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ARTICLE

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Increasing cell-free gene expression yields from linear templates in *Escherichia coli* and *Vibrio natriegens* extracts by using DNA-binding proteins

Bo Zhu[1] | Rui Gan[2] | Maria D. Cabezas[2] | Takaaki Kojima[1] | Robert Nicol[3] | Michael C. Jewett[2,4,5,6,7] | Hideo Nakano[1]

[1]Laboratory of Molecular Biotechnology, Graduate School of Bioagricultural Sciences, Nagoya University, Nagoya, Japan

[2]Department of Chemical and Biological Engineering, Northwestern University, Evanston, Illinois

[3]Broad Institute of MIT and Harvard, Cambridge, Massachusetts

[4]Center for Synthetic Biology, Northwestern University, Evanston, Illinois

[5]Simpson Querrey Institute, Northwestern University, Evanston, Illinois

[6]Chemistry of Life Processes Institute, Northwestern University, Evanston, Illinois

[7]Robert H. Lurie Comprehensive Cancer Center, Northwestern University, Evanston, Illinois

Correspondence
Michael C. Jewett, Department of Chemical and Biological Engineering, Northwestern University, 2145 Sheridan Road, Evanston, IL 60208.
Email: m-jewett@northwestern.edu

Hideo Nakano, Laboratory of Molecular Biotechnology, Graduate School of Bioagricultural Sciences, Nagoya University, Furo-cho, Chikusa-ku, Nagoya 464-8601, Japan.
Email: hnakano@agr.nagoya-u.ac.jp

Present address
Bo ZHU, Laboratory for Chemistry and Life Science, Institute of Innovative Research, Tokyo Institute of Technology, Yokohama., Japan.

Rui Gan, Broad Institute of MIT and Harvard, Cambridge, Massachusetts.

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Abstract

In crude extract-based cell-free protein synthesis (CFPS), DNA templates are transcribed and translated into functional proteins. Although linear expression templates (LETs) are less laborious and expensive to generate, plasmid templates are often desired over polymerase chain reaction-generated LETs due to increased stability and protection against exonucleases present in the extract of the reaction. Here we demonstrate that addition of a double stranded DNA-binding protein to the CFPS reaction, termed single-chain Cro protein (scCro), achieves terminal protection of LETs. This CroP-LET (scCro-based protection of LET) method effectively increases superfolder green fluorescent protein (sfGFP) expression levels from LETs in *Escherichia coli* CFPS reactions by sixfold. Our yields are comparable to other strategies that provide chemical and enzymatic DNA stabilization in *E. coli* CFPS. Notably, we also report that the CroP-LET method successfully enhanced yields in CFPS platforms derived from nonmodel organisms. Our results show that CroP-LET increased sfGFP yields by 18-fold in the *Vibrio natriegens* CFPS platform. With the fast-expanding applications of CFPS platforms, this method provides a practical and generalizable solution to protect linear expression DNA templates.

KEYWORDS

cell-free protein synthesis, CroP-LET, in vitro transcription/translation, linear expression template, scCro, *Vibrio natriegens*

Abbreviations: CFPS, cell-free protein synthesis; LET, linear expression template; scCro, single-chain derivative of the bacteriophage lambda Cro repressor; sfGFP, superfolder green fluorescent protein.

Bo Zhu and Rui Gan contributed equally to this work.

1 | INTRODUCTION

Crude extract-based cell-free protein synthesis (CFPS) provides a practical in vitro approach for protein expression. By combining the translation machinery present in the cell extract with additional enzymes, cofactors, amino acids, transfer RNAs (tRNAs), energy sources, and other small molecules in a test tube, this approach can produce functional proteins within hours from a plasmid or linear expression template (LET; Carlson, Gan, Hodgman, & Jewett, 2012; Silverman, Karim, & Jewett, 2020). While CFPS conditions may vary according to the unique transcription/translation requirements for the synthesis of individual proteins, these reactions can be tailored by optimizing concentrations of the CFPS reagents. As such, CFPS has enabled a wide range of applications in directed evolution, synthetic biology, glycoscience, metabolic engineering, and education (Des Soye, Gerbasi, Thomas, Kelleher, & Jewett, 2019; Harris & Jewett, 2012; Karim & Jewett, 2016; Karim et al., 2020; Kightlinger et al., 2019; Lin et al., 2020; Martin et al., 2018; Silverman et al., 2020; Stark et al., 2019; Thavarajah et al., 2020). LETs offer a unique advantage over their circular counterparts because extensive plasmid construction steps are not required. These leads to several important features. For example, skipping the in vivo transformation could enable the expression and analysis of toxic proteins. High yield cell-free expression from LETs can be achieved entirely in vitro in few hours for rapid prototyping of synthetic biological circuits (Sun, Yeung, Hayes, Noireaux, & Murray, 2014) and accelerating the optimization of metabolic engineering pathways (Karim et al., 2020). LETs are also essential materials when performing in vitro biomolecule display for directed evolution of proteins, such as microbead display (Zhu, Mizoguchi, Kojima, & Nakano, 2015) and complementary DNA display (Ueno et al., 2012). In addition, the LETs can contribute to the high-throughput screening of antibodies from single B-cells by sequential combination of single cell reverse transcription, polymerase chain reaction (PCR), and CFPS (Ojima-Kato, Nagai, & Nakano, 2017). However, LET degradation by exonucleases present in the cell extract still remains a significant challenge that prevents the wide use of LETs for CFPS (Michel-Reydellet, Woodrow, & Swartz, 2005).

Frequently, exonucleases present in crude cell extracts are responsible for LET degradation in the CFPS reaction (Hoffmann, Nemetz, Schweizer, Mutter, & Watzele, 2002; Michel-Reydellet et al., 2005). Previous works in *Escherichia coli-based CFPS* have addressed this problem using different approaches. Introducing modifications to the termini of LETs, such as introducing unnatural 3′-end adenosines and addition of loop ends, achieved four- to sixfold and 7- to 20-fold protein yield, respectively (Hoffmann et al., 2002). Threefold improvement of protein yield was also observed by adding GamS, a RecBCD inhibitor protein, to the CFPS reaction (Sun et al., 2014). Supplementing chi-site double stranded DNA (dsDNA) to the CFPS reaction gave a threefold protein yield compared to adding the same amount of dsDNA without chi-site sequences (Marshall, Maxwell, Collins, Beisel, & Noireaux, 2017). However, these strategies may not be applicable to CFPS systems derived from nonmodel organisms. For example, the LET-stabilization effect was not observed in *Vibrio natriegens*-based CFPS in the presence of GamS, where a yield of superfolder green fluorescent protein (sfGFP) at 0.02 mg/ml from 30 nM LET was detected (Wiegand, Lee, Ostrov, & Church, 2018), Another common strategy involves engineering strains to remove proteins and enzymes that degrade linear templates. Previously, the Swartz group developed a genetically modified *E. coli* strain (A19) to stabilize the DNA template by removing endA (endonuclease I) and RecBCD from the genome. While these strategies showed increased stability of the DNA template and improved protein production yields for *E. coli* CFPS (Michel-Reydellet et al., 2005), these methods require strain engineering efforts that might not port to all organisms and are not off-the-shelf solutions (Kelwick, Webb, MacDonald, & Freemont, 2016; Li, Wang, Kwon, & Jewett, 2017; Martin et al., 2017; Wang, Li, & Jewett, 2018).

To address this issue, we identified a DNA binding protein that provides increased stability to LETs against exonuclease degradation. This dsDNA-binding protein, termed single-chain bacteriophage lambda Cro repressor (scCro), directly protects the free termini of the LET with a dsDNA-binding protein by sterically blocking the progressive degradation caused by various exonucleases in the crude cell extract (Figure 1a). In this CroP-LET (scCro-based Protection of LET) method, the scCro specifically binds to a 17-bp dsDNA operator recognition consensus (ORC) sequence at a high affinity with a K_D in the range of 4 pM to 1.8 nM (Jana, Hazbun, Fields, & Mossing, 1998; Kojima et al., 2018; Nilsson & Widersten, 2004). The three-dimensional structure revealed that binding specificity is accomplished by direct hydrogen-bonding and the van der Waals interactions between the protein and the exposed bases of both strands (Figure 1b) within the major groove of the DNA (Albright & Matthews, 1998; Nilsson & Widersten, 2004). Moreover, the binding affinity ratio between the 17-bp ORC and nonspecific DNA with scCro is 10,000:1, which indicates a low probability of interference with any other sequence than the ORC (Kim, Takeda, Matthews, & Anderson, 1987). Leveraging the high affinity and specificity, scCro has been successfully utilized for protein immobilization in microbead display (Kojima et al., 2016; Zhu et al., 2015) and to control the spatial arrangement of enzymes on DNA scaffolds for designing reaction cascades (Kojima et al., 2018).

In this study, we develop a generalizable, easy-to-use method called CroP-LET for improving the stability of LETs using scCro. We demonstrate that this approach can be applied to both *E. coli* and *V. natriegens* CFPS platforms. First, we show that sfGFP yield in *E. coli* CFPS increased by sixfold when the LET was terminally protected by scCro thus achieving yields comparable to RecBCD inhibition with GamS. Second, we show host-versatility of this approach by applying the scCro-based protection method to nonmodel CFPS platforms, specifically for *V. natriegens*. Notably, the yield sfGFP expression from LET in the *V. natriegens* CFPS system increased by up to 18-fold to 0.3 mg/ml. Given the accelerated discovery of novel CFPS systems, the CroP-LET method presented here provides a rapid and cross-species compatible solution for protecting LETs. We anticipate that our results will accelerate the characterization of unknown gene

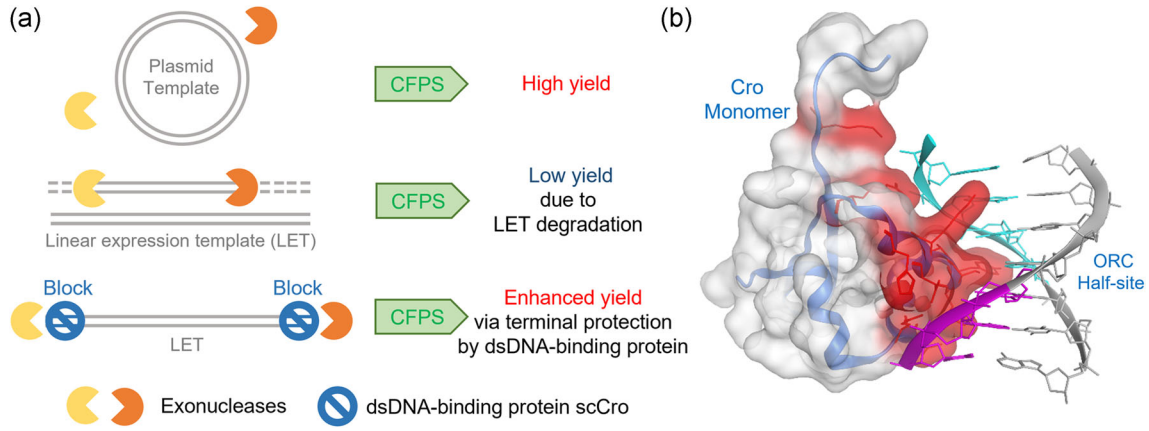

FIGURE 1 LET terminal protection prevents exonuclease degradation and increases protein yields in CFPS. (a) Proposed mechanism of LET terminal blocking by scCro. (b) Three-dimensional structure of lambda Cro repressor monomer and an operator recognition consensus sequence (ORC) half-binding site complex (PDB code: 6CRO). The surface of the Cro monomer is shown in transparent mode. The blue ribbon represents the main chain of the Cro protein. The residues interacting with the ORC half-site are colored in red. The gray ribbon indicates the dsDNA sequence of the ORC half-site TATCACC. The nucleotides interacting with the Cro protein were labeled in magenta or cyan for the sense and antisense strand, respectively. CFPS, cell-free protein synthesis; dsDNA, double stranded DNA; ORC, operator recognition consensus; scCro, single-chain Cro protein [Color figure can be viewed at wileyonlinelibrary.com]

functions (Salzberg, 2019) and enable the rapid synthesis of template libraries (Shrestha, Smith, & Bundy, 2014) for in vitro directed evolution studies (Ueno et al., 2012; Zhu et al., 2015), among other applications by utilizing low-cost commercially synthesized LETs in high-throughput CFPS-based screening platforms.

2 | MATERIALS AND METHODS

2.1 | Reagents and buffers

Chemicals were purchased from Sigma-Aldrich unless designated otherwise. DNA polymerase (Phusion), CpG methyltransferase (M.SssI), dam methyltransferase, RecBCD (exonuclease V), were purchased from New England Biolabs (NEB). T7 RNA polymerase was prepared as previously described (Swartz, Jewett, & Woodrow, 2004). Plasmids were extracted using a Plasmid Miniprep Kit (Omega Bio-Tek). All DNA oligonucleotides were purchased from Integrated DNA Technologies, Inc. (Table S1).

2.2 | LETs preparation

To test the effect of LETs in CFPS, various LET sequences were prepared by PCR amplification (Figures 2a and 3a). LET1 was obtained by amplifying the full length of the plasmid pJL1-sfGFP (Li, Wang, & Jewett, 2018; Pedelacq, Cabantous, Tran, Terwilliger, & Waldo, 2006) (Sequence S1) via an inverse PCR using DNA oligos G302-f and G302-r. As a result, the final LET had the same length and nucleotide sequence as the original plasmid. LET2 was prepared by amplifying the full length of the pJL1-sfGFP plasmid via inverse PCR using DNA oligos G350-f and G350-r. The scCro protein-binding sites with the ORC sequence (TATCACCGCGGGGTGATA) were introduced at the free end of the PCR products by G350-f and G350-r. LET3 was prepared by amplifying the sfGFP expression cassette from the pJL1-sfGFP plasmid via a PCR using DNA oligos G369-f and G369-r, which annealed to the T7 promoter and T7 terminator, thus the PCR product does not carry long buffering sequences at either upstream or downstream regions of the expression cassette. In this way, the LET3 sequence only presents scCro binding sites at the free ends. LET4 was prepared by amplifying the sfGFP expression cassette from the plasmid pJL1-sfGFP via a PCR using the DNA oligos G370-f and G370-r. LET5 was prepared by amplifying the sfGFP expression cassette via a PCR using the DNA oligos G243-f and G243-r that contain three phosphorothioate bonds modifications at the 5′ ends to prevent the hydrolysis of phosphodiester bonds caused by other exonucleases (Putney, Benkovic, & Schimmel, 1981; Yang, Sismour, & Benner, 2007) outside of RecBCD. The PCR products mentioned above were resolved on 1.2% agarose gel (Invitrogen) and purified by the QIAquick PCR Purification Kit (Qiagen). All DNA samples were quantified by the Nanodrop 2000c spectrophotometer (Thermo Fisher Scientific).

2.3 | LET methylation

The LET2 was methylated with dam or CpG methyltransferases following the manufacturer's instructions. The reactions were then purified by the QIAquick PCR Purification Kit (Qiagen) and quantified using a Nanodrop 2000c spectrophotometer.

2.4 | scCro protein expression and purification

The scCro expression plasmid pET22-scCro (Sequence S2) previously described (Kojima et al., 2016) was transformed into the *E. coli* strain

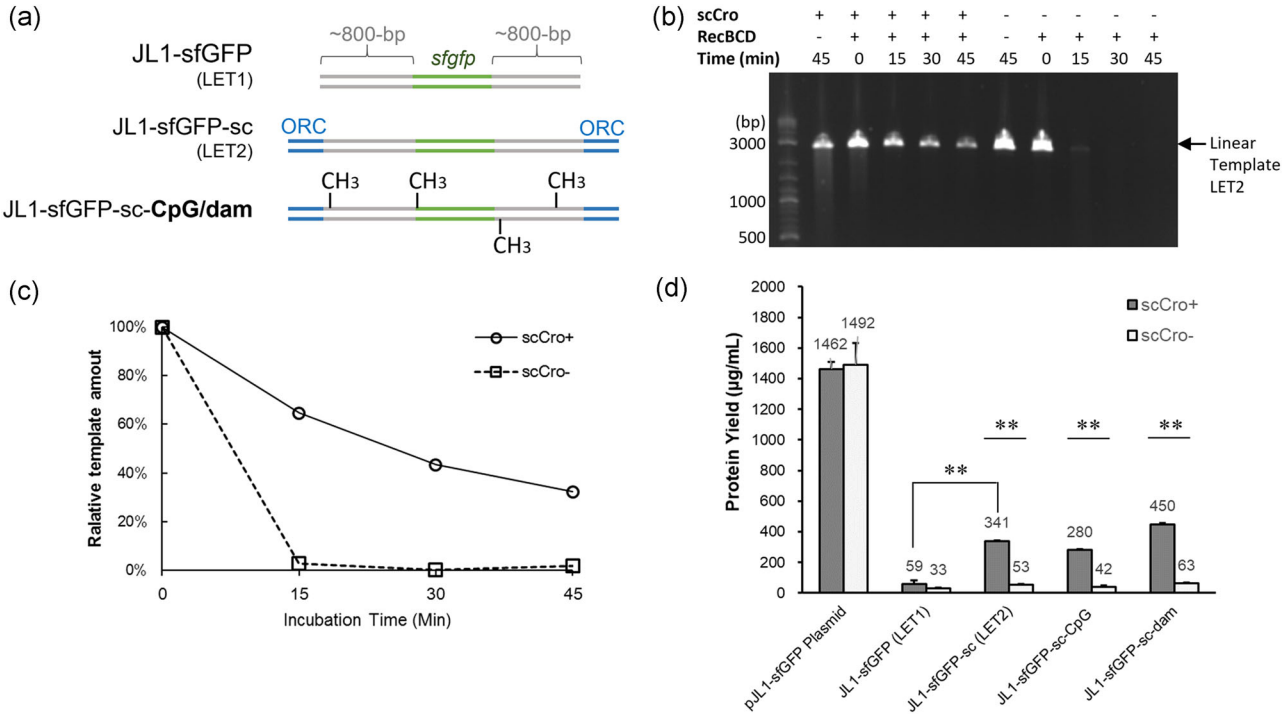

FIGURE 2 Effect of scCro-based protection of LETs on sfGFP yields in *Escherichia coli* CFPS. (a) LET sequences used in this study. *sfgfp* corresponds to the sfGFP operon. ORC refers to the scCro-binding site. JL1-sfGFP (LET1): the linearized full-length plasmid pJL1-sfGFP with buffer regions at each end marked in gray generated by PCR; JL1-sfGFP-sc (LET2): the JL1-sfGFP sequence with buffer regions marked in gray and one ORC at each end of the LET marked in blue; JL1-sfGFP-sc-CpG/dam: the JL1-sfGFP-sc (LET2) template with further methylation by CpG or *dam* methyltransferases. (b) Degradation of linear template JL1-sfGFP-sc by RecBCD in the presence of scCro. (c) Gel quantification analysis of the scCro-protected LET using ImageJ. (d) Yields of sfGFP using scCro-protected and methylated LETs in CFPS. scCro+ indicates the addition of scCro to DNA templates before the CFPS reactions while scCro− indicates that scCro was absent. The mean and standard deviations are shown for $N = 4$. p values were determined using the Welch's t test; $^{**}p < .0005$. CFPS, cell-free protein synthesis; LET, linear expression template; ORC, operator recognition consensus; PCR, polymerase chain reaction; scCro, single-chain Cro protein [Color figure can be viewed at wileyonlinelibrary.com]

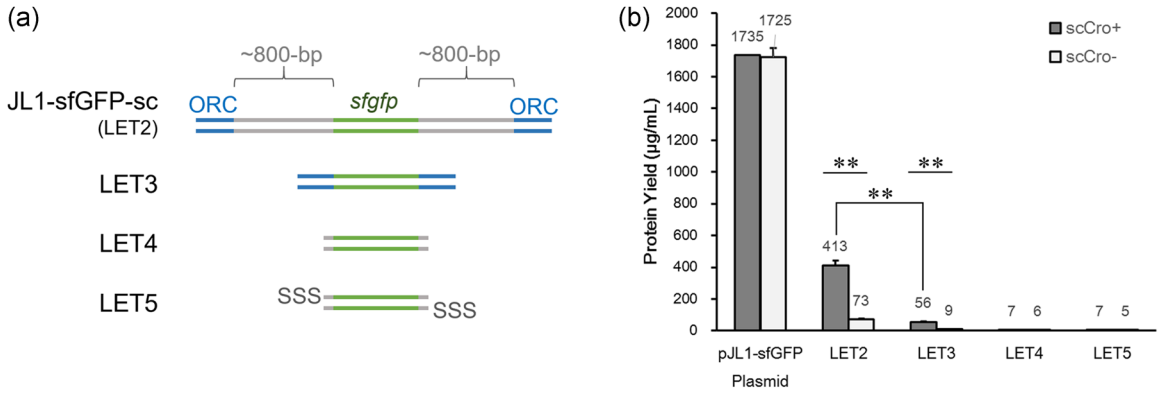

FIGURE 3 Synergetic effects between scCro-based protection and buffering sequences. (a) Diagram describing LETs used in this study. The regions colored in green correspond to the operon of *sfgfp*. The regions in blue ORC refer to the scCro-binding site. JL1-sfGFP-sc (LET2): the linearized full-length plasmid pJL1-sfGFP generated by PCR with one ORC at each end, and the PCR-amplified gray regions flanking outside the sfGFP operon are referred as the buffer sequences in this study. LET3: short LET without buffer sequences, only ORC regions in blue; LET4: short LET without buffer sequence and ORC; LET5: short LET (contains neither buffer sequence nor ORC) with three 5′ phosphorothioate bonds (SSS) at each end. (b) sfGFP yield from different LETs expressed in CFPS. scCro+ indicates that scCro was added to samples before the CFPS reactions. scCro− indicates that scCro was not added to samples. The mean and standard deviations are shown ($N = 4$). p values were determined using the Welch's t test; $^{**}p < .0005$. CFPS, cell-free protein synthesis; LET, linear expression template; ORC, operator recognition consensus; PCR, polymerase chain reaction; scCro, single-chain Cro protein [Color figure can be viewed at wileyonlinelibrary.com]

BL21(DE3). A 100 ml of ×2 YT medium containing 50 μg/ml carbenicillin was inoculated with 1 ml of overnight preculture. Cells were grown at 37°C to OD_{600} ~0.5, then the expression of scCro was induced with 1 mM isopropyl β-D-1-thiogalactopyranoside for 5 hr at 37°C. Next, cells were harvested by centrifugation at 6,000 *g* for 10 min at 4°C, and stored at −25°C. The frozen pellet (from 50 ml of culture) was thawed and suspended in 2 ml (6 ml/g of wet pellet) of binding buffer (50 mM sodium phosphate, 300 mM KCl, 10 mM imidazole, and 1.4 mM 2-mercaptoethanol, pH 8) containing 1 mM phenylmethylsulfonyl fluoride and 1 mg/ml of lysozyme. A 1 ml cell suspension was incubated at 4°C for 30 min and ultrasonicated on ice (30 s × 2, approx. 300 J) by Q125 Sonicator (Qsonica) with a 3.175 mm diameter probe at a frequency of 20 kHz and 50% of amplitude. The lysate was recovered by centrifugation at 12,000 *g* for 20 min at 4°C. Following lysate recovery, 900 μl of the supernatant was passed through an Ni-NTA spin-down column (Qiagen) according to the manufacturer's instructions. The column was then washed three times with 450 μl of washing buffer (50 mM sodium phosphate, 300 mM KCl, 50 mM imidazole, and 1.4 mM 2-mercaptoethanol, pH 8). Proteins bound to the resin were eluted in four fractions with 450 μl of elution buffer (50 mM sodium phosphate, 300 mM KCl, 500 mM imidazole, and 1.4 mM 2-mercaptoethanol, pH 8). Elution fractions were assessed by sodium dodecyl sulphate-polyacrylamide gel electrophoresis, and the E3 and E4 fractions were combined and dialyzed twice against 500 ml of S30 buffer 2 (10 mM Tris-OAc, 14 mM $Mg(OAc)_2$, 60 mM KOAc, 1 mM dithiothreitol, pH 8.2) and once against 500 ml of S30 buffer 2 containing 50% glycerol. Finally, the concentration of purified scCro was determined using the Quick Start™ Bradford Protein Assay Kit (Bio-Rad) and the sample was stored at −25°C (Figure S1).

2.5 | scCro protection prevents RecBCD degradation of LETs

The RecBCD degradation test was performed following the instructions provided by NEB with a minor modification detailed as follows. LET2 and scCro were premixed in a 1.5 μl mixture at room temperature for 60 min to allow binding of scCro protein to linear DNA templates and added to a 10 μl of RecBCD degradation reaction containing ×1 NEB buffer 4, 1 mM of adenosine triphosphate (ATP), and 0.2 U/μl of RecBCD. For the time-course study, samples were harvested at 15 min intervals, and the reaction was immediately terminated by diluting with an equal volume of 30 mM ethylenediaminetetraacetic acid solution followed by phenol-chloroform extraction. The mixture was centrifuged for 1 min at maximum speed, and 10 μl of the supernatant was recovered and resolved using a 1% agarose gel followed with SYBR Safe DNA gel staining. The band intensity of the LET was analyzed using ImageJ (Schneider, Rasband, & Eliceiri, 2012) according to the user manual. Briefly, the gel image was converted to an 8-bit greyscale image via the function in the Image/Type menu, and the integrated intensity checkbox was selected in the Set Measurements window. Each LET band was selected using the rectangular selection tool with the same area size, and the band intensity was measured using the Analyze/Measure function. The background intensity was subtracted from each band.

2.6 | sfGFP expression in CFPS from LETs

Expression of sfGFP in *E. coli*-based CFPS was performed according to a previously published report with minor modification (Jewett & Swartz, 2004; Kwon & Jewett, 2015). Briefly, the C321.ΔA.759 (*endA*$^-$ *gor*$^-$ *rne*$^-$ *mazF*$^-$) (Martin et al., 2018) *E. coli* strain was used for preparing the S12 extract. The purified scCro and the plasmid or LETs mixture (2-μl volume) was incubated at room temperature for 1 hr before adding into the CFPS reaction. This preincubation step is critical to get a sufficient protection result. The final concentrations of scCro and expression template were 2 and 8 nM, respectively, unless stated otherwise. Thereafter, these pretreated LETs were directly added to a final 15 μl *E. coli* CFPS reaction for a 16-hr incubation at 30°C. The CFPS reaction consists of the following components other than the template DNA and scCro: 57 mM HEPES-KOH (pH 7.5); 12 mM magnesium glutamate; 10 mM ammonium glutamate; 130 mM potassium glutamate; 1.2 mM ATP; 0.85 mM each of GTP, UTP, and CTP; 34.0 μg/ml folinic acid; 170.0 μg/ml of *E. coli* tRNA mixture (from strain MRE600); 2 mM each of 20 standard amino acids; 33 mM phosphoenolpyruvate; 0.33 mM nicotinamide adenine dinucleotide; 0.27 mM coenzyme-A; 4 mM sodium oxalate; 1 mM putrescine; 1.5 mM spermidine; 100 μg/ml T7 RNA polymerase, and 27% v/v of cell extract. The GamS-based inhibition of RecBCD was performed according to a previously published report (Sun et al., 2014).

The *V. natriegens* S30 extract preparation and CFPS reaction was performed according to previous publication without any modification (Des Soye et al., 2018). For protection, LET was mixed with scCro protein in a 3-μl volume for binding at room temperature for 1 hr. In parallel, nonprotected LET was prepared in the same way except no scCro supplied. Thereafter, these pretreated LETs were directly added to a final 15 μl of *V. natriegens* CFPS for a 16-hr incubation at 30°C. Plasmid pJL1-sfGFP was used as a circular template control. In *V. natriegens* CFPS, LET was supplied at four different final concentrations: 8, 16, 32, and 64 nM while the final concentration of scCro protein was fixed at 2 μM for all samples.

2.7 | Quantification of synthesized sfGFP

The CFPS reactions were diluted 1:25 in purified water to a final volume of 50 μl. The fluorescence was measured using a Synergy 2 plate reader (BioTek) with excitation at 485 nm, emission at 528 nm (cutoff at 510 nm) in 96-well half area black plates (Costar 3694; Corning). The sfGFP yield was calculated from the fluorescence units using a standard curve established with ^{14}C-Leu quantified sfGFP as previously described (Hong et al., 2014).

3 | RESULTS AND DISCUSSION

3.1 | Terminal protection of LET increases linear DNA stability in *E. coli* CFPS

We first generated two LETs to probe whether scCro could be used for effective terminal blocking in CFPS (Figure 2a). LET1 was designed as a linear counterpart to the plasmid template, with buffer sequences added to each end. LET2 comprises the same elements of LET1, but also includes the addition of terminal ORC binding sites that could be used to assess the effect of scCro-based terminal blocking. To confirm LET protection by scCro, we initially tested the susceptibility of LET2 degradation in the presence of *E. coli* exonuclease RecBCD at a concentration of 0.2 U/μl (Figure 2b). As expected, RecBCD degraded the unprotected LET2 rapidly, within 15 min of incubation. We also observed that terminal blocking with scCro protected 65% of the LET2 from degradation after 15 min of incubation with RecBCD, while only 3% of the LET2 remained full length in the absence of scCro (Figure 2c). These data suggest that scCro sterically hinders RecBCD association with the LET2 ORC and prevents degradation.

With LET2 having demonstrated stabilization in the presence of exonucleases, we next tested the impact of scCro protected DNA in CFPS. sfGFP expression levels were compared in the presence and absence of scCro in the CFPS reaction (Figure 2d). Cell extract was prepared from *E. coli* strain *C321.ΔA.759*, in which DNA endonuclease I (*endA*−) and ribonuclease E (*rne*−; Martin et al., 2018) were inactivated to minimize the effect endonuclease and RNA degradation on the final yield of sfGFP. As a control, addition of scCro to a plasmid-based CFPS reaction did not have a significant effect on sfGFP yields (Figure 2d) and the observed yields are comparable to our previously published results. When the LET does not contain any scCro-binding sites—as is the case in the LET1 sequence—the LET is still susceptible to degradation resulting in poor sfGFP yields ~0.05 mg/ml. In contrast, addition of scCro to the CFPS reaction expressing the LET2—which contains terminal binding sites for scCro—resulted in a sixfold protein yield improvement over the condition without scCro (Figure 2d).

We also compared our approach with DNA methylation strategies used to stabilize DNA templates. We observed methylation of LET2 using *dam* methyltransferase further increased sfGFP yield by 32%, while modification with CpG methyltransferase reduced sfGFP yield by 18% in the absence of scCro (Figure 2d). Furthermore, the synergistic effect of LET protection and DNA methylation did not enhance sfGFP expression significantly. From these results, we conclude that the effect of LET methylation on sfGFP production is not significant. Therefore, unmethylated LETs were used in the experiments described below.

Another common approach to prevent LET degradation in *E. coli* CFPS is to supplement the reaction with exonuclease V inhibitor protein GamS. Our results show that addition of either GamS or scCro resulted in comparable levels of sfGFP expression (Figure S2). While GamS is known to fully inhibit RecBCD exonuclease activity, we hypothesize that scCro offers a broader range of protection against degradation by exonucleases—including RecBCD—present in the extract. For this reason, we tested the synergistic effects of adding both GamS and scCro. However, we found no significant synergistic effect (Figure S2). The combination of two methods provided 1.3-fold yield improvement compared with GamS only result. Next, we monitored the blocking effect of scCro at a range of concentrations 5–40 μg/ml (corresponding to 0.28–2.2 μM) in the presence of 8 nM LET and found that degradation can be inhibited at scCro concentrations as low as 0.28 μM (Figure S3). Previously, a concentration of 1 μM of GamS with 2 nM LET was sufficient to prevent degradation and improve the expression of dual emission green fluorescent protein in *E. coli* CFPS (Sun et al., 2014). In this study, our results indicate that sufficient protection of LET can be achieved at relatively lower scCro concentrations compared to GamS because of the high affinity between scCro and the ORC (Jana et al., 1998; Kojima et al., 2018; Nilsson & Widersten, 2004).

3.2 | Synergetic effects between scCro-based protection and buffer sequences

We next evaluated if the DNA bases upstream and downstream of the linear *sfgfp* operon are required for CroP-LET mediated protection. Previously, DNA sequences flanking the *sfgfp* operon (i.e., buffer sequences), which originate from the amplification template used to make the LET, have been shown to sufficiently alleviate some LET degradation in *E. coli* CFPS (Sun et al., 2014). To test whether introducing buffer sequences (~800-bp buffer sequence at both ends) between the *sfgfp* operon and ORC binding sites would provide additional stability of LET2 alone, we compared LET2 to LET3, a counterpart linear template to LET2 which has no buffer sequences, and tested these LETs in CFPS with and without scCro (Figure 3a). The presence of buffer sequence, as shown in LET2, contributed to ~7-fold yield increase in CFPS regardless of the presence of scCro protein (Figure 3b); this demonstrates that a long buffer sequence is able to protect LETs. When scCro was present, we observed a ~6-fold improvement in sfGFP yields for both LET2 and LET3 (Figure 3b), which implies that the effect of scCro protection is independent of the buffer sequence. These results suggest there is a synergetic effect between the scCro-based protection and the presence of the buffer sequences. This observation could be because buffer sequences allow scCro to bind the 5′-end of the LETs without inhibiting transcription. Previously, it has been shown that phosphorothioate bond modifications can inhibit exonucleases (Putney et al., 1981; Yang et al., 2007) and introducing this type of modification potentially stabilizes LETs. We therefore tested whether adding phosphorothioate modifications (LET5) affected protein synthesis from LET. However, same as the LET4, LET5 only produced a low amount (5–10 μg/ml) of sfGFP.

3.3 | scCro prevents LET degradation in the *V. natriegens* CFPS system

Recently, a novel high-yielding CFPS platform derived from *V. natriegens* was developed (Des Soye, Davidson, Weinstock, Gibson, & Jewett, 2018; Wiegand et al., 2018). This nonmodel organism has a fast doubling time (~10 min) and the potential to serve as a robust alternative for the cell-free production of proteins, commodity chemicals and other synthetic biology applications (Des Soye et al., 2018; Failmezger, Scholz, Blombach, & Siemann-Herzberg, 2018; Wiegand et al., 2018). While sfGFP yields up to ~1.6 mg/ml have been achieved in the *V. natriegens* CFPS platform from a plasmid template, only yields ~0.02 mg/ml of sfGFP from a 30 nM LET have been reported, thus a solution is required to improve protein yields from LET-based systems (Wiegand et al., 2018). Given that scCro prevents degradation of LETs in *E. coli* CFPS, we decided to explore scCro as an alternative solution to improve yields from LETs in the *V. natriegens* CFPS system (Figure 4). Similar to our *E. coli* experiments, we incubated scCro with LETs before the CFPS reaction. In both *E. coli* and *V. natriegens* CFPS platforms, we observed sfGFP expression levels comparable to previous reports, and the addition of scCro did not have a significant impact on sfGFP expression. Without ORC binding sites, expression from LET1 yielded <10% of sfGFP in the *V. natriegens* system compared to the *E. coli* CFPS platform; this result points out that nucleases in the *V. natriegens* CFPS are more active. Interestingly, we observed an eightfold increase corresponding to 0.03 mg/ml of overall sfGFP production from 8 nM LET2 (Figure 4). Although this amount is 10% lower (~0.4 mg/ml) than the yield observed in *E. coli* CFPS, we hypothesize that endogenous nucleases specific to *V. natriegens* are responsible for LET degradation. We observed that the sfGFP yield increased proportionally with the concentration of LET2. In this way, we achieved sfGFP yields of up to 0.324 mg/ml with 64 nM of LET2, while keeping the concentration of scCro constant at 2 μM for all conditions (Figure 4). We found that scCro-based protection became more significant at higher LET concentrations. With 64 nM of LET2 in the CFPS reaction, scCro-protected template showed an 18-fold improvement in sfGFP yield over the nonprotected template, thus 2 μM of scCro is sufficient to protect up to 64 nM of the LET. While further increasing the DNA concentration is expected to enhance sfGFP yield, we anticipate that it would be challenging to assemble CFPS reactions at concentrations beyond 64 nM of LET template due to volume limitations. That said, protein yields of ~0.3 mg/ml are sufficient to enable a wide range of high-throughput screening applications, including directed evolution of enzymes, prototyping of synthetic biological circuits, and optimization of metabolic engineering pathways.

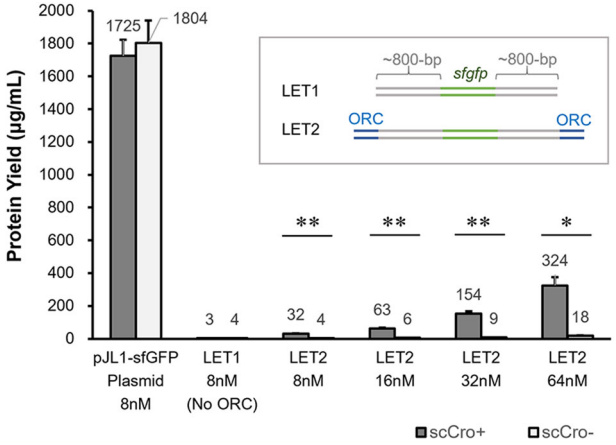

FIGURE 4 scCro-based protection of LETs boosts sfGFP yields in the *Vibrio natriegens* CFPS system. LET1 and LET2 are the same templates described in Figure 2a. scCro+ indicates that scCro was added to the samples before the CFPS reactions. scCro− indicates that scCro was not added to templates. The mean and standard deviations are shown ($N = 4$). p values were determined using the Welch's t test; $^{*}p < .005$, $^{**}p < .0005$. CFPS, cell-free protein synthesis; LET, linear expression template; scCro, single-chain Cro protein [Color figure can be viewed at wileyonlinelibrary.com]

4 | CONCLUSIONS

In this study, we developed a novel method termed CroP-LET that increases protein yields in CFPS systems by terminally blocking degradation of LETs with the dsDNA-binding protein scCro. This method only requires the addition of a 17-bp scCro-binding site sequence at the 5′-end of the primers used to amplify LETs. The scCro protein can be easily obtained via overexpression in *E. coli* followed by a one-step His-tag purification. Equally important, this method is successful both in the *E. coli* and *V. natriegens* CFPS systems, providing a generalizable solution that is independent of the hosts' genetic and biochemical background and can be applied CFPS systems derived from nonmodel organisms. Taken together, our method provides a simple and cross-species tool that will enable nonmodel CPFS applications.

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CONFLICT OF INTERESTS

The authors declare that there are no conflict of interests.

AUTHOR CONTRIBUTIONS

B.Z., R.G., T.K., M.C.J., and H.N. designed the experiments. B.Z. and R.G. conducted the experiments. M.D.C. prepared *V. natriegens* cell-free extract. B.Z., R.G., M.C.J., and H.N. wrote the paper. All authors discussed the results and edited the manuscript.

DATA AVAILABILITY STATEMENT

All data generated or analyzed during this study are included in this published article (and its supplementary information file).

ORCID

Bo Zhu http://orcid.org/0000-0002-4001-6045
Maria D. Cabezas http://orcid.org/0000-0002-0861-9735
Takaaki Kojima http://orcid.org/0000-0001-7282-121X
Michael C. Jewett http://orcid.org/0000-0003-2948-6211
Hideo Nakano http://orcid.org/0000-0001-6133-9794

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