



Repurposing ribosomes for synthetic biology

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The translation system is the cell's factory for protein biosynthesis, stitching together hundreds to thousands of amino acids into proteins, which are required for the structure, function, and regulation of living systems. The extraordinary synthetic capability of this system, which includes the ribosome and its associated factors required for polymerization, has driven extensive efforts to harness it for societal use in areas as diverse as energy, materials, and medicine. A powerful example is recombinant protein production, which has impacted the lives of patients through the synthesis of biopharmaceuticals such as insulin. In nature, however, only limited sets of monomers are utilized, thereby resulting in limited sets of biopolymers (i.e., proteins). Expanding nature's repertoire of ribosomal monomers could yield new classes of enzymes, therapeutics, materials, and chemicals with diverse, genetically encoded chemistry. Here, we discuss recent progress towards engineering ribosomes both *in vivo* and *in vitro*. These fundamental and technical breakthroughs open doors for advanced applications in biotechnology and synthetic biology.

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Introduction

The translation apparatus is the cell's factory for protein biosynthesis, stitching together L- α -amino acid substrates into sequence-defined polymers (i.e., proteins) according to a defined genetic template. With protein synthesis rates of up to 20 amino acids per second at an accuracy of 99.99% [1,2], the extraordinary catalytic capacity of the translation apparatus has attracted extensive efforts to repurpose it for novel functions [3–6]. Previous

pioneering works have shown site-specific incorporation of more than 150 non-canonical amino acids (ncAAs) into proteins using an engineered translation apparatus to generate biological insights and new applications [3–5]. As a result of these impressive efforts, expanding the genetic code has emerged as a major opportunity in synthetic and chemical biology [7–10].

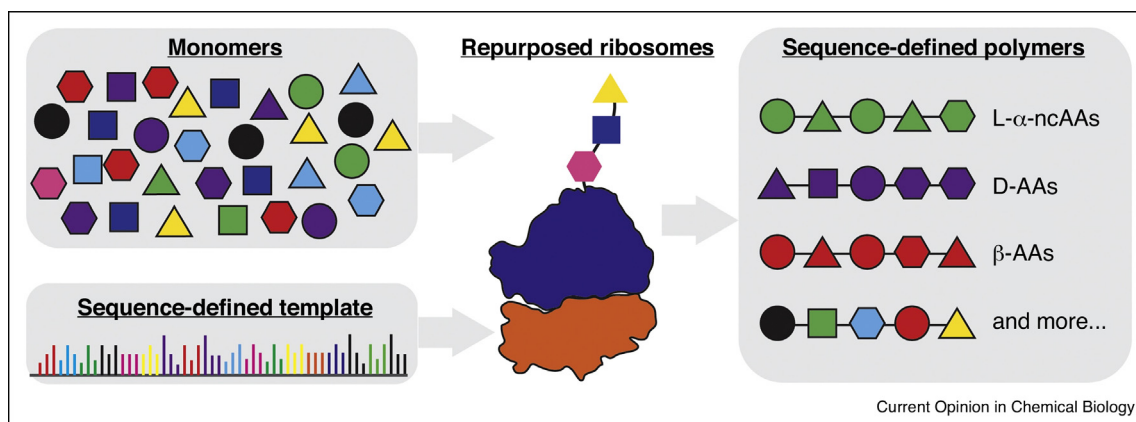
Unfortunately, expanding the range of genetically encoded chemistry into proteins presents a complex and formidable challenge for several reasons [3]. First, the components of engineered orthogonal translation systems that specifically utilize ncAAs suffer poor enzymatic efficiencies relative to native translational machinery [3]. Second, the focus of most engineering efforts remains on evolving orthogonal translation system components by targeting only a small number of individual parts, rather than coordinately tuning and optimizing all biological components involved in the complex system of protein biosynthesis [11•]. Third, certain biological constraints — especially that of the ribosome, the protein polymerase core of the translation apparatus — limit the scope of ncAA diversity. Because ribosome function is necessary for life, cell viability restricts the changes that can be made to ribosomes for expanding the range of substrates beyond those found in nature.

This review focuses on recent developments in repurposing the translation system for novel functions, with a focus on engineering the bacterial *Escherichia coli* ribosome (Figure 1). We first describe the state-of-the-art in the ribosome's ability to process ncAAs. Next, we highlight recent progress towards engineering ribosomes both *in vivo* and *in vitro*. We end with a discussion of current challenges in the field and provide commentary on future opportunities.

Repurposing ribosomes

The *E. coli* 70S ribosome is a ~2.4 MDa macromolecular machine made up of two subunits, the 50S large subunit, comprised of 33 ribosomal proteins (r-proteins), 23S ribosomal RNA (rRNA), and 5S rRNA, and the 30S small subunit, comprised of 21 r-proteins and 16S rRNA [12]. The 16S rRNA of the 30S subunit accommodates ribosomal monomers, aminoacyl-transfer RNAs (aminoacyl-tRNAs), and decodes mRNA. The 23S rRNA of the 50S subunit primarily makes up the peptidyl transferase center, which catalyzes the polymerization of amino acids into proteins via peptide bonds, and the nascent peptide exit tunnel, through which newly synthesized proteins leave the ribosome. Previous works have shown the possibility of using natural ribosomes to site-specifically

Figure 1



Engineering the translation apparatus to manufacture sequence-defined polymers. Expanding the repertoire of ribosome substrates and functions has the potential to not only create novel biopolymers, but also open new areas of research in materials science and synthetic biology.

incorporate ncAAs into polypeptides, including α,α -disubstituted amino acids, D-amino acids, β -amino acids, N-alkyl amino acids, and N-methyl amino acids [13–16,17*,18–20,21*,22*]. Since sequence defines structure and structure defines function, expanding the repertoire of ribosome substrates and functions has the potential to create polymers with even greater functional breadth. For example, the ribosome has been shown to be capable of producing polymers with non-peptide backbones such as polyesters. Over forty years ago, Fahrenstock and colleagues first demonstrated that the ribosome polymerizes phenyllactic acid in a template-directed manner [23]. More recently, Suga and colleagues synthesized polyesters up to ~ 10 units long containing up to three different side chains by genetic code reprogramming [24*,25].

Despite these advances, engineering the translation machinery can be hampered by low efficiencies of the ribosome to accept non-proteinogenic building blocks. The structural, physiochemical, and dynamic properties of the ribosome have been evolutionarily optimized to translate native proteins from the 20 canonical amino acids. To address this concern, the ribosome can be manipulated through directed evolution to accommodate non-canonical monomers, although there are relatively few examples. Hecht and colleagues evolved the peptidyl transferase center to enable exotic monomer incorporation, such as D-amino acids [26,27*] and β -amino acids [18,19]. More recently, Czekster and colleagues generated additional ribosome mutations to show, for the first time, the ability to incorporate these exotic monomers in a living cell [28*]. Even with site-directed evolution of the ribosome, efficiencies can be low. How might the efficiencies and utilities of engineered ribosomes be improved? There are some recent indications that modifying non-ribosomal factors involved in translation can

also lead to improved non-canonical monomer incorporation. For example, Suga and colleagues recently showed that modifying the concentrations of translation factors (e.g., Initiation Factor 2, Elongation Factor Tu, and Elongation Factor G) and using tightly binding elongator tRNAs can enhance multi-site incorporation of D-amino acids for the synthesis of novel macrocyclic peptides [21*]. Similarly, Huang *et al.* demonstrated that multiple D-amino acid incorporation could be enabled by using Elongation Factor P to resolve peptidyl transferase stalling (biorxiv.org/content/early/2017/04/10/125930).

Although the ribosome can feasibly accept non-canonical building blocks and be tolerant of modifications that enable increased promiscuity, constraints imposed by living cells have hindered efforts to engineer ribosomes effectively. In particular, dominant growth defects caused by mutations in the ribosome can preclude identification of mutants that confer desired functions [29,30]. This has motivated the need to develop new technology platforms for engineering ribosomes both *in vivo* and *in vitro*, which we describe next.

Engineering ribosomes *in vivo*

Expanding the decoding and catalytic capabilities of the ribosome is often at the expense of diminishing its endogenous function in protein synthesis. To bypass this limitation, recent developments in cells have focused on the creation of specialized ribosome systems. The concept is to create an independent, or *orthogonal*, translation system within the cell while wild-type ribosomes continue to synthesize genome-encoded proteins to ensure cell viability and productivity. The orthogonal ribosome is thus excluded from the production of endogenous polypeptides and, ideally, exclusively translates specific, targeted mRNA(s). Therefore, the orthogonal translation apparatus can be engineered to carry out new functions,

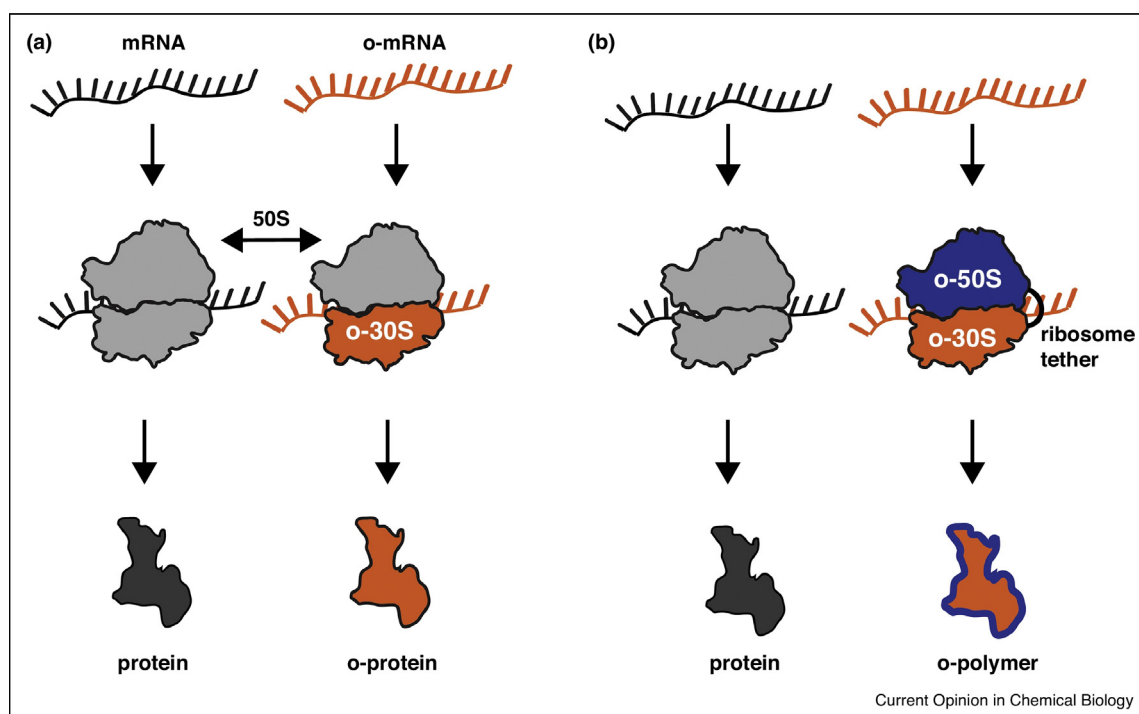
even if such modifications may negatively affect the operation of the orthogonal ribosome in normal translation. The principle of orthogonality is achieved through the bacterial small ribosomal subunit. Recognition of the start codon in bacteria relies on complementary interactions between the purine-rich Shine-Dalgarno (SD) region, which precedes the initiator codons of bacterial open reading frames, and the pyrimidine-rich ‘anti-SD’ (aSD) sequence at the 3′-end of the 16S rRNA in the 30S subunit [31]. Thus, by modifying the SD sequence of an mRNA and the corresponding aSD sequence in 16S rRNA, it is possible to create specialized ribosomes capable of translating only a specific kind of engineered mRNAs, while simultaneously excluding translation of endogenous cellular mRNAs (Figure 2a). Initially, the concept of orthogonal ribosomes was pioneered by Hui and deBoer [32–34], and then was extended and improved in several ways by Chin and colleagues. Rackham and Chin, for example, generated random mutagenesis libraries of possible 16S rRNA and mRNA pairs with complementary SD/aSD sequences, then selected for pairs that can robustly and exclusively translate orthogonal message without crosstalk with native translation processes [35•]. Chubiz and Rao developed a computational model to

rationally design orthogonal SD/aSD sequences in order to explore a larger mutational space, with similar results as they discovered several orthogonal 16S and mRNA pairs without toxicity effects on the host strain [36].

Leveraging these advances, orthogonal 30S subunits have been engineered to preferentially bind to the amber suppressor tRNA over RF-1 to improve ncAA incorporation efficiency [37], select for opal suppressor tRNA over RF-2 [38], decode quadruplet codons towards genetic code expansion [39•], and enable orthogonal transcription-translation networks [40]. These innovations have enabled the creation of engineered ribosomes with altered substrate preferences *in vivo*. However, until two years ago, such techniques have been limited to the 30S small subunit because 50S large subunits freely exchange between pools of native and orthogonal 30S subunits. This has previously constrained the engineering potential of the large subunit, which includes functionally important domains such as the peptidyl transferase center and the exit tunnel.

Recently, the covalent linking of the core ribosomal RNA of the large and small subunits of the orthogonal ribosome

Figure 2



Approaches to orthogonal ribosomes. **(a) 30S orthogonality.** 30S subunits (o-30S), with the anti-Shine-Dalgarno (aSD) sequence of its 16S rRNA modified to bind only to RNA messages (o-mRNA) with the complementary Shine-Dalgarno (SD) sequence, translate proteins (o-protein) orthogonal and parallel to the native translation process (gray). However, the 50S subunit is allowed to freely associate between native 30S and o-30S. **(b) A fully orthogonal 70S.** 50S and 30S subunits are connected by an RNA tether, preventing free association of native and orthogonal species.

has enabled the first completely orthogonal ribosome-mRNA system where mRNA decoding, catalysis of polypeptide synthesis, and protein excretion can all be optimized for new substrates and functions [41^{••},42[•],43]. Orelle and colleagues described the first successful construction of a ribosome with covalently tethered subunits, termed Ribo-T, capable of carrying out protein synthesis (Figure 2b) [41^{••}]. Specifically, they engineered a ribosome whose core 16S and 23S rRNAs form a single chimeric molecule with a covalent connection between the 23S rRNA termini within the loop of helix 101 (H101) and the apex loop of the 16S rRNA helix 44 (h44). Not only could this hybrid rRNA support the assembly of a functional ribosome in a cell, but surprisingly Ribo-T could also maintain bacterial growth even in the absence of wild-type ribosomes. Orelle and colleagues also used Ribo-T to create a fully orthogonal ribosome-mRNA system [41^{••}]. They demonstrated its evolvability by selecting otherwise dominantly lethal rRNA mutations in the peptidyl transferase center that facilitated the translation of problematic protein sequences. Fried and colleagues also demonstrated a linked ribosome design capable of sequestering dominant lethal mutations in a fully orthogonal ribosome using a different set of linkers, or ‘staples’ [42[•]]. Collectively, these findings uncover new directions in biomolecular engineering and synthetic biology. Looking forward, tethered ribosomes can be used for exploring poorly understood functions of the ribosome (e.g., antibiotic resistance mechanisms), enabling orthogonal genetic systems, and engineering ribosomes with altered chemical properties. Future challenges include resource re-allocation of the cell’s translational capacity and shared ribosomal protein pool, as well as optimizing the expression levels of tethered ribosomes in the background of high concentrations of endogenous ribosomes.

Engineering ribosomes *in vitro*

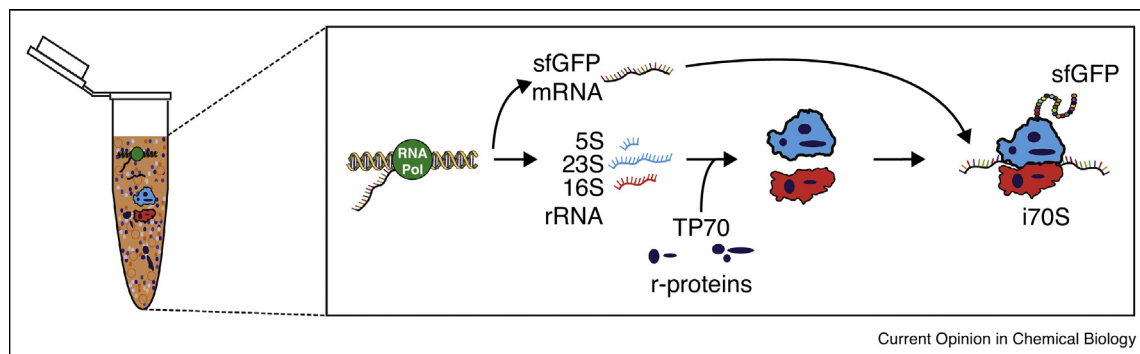
As a complement to engineering ribosomes *in vivo*, *in vitro* approaches offer potential advantages to precisely control the reaction environment in a manner that may allow for the isolation of certain mutant ribosomes not possible in cells, such as those in non-physiological pH, temperature, and redox levels. *In vitro* translation systems, both reconstituted from purified parts or from crude cell lysates, have shown promise for applications stemming from recent advances that alleviate possible ribosomal limitations and increase yields [44–47]. *In vitro* reconstitution of *E. coli* ribosomes from their individual components was first achieved over 40 years ago [48,49]. Despite relatively efficient reconstitution with natural components, the use of *in vitro* transcribed rRNA, which lack naturally occurring post-transcriptional modifications, is less efficient than *in vivo* transcribed versions [50,51]. This is a particular concern for the *E. coli* 50S subunit, where peptidyl transferase activity from reconstituted 50S subunits using *in vitro* transcribed 23S rRNA

is diminished ~10,000-fold relative to those with naturally derived 23S rRNA. Low reconstitution efficiencies from *in vitro* transcribed rRNA have represented one of the most significant bottlenecks to *in vitro* ribosome engineering.

Several efforts are underway to move beyond previous limitations. One method is to leverage purified translation systems, such as the PURE system with no endogenous ribosomes, to build new ribosomes in ways similar to strategies used in cells [52–54]. In a key milestone this year, Li and colleagues showed that ribosomal proteins generated *in vitro* could be used alongside *in vitro* transcribed rRNA to build a functional small ribosomal subunit [54]. In another approach, Jewett *et al.* developed an integrated synthesis, assembly, and translation method, termed iSAT, that enabled efficient one-step co-activation of rRNA transcription, assembly of transcribed rRNA with native ribosomal proteins into *E. coli* ribosomes, and ribosomal synthesis of functional proteins in a ribosome-free S150 extract [55] (Figure 3). Notably, iSAT mimics co-transcription of rRNA and ribosome assembly as it occurs in cells.

The iSAT system’s utility was improved over the past four years, where the activity of iSAT was increased by more than three orders of magnitude through optimization of extract preparation methods, rRNA transcription turning, substrate limitation alleviations, and the use of macromolecular crowding and reducing agents [55–58]. In one instance, Fritz and Jewett increased transcriptional efficiency through 3′-modifications in rRNA gene sequences, optimized plasmid and polymerase concentrations, and demonstrated the use of a T7-transcribed rRNA operon for stoichiometrically balanced rRNA synthesis and native rRNA processing [56]. These modifications produced a 45-fold improvement in iSAT protein synthesis activity. In another advancement, Liu and colleagues determined substrate depletion and toxic byproduct accumulation to be causes of reaction termination in iSAT, and alleviated these constraints using a semi-continuous reaction format [57]. Another study demonstrated that macromolecular crowding and reducing agents (6%, w/v, Ficoll 400, and 2 mM DTBA) yielded approximately a five-fold increase in overall iSAT protein synthesis activity [58]. By utilizing a fluorescent RNA aptamer, fluorescent reporter proteins, and ribosome sedimentation analysis, Fritz and colleagues showed that crowding agents increased iSAT yields by enhancing translation while reducing agents increase rRNA transcription and ribosome assembly [58]. These efforts demonstrated that iSAT ribosomes possess ~70% of the protein synthesis activity compared to *in vivo*-assembled *E. coli* ribosomes, which surpasses an important benchmark: iSAT ribosomes are now capable of translating >8,000 peptide bonds per ribosome — enough peptide bonds for the translation of a complete

Figure 3



Integrated synthesis, assembly, and translation (iSAT) method for ribosome construction *in vitro*. In cell-free, ribosome-free S150 extract, reporter mRNA and rRNA are transcribed by RNA polymerase (RNA Pol) and the rRNA assembled into ribosomal subunits with added total r-proteins of the 70S (TP70). iSAT-assembled ribosomes then translate the reporter, here superfolder green fluorescent protein (sfGFP), as a measure of ribosome activity.

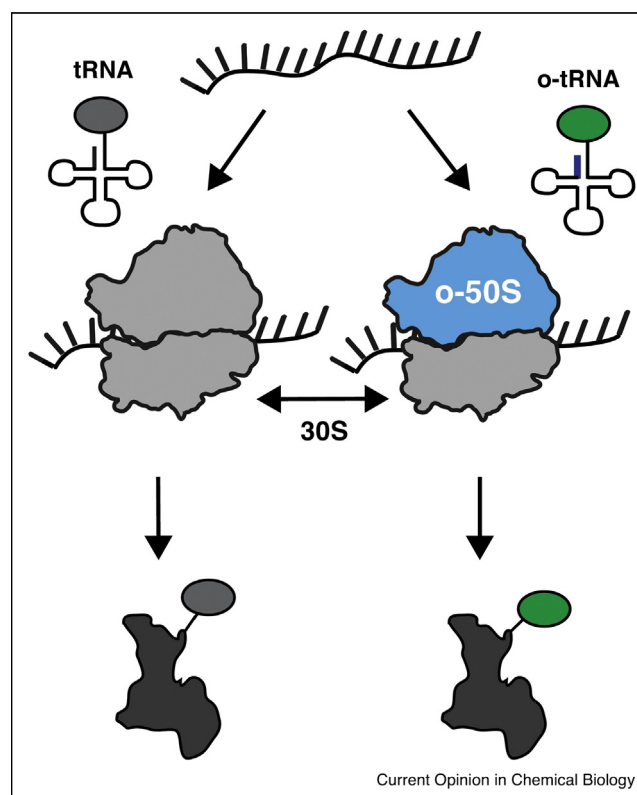
set of ribosomal proteins [55]. The iSAT system can also be encapsulated inside giant liposomes in a cell-like compartment which could facilitate *in vitro* evolution [59].

A key feature of the iSAT system is the ability to generate ribosomal variants by simply changing the DNA input, which allows for the facile construction of modified ribosomes with mutations in any desired domain. For example, ribosomes highly resistant to the lincosamide antibiotic clindamycin were readily constructed via targeted mutations in rRNA sequences [55], showcasing the ability of the iSAT system to generate functional modified ribosomes. Other approaches have shown the ability to evolve ribosomes *in vitro*. To select mutants of 23S rRNA, which contain the peptidyl transferase center, Cochella and Green developed a hybrid *in vivo/in vitro* approach [29]. Their strategy involved, first, *in vivo* assembly of tagged ribosomal mutants with variant 23S rRNAs (mutant rRNAs that are co-expressed with native rRNAs), second, isolation of tagged ribosomes by affinity purification, and third, *in vitro* selection of ribosome mutants using ribosome display. Employing this approach, the authors isolated functionally competent 23S rRNAs that were resistant to clindamycin and were not viable *in vivo* [29]. While this hybrid strategy enables *in vitro* selection of mutant ribosomes based on functional properties that cannot be accessed *in vivo*, it suffers from limited diversity resulting from the need to transform a mutant library of 23S rRNA genes into cells, as well as the challenge of separating mutant ribosome pools from native ones. This provides a robust opportunity to use iSAT for evolving modified ribosomes with altered substrate preferences.

Beyond modifying the active site of the ribosome for altered catalytic function, mutations elsewhere could allow the ribosome to use orthogonal tRNAs (Figure 4).

In pioneering work, Terasaka and colleagues demonstrated that the universally conserved 3'-terminal CCA sequence in tRNA molecules could be changed to CGA or GGA without loss of function, provided that three

Figure 4



Adapting the ribosome to unique tRNA pools. 50S subunits (o-50S) are modified in the 23S rRNA to bind only to orthogonal tRNA (o-tRNA) with a complementary sequence at the 3' tail. This can result in two species of protein translated from one RNA message. The 30S subunit freely associates between the two 50S species.

residues of the ribosomal peptidyl transferase center (P site G2251 and G2252, and A site G2553) were altered to retain base pairing with the tRNA terminus [60**]. To do this, they first generated synthetic tRNAs [61] bearing mutations at the 3' end at either one or two sites (C74G and/or C75G), and found that 3'-CGA-tRNA and 3'-GGA-tRNAs were not compatible with wild-type ribosomes and thereby orthogonal. Ribosomes with 50S subunits possessing complementary single (G2252C), double (G2251C and G2253C), and triple (G2251C, G2252C, and G2253C) mutations in the 23S rRNA were purified and their activity coupled with and without orthogonal tRNAs were assessed for translation using a flexible *in vitro* translation (FIT) system of purified parts [60**,62]. The authors found that the double mutant ribosome paired with 3'-CGA-tRNA was able to synthesize a separate species of peptide bearing an ncAA from a single mRNA, while wild-type ribosomes translated a peptide without an ncAA. This advancement suggests the possibility of establishing orthogonal coding channels for the biosynthesis of novel synthetic polymers capable of incorporating multiple ncAAs without crosstalk with canonical amino acids and the native translation system.

Conclusions

The construction of engineered ribosomes is poised to enable new opportunities to manufacture synthetic sequence-defined polymers that span vast structural and functional diversity, yet remain unattainable through existing methods in synthetic or biological chemistry. Despite these opportunities, many challenges remain. First, the fundamental constraints on the chemistry that the ribosome's RNA-based active site can carry out are unknown. By creating machines of translation that move beyond nature's processes and standard monomers, future work could elucidate a new understanding of the science of protein synthesis through construction. Second, the resolution of the crystal structure of the bacterial ribosome has provided newfound insights into the functional operation and mechanism of translation. Yet, repurposing ribosomes with new substrate preferences will require computational tools, as well as predictive models, to guide any fundamental redesign of the translation apparatus for new chemical activities. This is especially challenging given the size and structural complexity of the ribosome. Third, the ribosome is only one component of the translation apparatus and building wholly orthogonal translation systems with high specificity and activity for unique non-canonical substrates is complex, especially given its milieu of moving parts. New approaches for systematically engineering multiple components of the translation machinery (e.g., ribosomes, tRNAs, aminoacyl-tRNA synthetases, and elongation factors) concurrently as a cohesive unit, rather than in isolation, will provide synergistic opportunities to enhance multi-site incorporation of ncAAs into proteins.

Overcoming these challenges will have both short and long term benefits. In the short term, ribosome repurposing will deepen our understanding of translation, expand the genetic code in a unique and transformative way, and reveal how evolution has guided the structure and function of the ribosome. In the long term, engineering the translation apparatus will expand the range of genetically encoded chemistry in proteins and biopolymers, forging a broad range of innovative technologies that have the potential to transform synthetic biology.

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