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Research Article

A *Streptomyces venezuelae* Cell-Free Toolkit for Synthetic Biology

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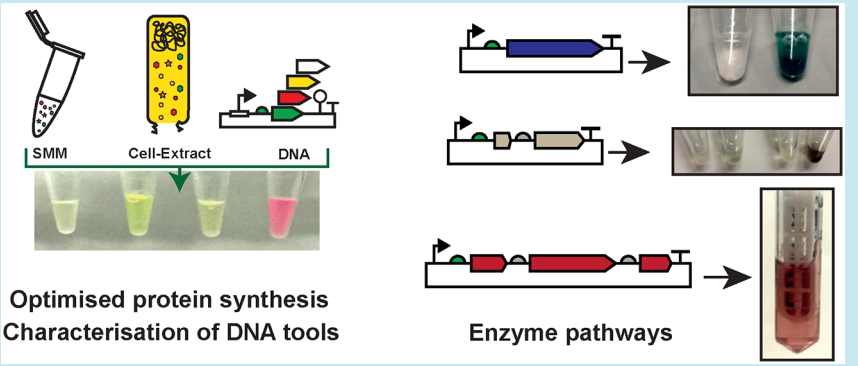

ABSTRACT: Prokaryotic cell-free coupled transcription−translation (TX-TL) systems are emerging as a powerful tool to examine natural product biosynthetic pathways in a test tube. The key advantages of this approach are the reduced experimental time scales and controlled reaction conditions. To realize this potential, it is essential to develop specialized cell-free systems in organisms enriched for biosynthetic gene clusters. This requires strong protein production and well-characterized synthetic biology tools. The *Streptomyces* genus is a major source of natural products. To study enzymes and pathways from *Streptomyces*, we originally developed a homologous *Streptomyces* cell-free system to provide a native protein folding environment, a high G+C (%) tRNA pool, and an active background metabolism. However, our initial yields were low (36 μg/mL) and showed a high level of batch-to-batch variation. Here, we present an updated high-yield and robust *Streptomyces* TX-TL protocol, reaching up to yields of 266 μg/mL of expressed recombinant protein. To complement this, we rapidly characterize a range of DNA parts with different reporters, express high G+C (%) biosynthetic genes, and demonstrate an initial proof of concept for combined transcription, translation, and biosynthesis of *Streptomyces* metabolic pathways in a single "one-pot" reaction.

KEYWORDS: *cell-free synthetic biology, Streptomyces, natural products, in vitro transcription−translation, cell-free protein synthesis*

INTRODUCTION

Streptomyces bacteria are environmental specialists (e.g., soil, marine, desert) that synthesize rich repertoires of natural products such as antibiotics. Much of this genetic information is locked up and cryptically regulated within biosynthetic gene clusters; regions of genomic DNA that harbor enzymes and other proteins (e.g., transporters, resistance markers). The key limitation in awakening these clusters for natural product discovery is silent gene expression and recalcitrant genetics. Traditional strategies to overcome this include genetic modification of the host organism to bypass native regulatory elements, and the "capture" of the cluster and expression in a heterologous host.[1] But this can take several weeks to months to complete with varying levels of success: some cryptic clusters remain dormant due to obscure native regulation. Fundamental tools that aid these efforts are of major interest to the natural product community.

Prokaryotic cell-free coupled transcription−translation systems are emerging as a new tool for studying natural product biosynthesis.[2−9] Cell-free transcription−translation uses a crude cell-extract or purified ribosomes and translation factors, the PURE system, in a "one-pot" reaction.[10,11] *E. coli* cell-extracts, referred to as either TX-TL[5,12,13] or cell-free protein synthesis (CFPS),[4,14] are low-cost, straightforward to prepare, and provide high recombinant protein yields, of up to 2300 μg/mL.[15] Moreover, metabolism is active,[16] providing ATP regeneration, while amino acid pathways are dynamic, providing additional ATP (through L-glutamate). In addition, certain amino acids deplete and become limiting for protein synthesis.[17] In summary, TX-TL provides distinct oppor-

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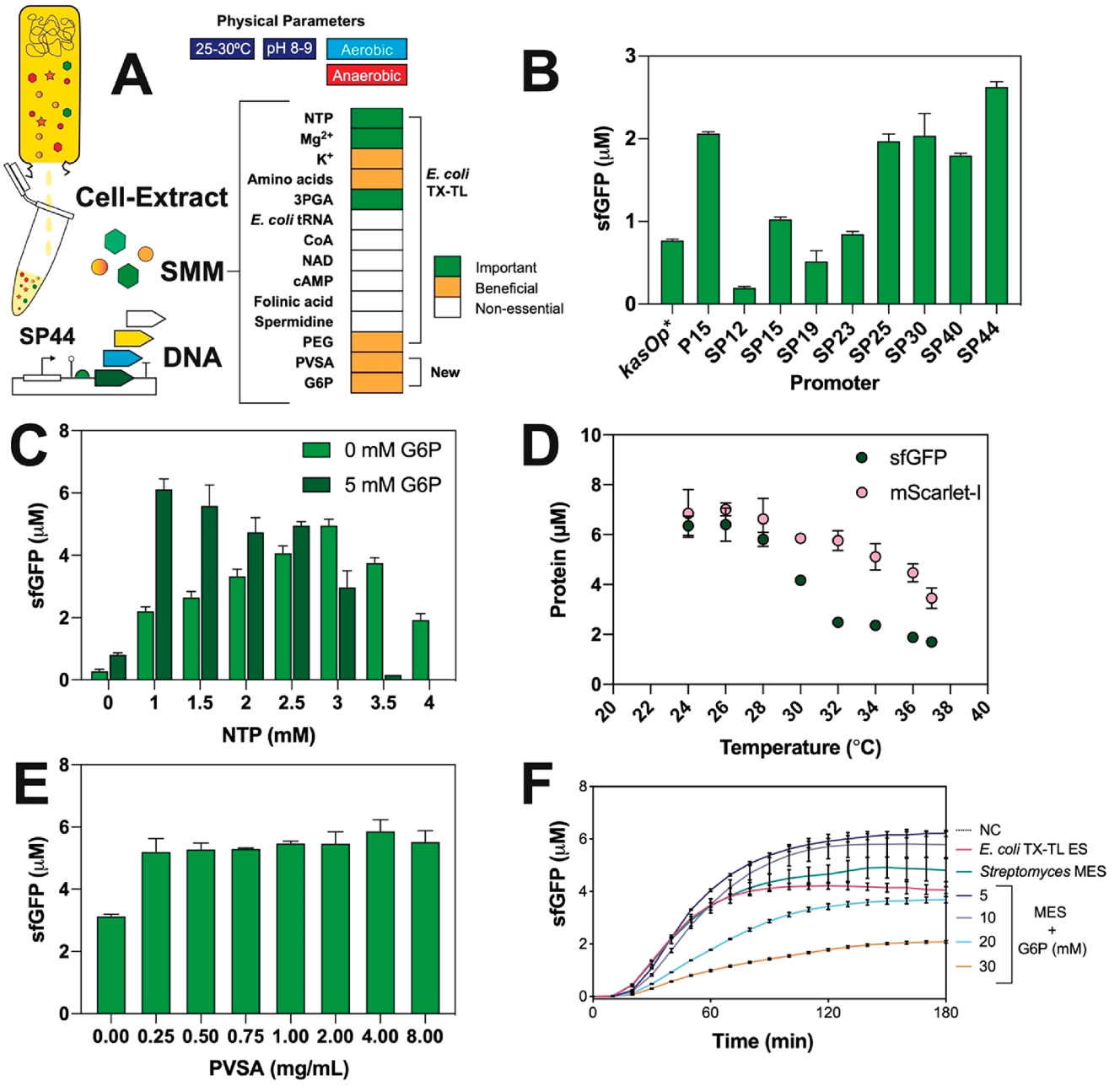

Figure 1. Overview of *Streptomyces* TX-TL optimization. (A) Outline of physical and biochemical parameters of *Streptomyces* TX-TL and SMM buffer system. Optimization of (B) promoter strength from Bai et al.;[19] (C) primary energy source; (D) temperature; (E) PVSA; and (F) G6P. Error bars are representative of three technical measurements.

tunities for natural product biosynthesis: precursors for biosynthesis, direct control to feed precursors, short experimental time scales (4−24 h), and stable yields. Moreover, we and others have shown the potential for automation in cell-free synthesis.[18−23] Specifically, we have screened up to 500 plasmid variants in 24 h.[23]

While *E. coli* TX-TL and the PURE system are promising for natural product biosynthesis,[2−4,9] *E. coli* has limited potential for studying biosynthetic gene clusters from *Streptomyces*, due to a number of genetic and metabolic differences. For example, the codon content between *Streptomyces* (∼70% G+C) and *E. coli* (51% G+C) is different, while the regulatory sequences that control transcription, post-transcription, and overall gene expression are distinct. Moreover, secondary metabolism in *E. coli* is not necessarily well-suited, and often requires further metabolic engineering. Notwithstanding, *E. coli* synthesis of heterologous proteins can result in poor expression and solubility.[5,24] Therefore, we anticipate that a dedicated *Streptomyces* TX-TL system for homologous protein synthesis, has several advantages for studying natural product biosynthesis. As a first step, we originally released a *Streptomyces venezuelae* DSM-40230 (ATCC 10712) TX-TL system, but this produced low protein yields (36 μg/mL) with high batch-to-batch variability. We chose *S. venezuelae* ATCC 10712 since it is well-suited to synthetic biology. *S. venezuelae* ATCC 10712 is fast-growing (40 min doubling time) and grows dispersedly in liquid culture; most *Streptomyces spp.* have slower doubling times and clump in mycelial aggregates. Moreover, *S. venezuelae* has a range of synthetic biology tools[25,26] and is an attractive host for industrial biotechnology.[27,28] In parallel

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to our studies, the Jewett group[7] also established a *Streptomyces lividans* CFPS system (yields ~50 μg/mL), which was further optimized.[29] A recent update to this system highlighted the need for adding individual purified translation factors[8] to elevate protein synthesis up to ~400 μg/mL.

On this basis, we rationalized that protein synthesis, in our original *S. venezuelae* TX-TL system, could be limited by the use of an energy solution derived for an optimal *E. coli* TX-TL protocol.[12] For a review of the biochemical role and origin of cell-free energy solutions, we refer the reader to Dopp et al.[30] In brief, TX-TL requires a cell-extract, a primary and secondary energy source, amino acids, cofactors, molecular crowding agents, and additives (e.g., Mg^{2+}, spermidine, folinic acid, tRNA) to support protein synthesis from a template DNA sequence. Some of these biochemicals are present in the cell-extract but may be rate-limiting. The energy source is composed of nucleotide triphosphates to drive initial mRNA and protein synthesis (primary energy source) and commonly 3-phosphoglyceric acid (3-PGA) or phosphoenolpyruvate (PEP) as the secondary energy source. 3-PGA or PEP provide ATP regeneration to leverage extended protein synthesis. Potentially, primary metabolism could be activated in TX-TL to provide reducing equivalents (e.g., NADH, FADH), extra energy, and building blocks (e.g., amino acids, malonyl-CoA) for natural product biosynthetic pathways, as shown in cell-extract metabolic engineering.[31] In this work, we focus on upgrading our *S. venezuelae* system to elevate protein synthesis. We also demonstrate its broader potential for cell-free synthetic biology, namely, for characterizing DNA parts and activating some model biosynthetic pathways. To achieve this, we made some simple modifications to the system, allowing yields of up to 266 μg/mL of expressed recombinant proteins. We also demonstrate combined transcription−translation and biosynthesis of some example natural product pathways, namely, melanin and haem biosynthesis. We report an easy-to-follow protocol that simply requires three components: DNA, cell-extract, and a master mix that we describe in detail. We believe this generic *Streptomyces* TX-TL toolkit will be of broad interest to the natural product community, complementing experimental wet-lab tools for genome mining studies.

RESULTS AND DISCUSSION

A High-Yield *Streptomyces* TX-TL Protocol. To provide an improved *Streptomyces* TX-TL toolkit for synthesis of high G+C (%) genes and pathways from *Streptomyces* spp. and related genomes, a key priority was to optimize protein production. Also, a straightforward protocol with minimal batch variation was essential, for ease of repeatability. Since bacterial transcription and translation is coupled, either these steps, physical parameters, or components from the energy solution, limit overall TX-TL activity. Therefore, to keep our protocol streamlined, we made the following changes: promoter strength, energy solution, ATP regeneration, and RNase inhibition. In doing so, we obtained a high-yield protocol with minimal variation between different cell-extract batches (Figure 1A).

Promoter Strength. Previously, we used the *kasOp** promoter to drive mRNA synthesis in *Streptomyces* TX-TL. This yielded up to 1.3 μM (36 μg/mL) of the model superfolder green fluorescence protein (sfGFP) in our previous work.[5] Promoter strength is a key limiting factor in heterologous expression systems. *kasOp** is a strong *Streptomyces* constitutive promoter, originally derived from the *kasO/cpkO/sco6280* promoter, with core-35 and -10 boxes of TTGACN and TAGART, respectively.[32] The *kasOp** promoter is active in a range of *Streptomyces* spp. through the endogenous RNA polymerases and HrdB house-keeping Sigma factor.[32] Bai et al. developed a synthetic promoter library based around *kasOp**, using fluorescence-activated cell sorting (FACS) to quantity *S. venezuelae* protoplasts.[25] This included the isolation of a synthetic promoter 44 (SP44), which is 1.87-fold stronger than *kasOp**.[25] We used *Streptomyces* TX-TL to test a panel of promoters developed by Bai et al., with SP44 being the strongest (2.63 μM sfGFP) and 2.2-fold more active than *kasOp** (Figure 1B). We also repeated this across four independent cell-extract batches, but still observed strong batch variation. However, SP44 provided a stronger reporter plasmid to continue the optimization process.

Energy Solution. Next, we focused on developing a minimal energy solution (MES) to identify any nonessential components. The standard *E. coli* TX-TL energy solution used previously,[5] is composed of HEPES buffer, ions (e.g., Mg-glutamate, K-glutamate), nucleotide triphosphates (NTPs - ATP, GTP, CTP, and UTP), secondary energy source [typically 3-phosphoglyceric acid (3-PGA) or phosphoenolpyruvate (PEP)], amino acids, molecular crowding agent, and a number of additives.[14] To establish a MES for *Streptomyces* TX-TL, we first eliminated a number of nonessential components from the energy solution. This included coenzyme A, tRNA (*E. coli*), NAD, cAMP, folinic acid, and spermidine (Figure S1A). While we did initially observe a positive response with cAMP, after several repeats in batches, this effect was not repeatable. For the HEPES buffer component, this was noninhibitory (10−100 mM) and provided optimum activity between pH 8−9 (Figure S1B). For the secondary energy source, we found 3-PGA was essential; the removal of 3-PGA decreased sfGFP synthesis by 98% (Figure S1C). We tried to replace 3-PGA with alternative secondary energy sources but observed only minimal activity: maltose (0.13 μM), sucrose (0.15 μM), and pyruvate (0.17 μM). Other potential sources such as glucose (with phosphate), PEP, and succinate were inactive (Figure S1C). 3-PGA is the preferred secondary energy source in a range of nonmodel cell-extract hosts,[33] due to its chemical stability and high energy potential, with an optimum concentration of 30 mM (Figure S1D). For the primary energy source (NTPs), there was some basal activity without additional NTPs, but addition of 3 mM ATP/GTP and 1.5 mM CTP/UTP provided peak activity (Figure S1E). Surprisingly, the removal of amino acids only decreased sfGFP synthesis by 45%, with 0.5−1.5 mM amino acids providing peak activity (data not shown). For a Mg screen, we found that $MgCl_2$, Mg-glutamate, or Mg-acetate were all active (Figure S1F), while high levels of K-glutamate (150−200 mM) stimulated increased sfGFP synthesis (Figure S1F). This is possibly due to additional ATP regeneration via entry of α-ketoglutarate into the TCA cycle, as previously shown.[34] Lastly, while we observed reasonable activity without PEG, 1% (w/v) PEG 6K was optimum, providing a 44% rise in activity (Figure S1G). However, it is desirable to omit PEG for downstream natural product analytical purposes (e.g., LC−MS). Finally, on the basis of these observations, we optimized our basic *Streptomyces* TX-TL MES system by individually fine-tuning the concentration of its core components (3-PGA, NTPs), while leaving DNA (40 nM), Mg-glutamate (4 mM), K-glutamate (150 mM), amino acids (1.25 mM), and PEG 6K

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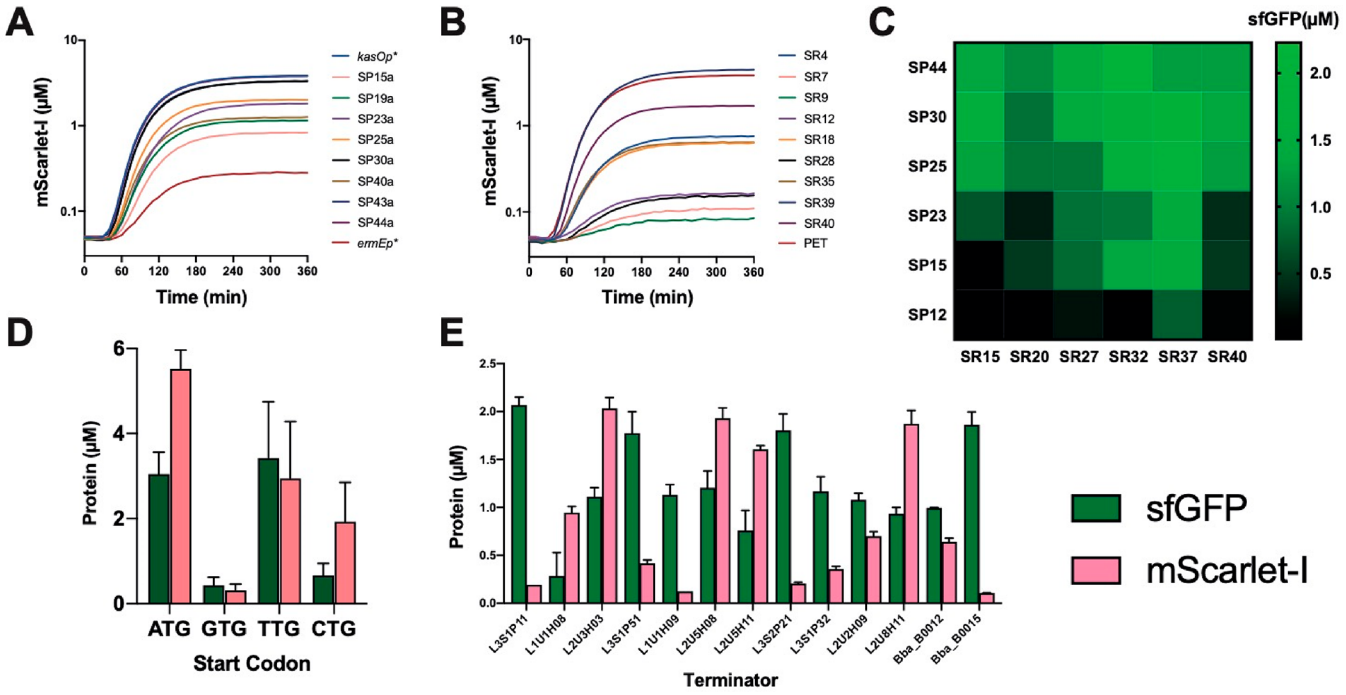

Figure 2. Part characterization of *Streptomyces* regulatory elements: (A) Promoter-R15 capsid RBS-mScarlet-I; (B) *kasOp**-RBS-mScarlet-I; (C) Promoter-RBS-sfGFP combinations; (D) variable start codons (with sfGFP and mScarlet-I); and (E) variable Rho-independent terminators from Chen et al.[34] For terminator plasmid design, see Moore et al.[38] 40 nM plasmid DNA was incubated in the optimized reaction conditions at 28 °C as a technical triplicate repeat and repeated on two separate days. Unless otherwise stated, the SP44 promoter, PET RBS and Bba_B0015 were used in constructs, assembled into either pTU1-A (*E. coli*) or pSF-1 (*E. coli* and *Streptomyces* shuttle vector). Error bars are representative of three technical measurements.

(1%) constant. 3-PGA was most optimum at 30 mM, while the NTP level (ratio of 2:1 ATP/GTP:CTP/UTP), showed biphasic activity, peaking at 3 mM ATP/GTP, with full inhibition at 4 mM. Specific data on Mg-glutamate and K-glutamate optimization with four different cell-extract batches is presented in Figure S2. As a combined result of this optimization process, sfGFP synthesis was increased to 4 μM, representing a 52% increase.

Additional ATP Regeneration Pathways. In a previous study, Caschera et al. highlighted that other glycolytic enzymes function in *E. coli* TX-TL, using the disaccharide maltose (or maltodextrin) combined with 3-PGA. This method extended protein synthesis up to 10 h, through inorganic phosphate recycling.[15] We investigated whether this part of the metabolism is functional in *Streptomyces* TX-TL. Therefore, we tested the *Streptomyces* MES system (with 3-PGA) with maltose, glucose, glucose-6-phosphate (G6P), or fructose-1,6-phosphate (F16P). Interestingly, maltose, glucose, Glc6P, and F16P all prolonged the length of *Streptomyces* TX-TL activity from 2 to 3 h. This was maximal with 5 mM Glc6P and 30 mM 3-PGA (Figure 1C), at an optimum temperature of between 24 and 28 °C (Figure 1D). All together we observed a 59% increase in sfGFP synthesis to 6.37 μM, but lower levels of NTP are required (Figure 1C)—equivalent to 1 mM ATP/GTP and 0.5 mM CTP/UTP. We speculate this could be related to ATP regulation of the glycolytic enzymes (e.g., hexokinase, fructokinase), leading to rapid depletion of ATP and inhibition of protein synthesis. However, this requires further investigation as there is limited literature on specific glycolytic enzymes from *Streptomyces*.

RNase Inhibition. As a final addition to the system, we tested the effect of the inexpensive RNase inhibitor, polyvinylsulfonic acid (PVSA). Recently, PVSA, an RNA-mimetic, was shown to improve mRNA stability in *E. coli* TX-TL, but did not increase protein synthesis.[35] In *Streptomyces* TX-TL, 1 mg/mL PVSA increased sfGFP synthesis up to 5.87 μM, in the basic MES system (Figure 1E). However, while we observed individual improvements with either the PVSA RNase inhibitor or the blended G6P/3-PGA secondary energy source, in combination, there was no significant additive effect with PVSA and G6P/3-PGA together. This suggested that other rate-limiting factors are at play.

In summary, we have made a specific energy solution for *Streptomyces* TX-TL with an overall 6-fold improvement in the system. This is attributed to the combined use of 3PGA and G6P as secondary energy sources and a stronger promoter system. Furthermore, we find this can be combined into a single *Streptomyces* master mix (SMM) solution, further streamlining the reaction process. With this simple modification, the TX-TL reaction requires three single components that minimize batch variation: SMM solution, plasmid DNA, and the cell-extract. Next, we sought to demonstrate the use of this simplified system for the testing of plasmid tools and regulatory elements for *Streptomyces* synthetic biology.

Cell-Free Characterization of *Streptomyces* Genetic Tools for Synthetic Biology. It is highly desirable to characterize standard DNA parts using rapid and iterative design−build−test−learn cycles, the central paradigm of synthetic biology. For *Streptomyces* and related strains, either conjugation or protoplast transformation is typically used to transfer self-replicating and integrative plasmids for the testing of DNA parts for *Streptomyces* synthetic biology.[25,26,32] DNA parts are small modular regulatory elements (e.g., promoter, insulator, tags, RBS, ORF, terminator) that facilitate down-

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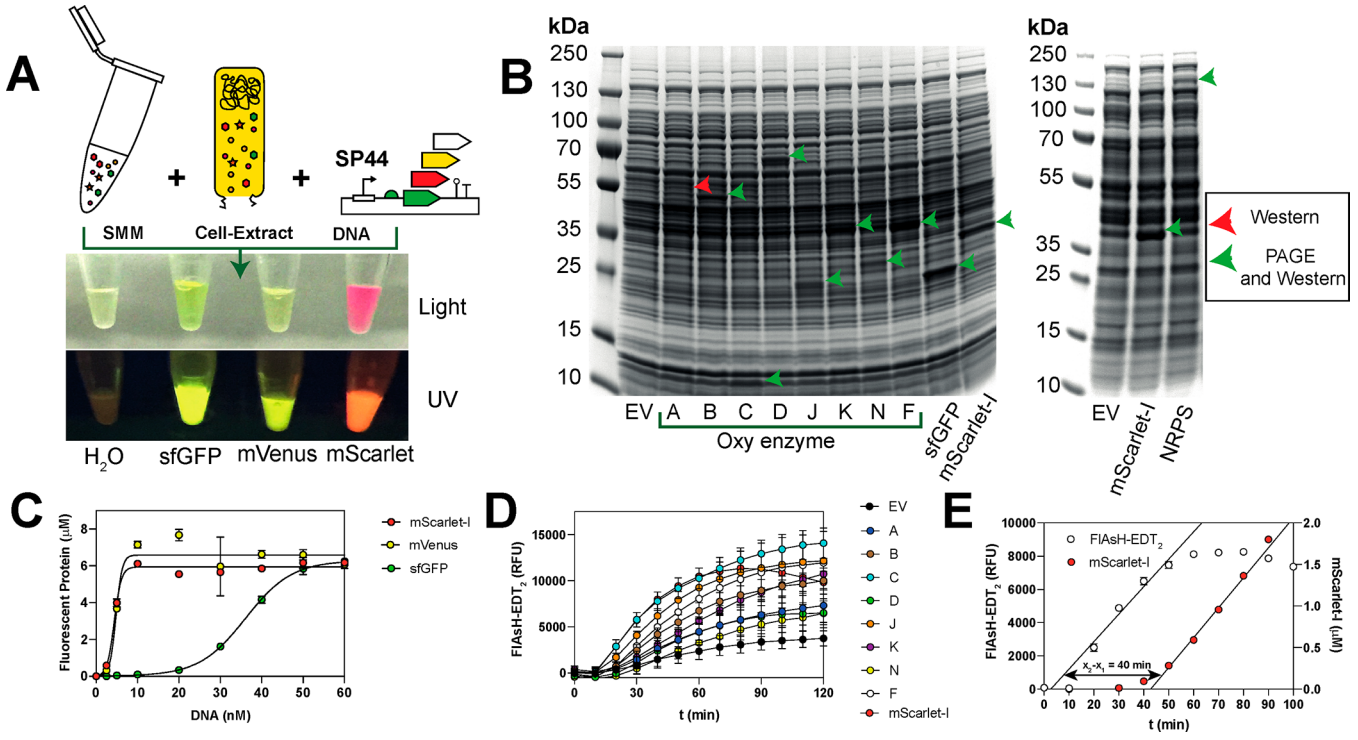

Figure 3. Robust and high-yield synthesis of high G+C (%) genes. (A) Synthesis of codon-optimized fluorescence proteins. (B) Denaturing PAGE of oxytetracycline biosynthetic proteins, fluorescence proteins, and a representative NRPS (NH08_RS0107360 from *S. rimosus*). (C) Saturation of protein synthesis for sfGFP, mVenus, and mScarlet-I with increasing DNA concentrations. (D) Real-time detection of protein synthesis with C-terminal FlAsH-EDT$_2$ tag system. (E) Estimation of mScarlet-I maturation time with real-time measurement of immature and mature protein synthesis. Error bars are representative of three technical measurements.

stream combinatorial DNA assembly workflows (e.g., Golden Gate) for refactoring gene expression pathways. While there are different approaches to quantitate gene expression,[26,36] Bai et al.[25] recently applied a lysozyme method, to study single-cell gene expression quantitation of *S. venezuelae* ATCC 10712 protoplasts using fluorescence-activated cell sorting.

We next tested the promoter and RBS elements from Bai et al.[25] in *Streptomyces* TX-TL, as well as two other important regulatory elements: alternative start codons[36] and terminators.[37] First, we built these DNA parts to be compatible with our previous DNA assembly method, EcoFlex.[38] For this we had to modify the promoter consensus (prefix renamed, *e.g.*, SP44a instead of SP44) to remove an internal BsmBI site to permit MoClo assembly. In addition, to provide comparative *in vivo* data, we built a new destination vector (cured of BsmBI and BsaI sites) from pAV-*gapdh* from Phelan et al.[26] and renamed this StrepFlex (pSF1). pAV-*gapdh* is an integrative shuttle vector developed as a synthetic biology plasmid tool for *S. venezuelae*.[26] First, for the promoter library (*kasOp**, SP15a, SP19a, SP23a, SP25a, SP30a, SP40a, SP44a, and *ermEp**), we assembled this with the RiboJ insulator, R15 capsid RBS, mScarlet-I, and the Bba_B0015 terminator. For the RBS library, *kasOp** was used as the promoter. For the promoter variants, activity ranged from 5% (*ermEp**) to 100% (*kasOp**). In contrast to earlier results (Figure 1B), the range of activities for the BsmBI cured promoter variants were between 30 and 50% less active across the library. For the activity of the RBS variants, this ranged from 0.7% (SR9) to 117% (SR39) activity relative to the R15 capsid RBS (Figure 2B). We also tested two-dimensional promoter and RBS space with sfGFP (Figure 2C). Lastly, to provide *in vivo* data, we characterized the mScarlet-I promoter and RBS plasmids (from Figure 2A,B) in *S. venezuelae* ATCC 10712 (Figure S3) following the approach by Phelan et al.[26] Interestingly, there was some significant outliers in the RBS library. SR39 (along with the *E. coli* PET-RBS) was the strongest RBS in contrast to SR40, which was unexpectedly weaker both *in vitro* and *in vivo*. In addition, SR4, an expected weak RBS, was strong in both *in vitro* and *in vivo* measurements (Figure 2A,B, Figure S3). This may reflect differences in the upstream 5′-untranslated (5′-UTR) region and the use of a different fluorescence reporter (mScarlet-I), in comparison to Bai et al.[25] However, overall the promoter and RBS strengths characterized were broadly consistent with the original publication.[25]

Another important regulator of gene expression is the start codon. In most bacteria, ATG is the preferred codon for translation initiation through fMet-tRNA. Previously, Myronovskyi *et al.* used a *β*-glucuronidase (GUS) reporter to show that the TTG codon was stronger than ATG for translation initiation by almost 2-fold in both *Streptomyces albus* J1074 and *Streptomyces sp.* Tu6071.[36] Using sfGFP and mScarlet-I as reporters, our findings suggest that, for *S. venezuelae* at least, ATG is equivalent in strength to TTG, followed by CTG and last GTG as the weakest (Figure 2C). This also likely changes with coding sequences and 5′-UTR. In comparison, for *E. coli* the order of strength goes as follows: ATG > GTG > TTG > CTG.[39] We expect this differs due to high GC codon bias in *Streptomyces*. Despite the use of different experimental conditions, our results confirm that TTG is a strong alternative start codon and that GTG is weak. Nevertheless, the role of GTG in regulation is unclear and intriguing due its high frequency in *Streptomyces* genomes.[40]

To the best of our knowledge, no studies have so far reported the use of terminators for controlling pathway

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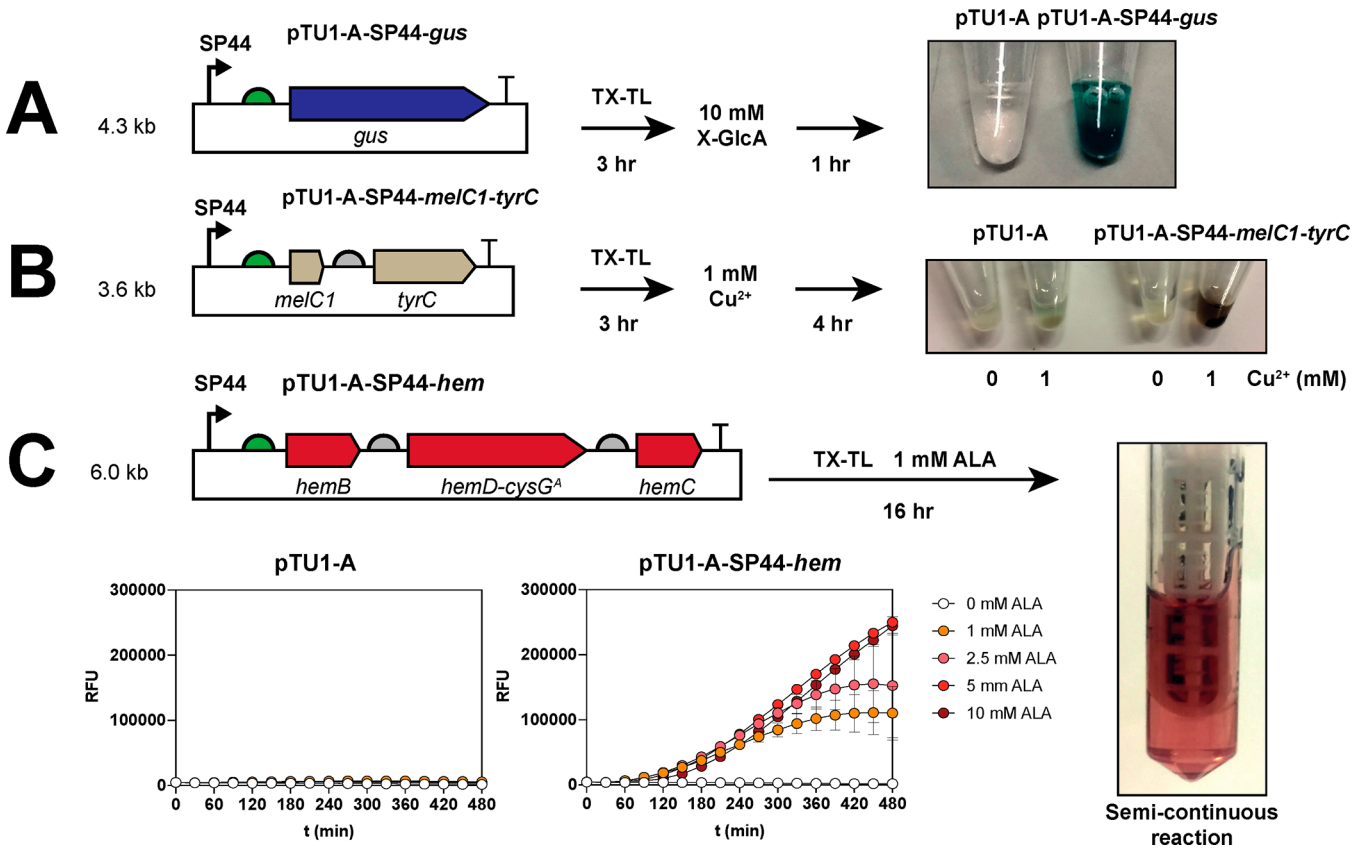

Figure 4. *Streptomyces* cell-free transcription, translation and biosynthesis. (A) Codon-optimized *E. coli* MG1655 GUS enzyme. (B) *S. venezuelae* DSM-40230 tyrosinase (TyrC) and copper metallochaperone (MelC1). (C) *S. venezuelae* DSM-40230 early stage haem biosynthetic pathway, HemB, HemD-CysG^{A} and HemC. Addition of individual substrates and approximate time scales are indicated within the diagram. For details of batch and semicontinuous reaction conditions, please refer to methods. For a summary of the chemical intermediates, please see Figure S9. Melanin is a mixed family of pigments spontaneously produced from air oxidation of L-DOPA. Fluorescence error bars are representative of three technical measurements.

expression in *Streptomyces*. Using the same experimental format as we previously used in EcoFlex,[38] we tested a selection of Rho-independent terminators from the iGEM catalogue (Bba_B0012, Bba_B0015) and from Chen et al.[41] in *S. venezuelae* TX-TL (Figure 2D). The latter terminators were designed to prevent repetition in DNA elements and protect against homologous recombination as previously highlighted.[41,42] In summary, the activities we observed, strongly follow our previous observations in *E. coli* cell-free.[38] For now, our TX-TL system demonstrates proof-of-concept data for prototyping DNA parts in *Streptomyces*. Rho-independent terminators may in future provide tools for refactoring metabolic pathways in engineered *Streptomyces* strains.

TX-TL synthesis of high G+C (%) genes. Previously, we found our *Streptomyces* TX-TL system was most active with 40 nM of plasmid DNA, using the *kasOp**-sfGFP reporter, to saturate protein synthesis.[35] In comparison to *E. coli* TX-TL, protein synthesis is saturated at around 5−10 nM of reporter DNA, which varies with different promoters and sigma factors.[43] We questioned whether DNA degradation led to this discrepancy since most *Streptomyces spp.* degrade methylated plasmid DNA with endonucleases.[44] To compare methylated and unmethylated plasmid DNA for methylation-specific endonucleases, we tested unmethylated and methylated SP44-sfGFP reporter plasmid in *Streptomyces* TX-TL. Interestingly, there was no major change in sfGFP synthesis between unmethylated and methylated plasmid DNA, across different DNA concentrations (Figure S4). We also tested relative plasmid DNA stability in *S. venezuelae* cell-extracts, with the standard MES energy solution, and incubated at different time-lengths, followed by re-extraction of the plasmid DNA (using the Qiagen plasmid DNA purification kit). The extracted plasmid DNA was then separated and visualized on a 1% (w/v) agarose gel. This indicated that methylated plasmid DNA is stable, during the time (0−4 h) when TX-TL is active (Figure S4). Further to this, we tested linear DNA for exonuclease activity. To protect the coding sequences, we PCR amplified about 150−250 bases upstream and downstream of the coding parts, using the standard SP44-sfGFP reporter plasmid. However, in the TX-TL reaction, linear DNA was 95% less active than circular DNA, at 40 nM of DNA (Figure S5). This suggests the *S. venezuelae* cell-extract has exonuclease activity, while endonuclease activity is minimal.

Since circular DNA degradation was not a limiting factor, we tested different fluorescent proteins (Figure 3A) to determine if the optimum plasmid DNA concentration for protein synthesis changes. First, we tested mVenus-I and mScarlet-I, combined with the strong SP44 promoter, and compared them to the SP44-sfGFP reporter. The maximum yields achieved for these three proteins were 6.48 μM sfGFP (174 μg/mL), 9.50 μM mScarlet-I (266 μg/mL), and 7.72 μM mVenus-I (224 μg/mL). Interestingly, this was tested in the extract batches presented in Figure S2, where both SP44-mScarlet-I and SP44-mVenus saturated protein synthesis with a lower DNA

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template (10 nM) than SP44-sfGFP (50 nM) (Figure 3B). This was surprising since the coding sequence of mVenus is 96% identical to sfGFP, with the exception of 30 mutations and an additional GTG (valine) at the second codon for mVenus-I. However, while the optimal sfGFP plasmid DNA concentration was 50 nM in this experiment, consistent with our previous work,[5] it was not consistent in all extract batches (Figure S4B). This contrasting result likely relates to either a difference in mRNA stability or translation initiation rate between the batches. Since little is known about how *Streptomyces sp*. control protein synthesis, this topic alone merits a separate in-depth investigation.

Second, we tested the robustness of the system for other proteins from high G+C (%) genes (Figure 3C). We expressed the oxytetracycline enzymes (OxyA, -B, -C, -D, -J, -K, -N, and -T) from *Streptomyces rimosus* that were previously only detectable by Western blotting in our original publication,[5] as well as three nonribosomal peptide synthetases (NRPS). The latter included the TxtA and TxtB NRPS enzymes from thaxtomin A biosynthesis in *Streptomyces scabiei* and an uncharacterized NRPS (NH08_RS0107360) from *S. rimosus*. Except for TxtA, most enzymes were discernible by either SDS-PAGE (Figure 3C), while for OxyA (47 kDa) and TxtB (162 kDa), low levels (<0.5 μM) were detected by Western blotting using an anti-Flag tag (data not shown). We also incorporated a C-terminal tetracysteine tag with the oxytetracycline enzymes and mScarlet-I, using the fluorogenic biarsenical dye fluorescein arsenical hairpin binder-ethanedithiol (FlAsH-EDT$_2$), to measure real-time nascent protein synthesis (Figure 3D). Most oxytetracycline enzymes showed a significant increase in FlAsH-EDT$_2$ fluorescence ($P < 0.05$), peaking at 120 min, with only OxyN producing the weakest response ($P = 0.056$). However, this was still clearly detectable by PAGE or Western. For mScarlet-I, the time-lag between the fluorescence signals for FlAsH-EDT2 (immature protein) and mScarlet-I (mature protein) allowed us to estimate a maturation time of 40 min for mScarlet-I (Figure 3E). This is in close agreement to a literature value of 36 min, calculated *in vivo*.[45] In summary, our *Streptomyces* TX-TL system is robust for expression of high G+C (%) genes, incorporates multiple tools (e.g., tags, plasmid systems) and is comparable to other bacterial TX-TL systems.

Transcription, translation, and biosynthesis. The next step was to reconstitute a biosynthetic pathway in *Streptomyces* TX-TL system. Initially, to show the synthesis of a single enzyme and its activity, we selected the GUS reporter enzyme. We synthesized the enzyme in the TX-TL reaction from 40 nM SP44-*gus*, left for 4 h at 30 °C. The GUS enzyme showed a clear band on SDS-PAGE at the expected size of 68 kDa (Figure S6). To test for GUS activity, an equal volume of the TX-TL extract, as well as a negative control reaction, was mixed with X-GlcA substrate in increasing concentrations (10, 25, and 50 mg/mL). Only the extract from the SP44-*gus* reaction developed a deep blue pigment within minutes, indicating strong GUS activity (Figure 4A).

Next, we selected two metabolic pathways to provide a further test for the TX-TL system. We selected two operons from *S. venezuelae* encoding the melanin and early stage haem biosynthetic pathways to provide a discernible output for testing (fluorescence and/or colorimetric). Also, both operons were selected from *S. venezuelae*, to improve expression in TX-TL since the codon usage is adapted to this host.

Melanin is a natural pigment that absorbs ultraviolet (UV) light to protect cells from DNA damage. Recently, Matoba et al. studied the mechanism of tyrosinase and the role of the "caddie" protein from *Streptomyces castaneoglobisporus* HUT6202.[46] Tyrosinase, TyrC, catalyzes the rate-limiting step in melanin biosynthesis. It oxidizes the phenol group (in L-tyrosine) into the *orthro*-quinone intermediate, which enters an autocatalytic cascade into the melanin pathway. TyrC is dicopper-dependent, with each Cu(II) atom coordinated by three His residues, facilitated by MelC1, a small (12.8 kDa) metallochaperone. The *S. venezuelae* tyrosinase operon encodes both MelC1 and TyrC. After TX-TL with SP44-*melC1-tyrC*, denaturing PAGE shows clear synthesis of TyrC at approximately 34 kDa (expected 31.4 kDa) although MelC1 was indistinguishable (Figure S7). In terms of activity, we observed brown pigment formation after ∼2 h, only with the addition of 1 mM $CuCl_2$ (Figure 4B). This indicates L-DOPA formation, which enters an autocatalytic cascade, leading to different melanin pigments. This suggests TyrC is active, despite the apparent absence of MelC1. Without the addition of $CuCl_2$ or tyrosinase plasmid, the cell-extracts remained clear. Previously, Matoba et al. showed that insertion of Cu(II) into TyrC by MelC1 involves a transient interaction, and that MelC1 is unstable and forms aggregates difficult to detect with PAGE.[46] Also, apo-TyrC is inactive with Cu(II) alone, which suggests that our TX-TL system supports the synthesis of both TyrC and MelC1.

Lastly, we tested a three-gene biosynthetic operon (*hemC-hemD/cysG^A-hemB*) that catalyzes the early stages of haem biosynthesis.[47] This pathway was selected since it contains a known fluorescence reporter enzyme CysG^A,[48] a methyltransferase naturally fused as HemD/CysG^A. We added a pTU1-A-SP44-*hemC-hemD/cysG^A-hemB* (pTU1-A-SP44-*hem*) plasmid into the TX-TL reaction, as well as a negative control plasmid (pTU1-A), both with and without 5-aminolevulinic acid (5-ALA), which is the substrate for the pathway. In the presence of pTU1-A and 1 mM ALA, there was some minor background fluorescence (Figure 4C), which we expected since haem biosynthesis is essential. In contrast, with pTU1-A-SP44-*hem* and 1 mM ALA, strong red fluorescence was generated, 20-fold higher than background levels in the control reaction (pTU1-A and 1 mM ALA). For protein synthesis, while we could detect HemB (35 kDa) and HemC (38 kDa), the fusion protein HemD/CysG^A was less clear, with other major bands at the expected mass, 58.3 kDa (Figure S6). To verify pathway function, we ran a semicontinuous reaction[7] to facilitate purification by separating the haem intermediates from the cell-extract proteins (inset image in Figure 4C). Interestingly, LC−MS analysis detected the air-oxidized product of the HemD enzyme (uroporphyrinogen III, 837 m/z), observed as a 6-electron oxidized uroporphyrin III (red fluorescent) intermediate at 831 m/z, typical for these air-sensitive intermediates (Figures S8 and S9). Since uroporphyrinogen III is colorless and nonfluorescent, we tried to minimize oxygen levels in the TX-TL reaction using a layer of mineral oil in small-scale batch reactions. Surprisingly, the pigment and fluorescence still accumulated, suggesting that dissolved oxygen levels remain stable in the cell-extract. Interestingly, we also found the TX-TL reactions were still active for sfGFP and mScarlet-I synthesis (data not shown). This anaerobic activity potentially suggests that oxygen is not rate-limiting at the current level of protein synthesis activity and is sufficient for folding of the fluorescence proteins. Further investigation is

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needed to determine whether oxidative phosphorylation is active in *Streptomyces* TX-TL and whether this presents a bottleneck to overall ATP regeneration. In summary, these results show that our *S. venezuelae* TX-TL system can support the synthesis of at least three enzymes from plasmid DNA in a combined "one-pot" translation, translation, and enzymatic pathway.

CONCLUSIONS

Our study complements a recent surge in interest in the use of cell-free systems for the study of biosynthetic pathways.[2,4,9,29] Here we wanted to expand the palette of plasmid tools for the further development of *S. venezuelae* as a synthetic biology chassis by developing an optimized streptomyces TX-TL toolkit.[5,25−27] Our combined findings show at least a 6-fold improvement in protein synthesis over our original *Streptomyces* TX-TL system, using the wild-type *S. venezuelae* ATCC 10712 strain. It is likely genetic modifications that either limit RNA degradation or increase translation rates will improve this current system. Indeed, Xu et al. recently showed translation factors are a clear rate-limiting step for other *Streptomyces* cell-free systems.[8] Finally, we demonstrate that the semicontinuous system permits reasonable milligram scale-up of biosynthetic metabolites and a clean route to purification and analysis. In conclusion, our results realize the early stage potential of *Streptomyces* cell-free for the study of synthetic biology for natural products. It provides a native prototyping environment for developing synthetic biology tools (e.g., promoters/RBS) and also for exploring biosynthetic pathways from these organisms.

METHODS

Molecular Biology. All plasmids were either prepared using EcoFlex cloning or by routine materials and methods, as previously described.[41] For the PCR of high GC genes and operons, Q5 polymerase (NEB, UK) was used, using standard cycling or touchdown (72−59 °C annealing) and the addition of 5% (v/v) DMSO. For tricky amplicons, the protocol was modified with an annealing time of 30 s and elongation temperature reduced to 68 °C. The following bacterial strains were used: *S. venezuelae* DSM-40230 and *E. coli* DH10β. Unmethylated plasmid DNA was prepared from an *E. coli* $dam^{-}dcm^{-}$ mutant (C2925) obtained from NEB. Plasmids and oligonucleotides are listed in Tables S1−S4.

Preparation of Cell-Extracts. *S. venezuelae* ATCC 10712 was grown in GYM (prepared in distilled water). The cell-extracts were prepared as described previously,[5] with the exception that β-mercaptoethanol was removed from the wash buffers and replaced with 2 mM dithiothreitol.

Energy Solution and Reaction Conditions. The reaction mixture contained 8 mg/mL cell-extract, 25 mM HEPES, 1 mM ATP, 1 mM GTP, 0.5 mM UTP, 0.5 mM CTP, 30 mM 3-PGA, 5 mM glucose-6-phosphate, 1.5 mM amino acids (1.25 mM L-leucine), 4 mM Mg-glutamate, 150 mM K-glutamate, 1% (w/v) PEG6K and 5 mg/mL PVSA. All reactions were incubated at 28 °C, with 40 nM pTU1-A-SP44-sfGFP and the MES or SMM buffer system, unless otherwise stated. At least three technical repeats were prepared (for fluorescence measurements) and repeated with at least two independent cell-extract batches (from A6-A9) prepared on separate days. (See Table S6 for chemicals in the SMM buffer.)

Denaturing PAGE. A 40 μL cell-free reaction (30 μL SMM + 10 μL plasmid DNA) was incubated in a 2 mL tube at 25−30 °C (no shaking) for 6 h. To precipitate proteins, 1 mL of ice-cold 100% (v/v) acetone was added. Samples were placed at −20 °C for 30 min, before centrifugation at 18 000*g*, 4 °C, for 10 min. The supernatant was removed, and the pellet was washed with 1 mL of ice-cold 70% (v/v) acetone. Centrifugation and supernatant removal steps were then repeated. The pellet was air-dried, before resuspending in 30 μL of ddH_2O and 10 μL of 4X NuPAGE lithium dodecyl sulfate (LDS) sample buffer (ThermoFisher) and boiled at 100 °C for 5 min. To ensure the pellet was solubilized, samples were aspirated with a pipet five times, and if necessary (a visible pellet remaining), left for an additional 5 min at 100 °C. An amount of 10−100 μg of total protein was then separated with a 4−12% (v/v) gradient Bis-Tris gel (ThermoFisher) run in an MES buffer system. Proteins were stained with InstantBlue (Generon) and destained with ddH_2O, and the images were recorded with the ChemiDoc XRS imaging system (Biorad).

TX-TL Fluorescence Measurements. Ten microliters of cell-free reactions was prepared in a 384-well black clear, F-bottom, low-binding plate (Greiner). Reactions were measured as a triplicate technical repeat and at least repeated with cell-extracts prepared from two separate days. They were measured in a 384-well plate. The plate was sealed with aluminum film, SILVERseal (Greiner), and briefly centrifuged at 2000*g* for 10 s. Real-time plate measurements were recorded in a CLARIOStar plate reader (BMG Labtech, Germany) at 30 °C with 10 s of shaking at 500 rpm prior to measurements, using either standard filters (Omega) or monochromator settings (CLARIOStar). Purified sfGFP, mVenus-I and mScarlet-I standards were purified, as described previously,[5] to estimate protein concentration during real-time fluorescence measurements.

Mass Spectrometry Analysis. TX-TL reactions were prepared as two components (A and B) in a semicontinuous reaction as follows: Component A: 100 μL of standard TX-TL reaction, in the absence of PEG, was injected into a Thermo Scientific Pierce 3.5K MWCO 96-well microdialysis device. Component B: 1.5 mL of SMM solution with 1 mg/mL carbenicillin was placed in a 2.5 mL tube. The microdialysis cassette was placed inside the 2.5 mL tube and incubated at 30 °C for 24 h with shaking (1000 rpm). Samples were acidified with 1% (v/v) HCl, centrifuged at 18 000*g* for 25 min at room temperature. The supernatant was loaded onto a Sep-Pak C-18 (50 mg sorbent) solid-phase extraction cartridge (Waters), washed with 10 mL of 10% (v/v) ethanol and eluted with 2 mL of 50% (v/v) ethanol. All solutions were acidified with 1% (v/v) HCl. Eluted samples were dried under vacuum at room temperature, using an Eppendorf Concentrator Plus. Samples were dissolved in 150 μL of 1% (v/v) HCl and centrifuged again at 18 000*g* for 25 min at room temperature. One microliter of supernatant was then analyzed by LC−MS, performed with an Agilent 1290 Infinity system with an online diode array detector in combination with a Bruker 6500 quadruple time-of-flight (Q-ToF) mass spectrometer. An Agilent Extend-C18 2.1 mm × 50 mm (1.8 μm particle size) column was used at a temperature of 40 °C with a buffer flow rate of 0.5 mL/min. LC was performed with a gradient of buffer A [0.1% (v/v) formic acid in water] and buffer B [0.1% (v/v) formic acid in acetonitrile]. Separation was achieved using 2% buffer B for 0.6 min, followed by a linear gradient to

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100% buffer B from 0.6−4.6 min, which was held at 100% buffer B from 4.6−5.6 min followed by a return to 2% buffer B from 5.6−6.6 min, along with 1 min post-run. Spectra were recorded between a mass range of 50−1700 m/z at a rate of 10 spectra per second in positive polarity.

■ ASSOCIATED CONTENT

Supporting Information

The Supporting Information is available free of charge at https://pubs.acs.org/doi/10.1021/acssynbio.0c00581.

Additional methods, *S. venezuelae* ATCC 10712 promoter and RBS platereader characterization; list of plamids created in this study, oligonucleotides, annealing oligonucleotides, sequencing primers, promoter, RBS, and RiboJ parts, DNA sequences; additional figures (PDF)

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Notes

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