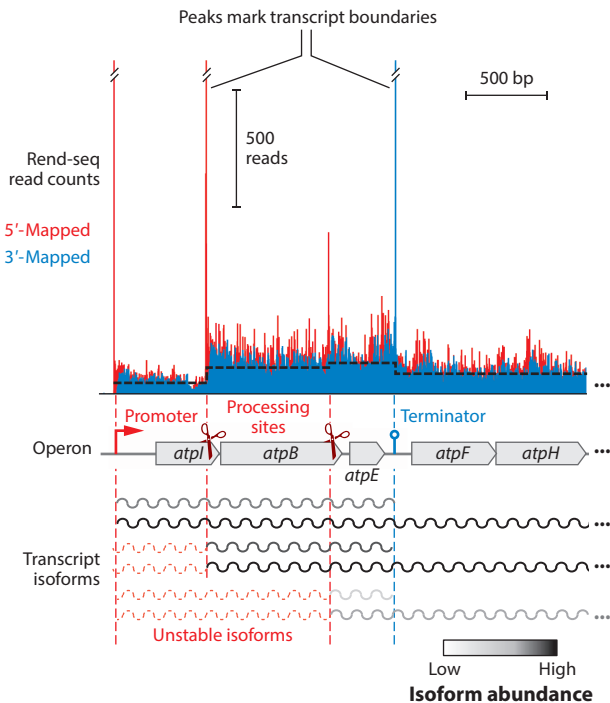


Figure 3

End-enriched RNA-seq (Rend-seq) data (from Reference 98) showing coverage trace for the *atp* operon in *Bacillus subtilis*, truncated to include only the first five genes. Peaks in 5'-mapped (red) and 3'-mapped (blue) reads mark mRNA boundaries. Two RNase Y cleavage sites (*scissors*), one promoter, and one intrinsic terminator are shown. mRNA processing sites validated through orthogonal experiments (not shown). Darker gray indicates higher abundance of transcript isoforms (as in Figure 2), and red, dashed isoforms are rapidly degraded and therefore undetectable.

to allow deviation from one-to-one stoichiometry for cotranscribed genes, despite differences in mRNA decay machinery.

4.2. Features Encoding Differential mRNA Stabilities

To understand how differential stabilities are encoded, one must first consider what makes an mRNA an efficient substrate for processing or degradation by key players in RNA decay. Among the best-characterized decay-initiating nucleases in bacteria, RNase E is thought to degrade mRNAs through an initial cleavage (through either 5'-end-dependent or direct entry pathways) followed by sequential cleavage events in the 5'→3' direction (allowing for 5'→3' decay in organisms lacking a 5'→3' exonuclease such as RNase J1) (reviewed in 10, 80, 120, 170). This activity can be inhibited by local secondary structure or other obstructions such as proteins bound to the mRNA (113, 141). Through selective capture of 5'-monophosphate-containing RNAs in a previously characterized temperature-sensitive RNase E allele, global cleavage profiles of both the *E. coli* and *Salmonella enterica* RNase E enzyme have been determined, revealing thousands of cleavage sites across the transcriptome (5, 29, 34). RNase E demonstrates a strong preference for unpaired, AU-rich substrates (113, 114), and for a U at position +2 relative to the position of cleavage, with the *S. enterica* RNase E recognizing a degenerate motif of the form RN↓WUU (29). RNase E can also interact with and be directed by stem-loop structures in its targets (7).

Because RNase E is membrane localized, substrate proximity to the membrane is also a determinant of RNase E activity (118).

In many bacteria lacking RNase E, particularly gram-positive bacteria such as *B. subtilis*, RNase Y is the primary endonuclease initiating RNA processing and decay. Akin to RNase E, RNase Y is thought to be sensitive to the 5' moiety of an mRNA (155), acting more efficiently on 5'-monophosphorylated RNAs in an end-dependent manner. However, RNase Y is also known to efficiently cleave internally within some mRNAs with a 5' triphosphate (184). As with RNase E, RNase Y is thought to prefer unstructured, AU-rich regions, with an apparent preference for structure downstream (110, 155). In *Staphylococcus aureus*, transcriptome-wide mapping of RNA 5' ends by EMOTE revealed a sequence preference for G at position -1 relative to the site of cleavage (89). Though RNase Y is thought to be the primary initiator of mRNA turnover in *B. subtilis* (53, 61, 96, 99, 170), its set of mRNA targets appears to be more limited in *S. aureus* and *Streptococcus pyogenes* (21, 89, 109), suggesting that the centrality of RNase Y in mRNA turnover may vary between organisms. The target repertoire of RNase Y in organisms more reliant on its activity, such as *B. subtilis*, remains to be exhaustively characterized.

Though mRNA processing and turnover are frequently initiated by endonucleases that are capable of cleaving RNA in a 5'-end-independent manner, both endonuclease and exonuclease activities can be stimulated by the presence of a 5'-monophosphate at the 5' end of an mRNA. Such a moiety can be generated either by endonucleolytic cleavage or by the activity of RNA pyrophosphohydrolase (RppH), which is present in both *E. coli* and *B. subtilis*. RppH plays a role in decay initiation for a subset of the transcriptome, with hundreds of transcripts enriched when RppH is deleted or inactivated in both organisms (45, 66), despite evidence that *B. subtilis* encodes multiple enzymes that can catalyze this activity (78, 142). *E. coli* RppH and *B. subtilis* RppH have differing sequence preferences, with *B. subtilis* demonstrating stricter requirements, including a strong preference for a G in position +2 (63, 78). Interestingly, in *E. coli*, RppH is much more active against a diphosphorylated 5' end, an apparently abundant moiety generated by an unknown phosphatase (107). In both *E. coli* and *B. subtilis*, RppH activity is strongly impeded by base-pairing at the 5' end of an mRNA (63, 78). Downstream of either RppH or endonuclease activity, 5' hairpins can additionally inhibit activity of RNase J1, which requires at least four unpaired nucleotides to initiate degradation (51). 3'-5' exonucleases can be similarly impeded by 3' hairpins (reviewed in 170). Terminal secondary structure can therefore both inhibit RNA decay initiation and stabilize decay intermediates.

The bacterial RNA decay machinery acts in concert with numerous RNA and protein factors that modulate their specificity, specifying locations of mRNA processing. Most known examples of mRNA processing in *B. subtilis* are dependent on a protein complex termed the Y-complex (YlbF, YmcA, and YaaT), which is known to physically interact with RNase Y (47, 48). Absence of any member of this complex ablates mRNA processing activity at tens of sites in the transcriptome (48), including the glycolytic operon (35) and the ATP synthase operon (**Figure 3**). In *E. coli*, a substantial network of small RNAs (sRNAs) contributes to mRNA processing through multiple modes of action. sRNA binding is able to direct cleavage by endonucleases, and RNase III and RNase E have both been implicated in sRNA-directed mRNA processing (9, 129). Beyond directing cleavage by endonucleases, sRNAs can inhibit exonuclease (or sequential RNase E) activity, resulting in differential stabilization of operon decay intermediates (reviewed in 9). Such a mechanism regulates glucose homeostasis in *E. coli* and may be a common occurrence in this organism (131).

Though we understand many of the major processes involved in differential stabilization of operonic genes, we still lack a predictive understanding of what makes an mRNA stable. Because the primary sequence determinants specifying decay initiation through endonucleases or RppH appear highly degenerate and some downstream products of RNA processing are inherently

unstable, it is difficult to precisely map the determinants of differential mRNA stabilities. Secondary structure plays a role in directing RNA processing events, but precisely attributing cleavage events to secondary structural motifs is constrained by our ability to precisely predict or measure mRNA folding transcriptome-wide (145). As an additional complication, RNA decay may be concurrent with transcription and translation, the latter known to potentially stabilize mRNAs through occlusion of RNA decay machinery (170, 185). Application of massively parallel reporter assays, extensively used to study transcription and translation but not yet RNA decay, may provide the degree of control needed to dissect determinants of efficient processing at known sites. Further work coupling perturbations to the RNA decay machinery with newly developed RNA-end-mapping techniques may also continue to yield a higher-resolution map of mRNA processing across transcripts and species.

Ribosome-binding site (RBS): feature in the 5' region of an mRNA; includes a Shine-Dalgarno sequence and start codon, which specify translation initiation

5. DIFFERENTIAL TRANSLATION EFFICIENCY TO TUNE PROTEIN PRODUCTION

For a given polycistronic mRNA isoform, each gene may be translated at a different rate. We refer to the rate of protein synthesis per copy of mRNA for a given gene as the translation efficiency (101). Different genes in the same transcript can have translation efficiencies that differ by up to 100-fold (102, 180), which is comparable to the magnitude that can be achieved by partial transcription termination. Interestingly, it is rare to find genes that have high transcription and low translation efficiency, a phenomenon that can be explained by an evolutionary trade-off between the cost and noise of expression (76). In this section, we discuss the molecular mechanisms that contribute to differential translation efficiency (101).

5.1. Autonomous Translation and Impact of Neighboring Genes

The translation efficiency of different genes in the same transcript may be dependent on or independent of each other. For many operons, every gene carries its own ribosome-binding site (RBS), which consists of a Shine-Dalgarno sequence and a start codon. Translation can thus initiate at each RBS regardless of its neighbors. There are also mechanisms that make translation of a gene dependent on translation of neighboring genes (30). Some of the best-characterized examples are specialized mechanisms at leader peptides whose translational stalling can alter mRNA folding and influence the accessibility of the RBS of the downstream genes (124, 125). These mechanisms have been exploited to create synthetic genes in a bicistronic context to enable controllable translation (27, 123). Because leader peptides are often not functional after their synthesis, this type of mechanism mainly serves as a way to regulate operon-wide expression and not relative stoichiometry.

Similar translational coupling between neighboring genes may be responsible for maintaining uniform translation efficiency across many ribosomal proteins encoded in the same operon. For example, ribosomal protein operons are often regulated by one of the proteins they encode, whereby an excess of unassembled subunits bind to and downregulate genes on the same mRNA (126). Coupled translation would potentially allow a single feedback regulator to control the translation of all genes stoichiometrically. Although it was originally proposed that the same ribosome would translate sequentially through such linked genes (154), more recent evidence has suggested that the dependency might be due to modulation of RBS accessibility for *de novo* initiation by the translation of upstream genes (111, 122, 146). Still, compared to well-characterized leader peptides, the exact mechanism leading to the equimolar production rates among translationally coupled genes is less clear.

For most operons, protein production is not equimolar and requires distinct translation efficiencies at each gene. As different genes are translated differentially, operon RNAs also form

distinct domains of secondary structures that are separated by gene boundaries (24). RNA-folding models based on genome-wide secondary structure probing have shown that intra-open reading frame (ORF) base-pairing is generally favored over inter-ORF base-pairing, except for genes that may be translationally coupled (24, 122). Intra-ORF base-pairing is intrinsic to the evolved RNA sequence and provides a blueprint for translation efficiency, as we discuss in the following section.

5.2. Determinants of Initiation Frequency

It is generally thought that translation efficiency is determined by the initiation rate, as opposed to elongation rates, because the steady-state flux of initiating ribosomes must be equal to the flux of peptide and ribosome release (93, 101, 163). To initiate translation, the RBS must not be base-paired to other regions of the mRNA. Indeed, large-scale studies based on massively recoded reporters in *E. coli* have shown that translation efficiency is anticorrelated with the thermodynamic stability of RNA folding for an RBS (13, 17, 18, 27, 57, 68, 94). Ribosome profiling data for endogenous genes also showed a consistent trend (102). These results suggest that the close relationship between RNA secondary structure and translation efficiency—originally observed for the polycistronic bacteriophage RNAs (105)—is a general mechanism across the host genome.

Typically, the region of mRNA containing the RBS is less structured than other parts of the gene body, which facilitates translation initiation (12, 58, 150). Avoidance of RNA secondary structure places a constraint on codon usage, an effect that is most pronounced for the N-terminal residues for which codon substitutions strongly influence translation efficiency via RNA folding (13, 18, 57, 94). These results offer an explanation for the intriguing phenomenon that rarely used codons are enriched at the 5' end of ORFs (172). Long-range base-pairing can also play a role in reducing the accessibility of the RBS, as synonymous codons further downstream in the gene can reduce translation efficiency if they are the reverse complement of the Shine-Dalgarno sequence (13, 86). The entirety of each coding sequence likely has evolved under this RNA folding constraint. Therefore, bacterial operons not only encode units of protein sequences but also specify the relative translation efficiency through ORF-wide secondary structures (24).

It should be noted that RNA secondary structures affect both translation efficiency and decay rates (46). Large-scale studies of the effects of gene sequence on translation have demonstrated a nearly universal correlation between protein levels and mRNA levels, making it difficult to disentangle the contribution of a synonymous variant to translation efficiency from the contribution to RNA decay (13, 17, 27, 57, 68, 94, 95). In the context of polycistronic operons, it remains to be determined how the distinct units of secondary structures and translation efficiency affect the stability of an entire mRNA.

In addition to secondary structures, the affinity of the Shine-Dalgarno sequence to the anti-Shine-Dalgarno region of the 16S rRNA is also relevant in *E. coli* (159). Although the correlation between the Shine-Dalgarno strength and translation efficiency is weak across endogenous *E. coli* genes (102), a stronger correlation can be observed once variations in secondary structure are controlled for—either using a deep mutational scanning library that only targets the Shine-Dalgarno sequence (95) or measuring the translation of orthogonal ribosomes that differ in the anti-Shine-Dalgarno region (147) (see the sidebar titled Orthogonal Ribosomes). Intriguingly, orthogonal ribosomes mostly initiate at the correct start codons despite the lack of corresponding orthogonal Shine-Dalgarno sequences, again suggesting that translation initiation sites on endogenous operons are primarily hard-coded in features such as the modular secondary structures.

5.3. Roles of Elongation Kinetics

Although elongation per se does not influence the steady-state flux of protein production, it may indirectly affect translation efficiency by either triggering premature ribosome release or reducing

ORTHOGONAL RIBOSOMES

Orthogonal ribosomes are ribosomes that harbor an anti-Shine-Dalgarno sequence that has been modified away from the native ribosome (138). These ribosomes allow for selective translation of transcripts with ribosome-binding sites that complement the new anti-Shine-Dalgarno sequence, with an orthogonal set of modified Shine-Dalgarno/anti-Shine-Dalgarno interactions. Orthogonal ribosomes permit disentangling of some of the different features (RNA secondary structure, ribosome-binding sites) contributing to translation initiation control (147) that are otherwise hard to decouple.

the initiation frequency (101, 163). In the first scenario, ribosomes may be released due to stalling, collision, or programmed frameshifts (59, 60, 175). In ribosome profiling data for *E. coli* and *B. subtilis*, premature release appeared to be uncommon, except for a few specific genes that utilize this mechanism to generate truncated proteins or regulate expression (15, 39, 62, 102, 117, 171). On the other hand, a large-scale study based on randomized N-terminal coding sequence in vivo, combined with single-molecule assays in vitro, showed that ribosome stalling may occur in the first three to five codons in a context-dependent manner. Consequently, ribosomes may drop off shortly after initiation, which would be difficult to detect by ribosome profiling (175). This early ribosome drop-off may further fine-tune the initiation rates that are mainly determined by RBS accessibility.

In the second scenario, whereby elongation rates affect initiation frequency, strong ribosome pausing may lead to a pileup of trailing ribosomes that eventually occlude the RBS from further initiation. This transition occurs when the pause duration becomes longer than the time between the native initiation events (60, 101). In vivo estimates of the translation kinetics showed that the average stepping time for elongation is approximately 60 ms per codon, whereas the time between initiation events is typically a few seconds (41, 70, 87, 102). Therefore, a pause that is >20 times longer than the average elongation step time is required to create a massive ribosome pileup that can lead to RBS occlusion. Although rare codons decoded by less abundant tRNAs may have slower elongation rates, they may not cause sufficient pauses in rich media to lead to ribosome queues given that the tRNA concentration differences are typically less than 20-fold (50). Updated ribosome profiling data support this view (119). Interestingly, it has been observed that codon usage correlates with proportional synthesis, with a more biased usage for more frequently translated genes (137). This is consistent with the general trend that highly expressed genes are enriched in codons that are decoded by more abundant tRNAs. Biased codon usage is likely a consequence of evolutionary pressures to balance the supply and demand for tRNAs (55) and maximize ribosome usage (93), instead of being a driving force for translation efficiency. When the tRNA supply and demand are imbalanced because of forced expression of exogenous genes, codon choice of the overexpressed gene can become important (17). Indeed, the extent of codon influence depends on the level of overexpression (27). For native operons with cotranscription, however, ORF-specific codon usage appears to be a consequence and not a driver of translation efficiency.

6. EFFECTS OF THE BROADER CONTEXT

Although colocalization along the chromosome is common for functionally connected genes, members of pathways are sometimes not in operons. In particular, pathways involving numerous proteins, such as mRNA translation, have participating genes scattered across the chromosome. Even subunits of obligate heteromeric complexes are occasionally not contiguous (102). Placement along the chromosome can influence gene expression: A self-contained construct including a gene and its *cis*-regulatory elements will produce quantitatively different amounts of protein when at

different genomic positions as a result of the local and long-range context. The precise requirements for stoichiometric production among proteins that span multiple distal operons suggest that the outputs of *cis*-regulatory elements have evolved to compensate for these position-dependent effects, through either feedback mechanisms (67) or hardwired sequence-level modulation. We briefly survey how chromosomal context affects expression.

At the simplest level, more proteins will be produced when multiple copies of the encoding gene are present in the cell. In fast-growing bacteria, single-copy genes still have different copy numbers (i.e., dosage) in the cell depending on their chromosomal position. Indeed, as one round of DNA replication initiates before completion of previous rounds, leading to multifork replication (38), genes near the origin of replication have a higher copy number compared to those close to the terminus. Quantitatively, the largest difference in gene dosage is between the origin and terminus, with a population-averaged origin-to-terminus dosage ratio higher than 3:1 in fast-growing *E. coli* (187). Measurements of gene expression output confirm that expression is directly proportional to chromosomal dose (16, 69, 151, 160). Importantly, the magnitude of the dosage difference can be larger than the measured stoichiometric production deviation in complexes and pathways (98, 102), so that the selective pressures sculpting *cis*-element activity are sensitive to these effects.

In addition to the changes in gene dosage, which gradually varies with chromosomal position, sharper local features can also influence gene expression. Concretely, gene-dosage-corrected expression typically spans a factor of 4 from position to position for insulated reporter cassettes (69, 152), or more for uninsulated ones (22). Scholz and coworkers (152) systematically investigated underlying causes of these differences, identifying AT content, binding of nucleoid-associated proteins, and proximity to high-transcription loci as features correlated with local expression propensity. Bacterial chromosomes are heavily decorated by a variety of proteins (178), and occupancy of these proteins can obstruct initiation and progression of the RNAP (reviewed in 157), leading to silencing of certain genomic regions. Furthermore, some promoters are sensitive to DNA supercoiling, which can be affected by local transcriptional activities or barriers to supercoiling spread (reviewed in 52). Additional effects involve the spatial context of a bacterial cell, with heterogeneous concentration of the central dogma machinery and specific chromosomal organization (respectively reviewed in 6 and 42). For example, the proximity of a gene locus to the inner membrane and mRNA degradation enzymes could affect its expression (118).

Overall, the nonuniform dependence of gene output on growth rate and local features raises an important question regarding how expression stoichiometry among different genes is maintained under changing environments. These results underscore that *cis*-regulatory elements ultimately cannot be considered in isolation and that a holistic view including local and broad genomic context effects is needed for a fully quantitative understanding.

7. CONCLUSION AND OUTLOOK

Though recent high-resolution measurements have provided insights into the regulatory landscape underpinning stoichiometric protein synthesis, our degree of predictive understanding for gene expression from these features remains relatively low. The activity of regulatory elements in bacterial operons is set by evolution to a precision at least one order of magnitude higher than what is currently achievable with the state-of-the-art synthetic biology toolbox. An aspirational challenge for the field will be to reach *de novo* any chosen relative expression between two exogenous genes within a factor of two or less. Currently, the best approach to achieve a prespecified stoichiometry remains to screen libraries of regulatory elements.

With limited spatial separation, the processes of bacterial gene expression are frequently highly coupled, making an understanding of transcription, translation, or RNA decay in isolation

inadequate. Indeed, mounting evidence suggests that lack of modularity of regulatory elements is the norm. Careful design of experiments is critical to isolate a perturbation to only one step in gene expression and quantify any secondary alterations to transcription, translation, and mRNA stability. Further, systematic assessment of these interactions might provide a path toward integration of these concurrent processes into a coherent framework. Importantly, the gene expression machinery displays fundamental differences across bacteria, as can be seen by the limited transcription-translation coupling in Firmicutes (84). This diversity limits the species-to-species portability of regulatory elements (186), and particular care must be taken when generalizing findings across bacterial species.

Questions remain regarding how stoichiometric production is maintained in different environments. Coregulated protein production presents a challenge for systems finely tuned for proportional protein synthesis: How do the regulatory elements, shaped in sequence by evolutionary pressures toward stoichiometric synthesis, respond to fluctuating cellular demands? Regulators acting on whole operons provide one clear solution, as described for some groups of *E. coli* ribosomal proteins, but many pathways demonstrate more complicated operon structures or span multiple genomic loci. More comprehensive characterization of the landscape of gene regulatory networks, and in particular autoregulation, may yet reveal new buffering and feedback mechanisms robust to the fluctuating environments bacteria have evolved in.

FUTURE ISSUES

1. Certain regulatory elements, such as intrinsic terminators and mRNA processing sites, are ripe for application of large-scale sequence-to-function characterization using massively parallel reporter assays.
2. Even for compact regulatory elements with extensive prior characterization, such as promoters, rational and model-based generation of libraries of maximally constraining elements is needed to efficiently explore the large DNA sequence space, with the particular goal of high generalizability of learned statistical or biophysical models.
3. The ever-increasing catalog of bacterial genomes holds potentially useful information about the regulatory code. Can evolutionary covariation analyses be used to constrain the quantitative sequence-to-function relationships of *cis*-elements?
4. Systematic quantification of regulatory elements should be undertaken in a wider diversity of bacteria to assess divergence in the regulatory code across the full bacterial phylogeny.
5. To what extent is expression stoichiometry conserved across additional cellular states that are different from steady-state growth, such as in stress or nutrient-poor conditions?
6. What design principles allow regulatory elements for genes in the same pathway, but discontinuous on the chromosome, to be seamlessly induced or repressed across various growth conditions?
7. Interaction between the various processes of the central dogma, and by extension between the underlying regulatory elements controlling these processes, should be explored systematically and at high throughput using tools similar to those already available to assess sequence-to-function relationships. Examples include interaction between translation initiation (ribosome-binding site) and endonuclease cleavage (cleavage site) and between transcription initiation (promoter) and transcription termination (terminator).

8. The underlying causes for the precise requirement for the observed expression stoichiometry for many proteins remain obscure.

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Errata

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