



Enhanced phosphoserine insertion during *Escherichia coli* protein synthesis via partial UAG codon reassignment and release factor 1 deletion

Ilka U. Heinemann^{a,1}, Alexis J. Rovner^{b,e,1}, Hans R. Aerni^c, Svetlana Rogulina^c, Laura Cheng^b, William Olds^b, Jonathan T. Fischer^a, Dieter Söll^{a,d}, Farren J. Isaacs^{b,e,*}, Jesse Rinehart^{c,e,*}

^a Department of Molecular Biophysics and Biochemistry, Yale University, New Haven, CT 06520-8144, USA

^b Department of Molecular, Cellular and Developmental Biology, Yale University, New Haven, CT 06520-8230, USA

^c Department of Cellular & Molecular Physiology, Yale University, New Haven, CT 06520-8026, USA

^d Department of Chemistry, Yale University, New Haven, CT 06520-8107, USA

^e Systems Biology Institute, Yale University, West Haven, CT 06516-7388, USA

ARTICLE INFO

Article history:

Received 30 July 2012

Revised 29 August 2012

Accepted 30 August 2012

Available online xxxx

Edited by Michael Ibba

Keywords:

Synthetic biology

Phosphoserine

Phosphoproteomics

Genetic code

Genetic code expansion

Genome engineering

ABSTRACT

Genetically encoded phosphoserine incorporation programmed by the UAG codon was achieved by addition of engineered elongation factor and an archaeal aminoacyl-tRNA synthetase to the normal *Escherichia coli* translation machinery (Park et al., 2011) Science 333, 1151 [2]. However, protein yield suffers from expression of the orthogonal phosphoserine translation system and competition with release factor 1 (RF-1). In a strain lacking RF-1, phosphoserine phosphatase, and where seven UAG codons residing in essential genes were converted to UAA, phosphoserine incorporation into GFP and WNK4 was significantly elevated, but with an accompanying loss in cellular fitness and viability.

© 2012 Federation of European Biochemical Societies. Published by Elsevier B.V. All rights reserved.

1. Introduction

Phosphorylation at serine residues is the most abundant phosphorylation event in eukaryotic signaling pathways. Given that these signaling networks form the basis for regulating most physiological processes, there exists a continued scientific interest in resolving the nature of these phosphorylation events. Chemical modification of proteins has enabled the study of functionally relevant phosphorylation sites within proteins but the use of this method is limited [1]. Recently, a new method for the study of phosphorylation via translational insertion of O-phosphoserine (Sep) has been developed. This SEP-system employs UAG codon (amber) suppression, an orthogonal aminoacyl tRNA synthetase/

tRNA pair (SepRS/tRNA^{Sep}), and an engineered elongation factor (EF-Sep) [2].

The use of UAG as a sense codon for Sep insertion results in low protein yields and truncated protein products due to the primary function of UAG as a stop codon [2]. While natural suppressor tRNAs are capable of efficient amber codon read-through in the presence of release factors [3], orthogonal suppressor systems remain less efficient at this process. Reported protein yields vary from ~micrograms with Sep-incorporation [2] to ~milligrams for other systems [4], depending on the employed unnatural amino acid and associated suppressor system. Thus, to achieve high yield production of Sep-proteins with the relatively inefficient SEP-system, release factor competition must be minimized.

The recognition of stop codons by release factors 1 (RF-1, encoded by *prfA*) and 2 (RF-2, encoded by *prfB*) leads to peptide chain termination during translation. Amber and ochre (UAG and UAA) stop codons are recognized by RF-1 while ochre and opal (UAG and UGA) stop codons are recognized by RF-2. RF-1 has been thought to be essential [5,6] in *Escherichia coli*. However, *prfA* deletion has recently been successful as employed by two different classes of approaches. Studies have reported that *prfA* deletion is possible if (1) the genomic background of *Escherichia coli* is

Abbreviations: GFP, green fluorescent protein; RF-1, release factor-1 (*prfA*); RF-2, release factor-2 (*prfB*); SepRS, phosphoserine-tRNA synthetase; WNK4, serine/threonine-protein kinase WNK4; Sep, phosphoserine; MAGE, multiplex automated genome engineering

* Corresponding authors at: Systems Biology Institute, Yale University, West Haven, CT 06516-7388, USA. (J. Rinehart and F.J. Isaacs)

E-mail addresses: farren.isaacs@yale.edu (F.J. Isaacs), jesse.rinehart@yale.edu (J. Rinehart).

¹ These authors contributed equally to this work.

significantly reduced and specific, accommodating mutations are introduced within *prfB* [7,8] or (II) essential TAG-terminating genes are supplied *in trans* as TAA-terminating alleles in the presence of an amber suppressor tRNA [9–11]. Thus, a defined set of genetic manipulations in *E. coli* might afford an efficient system for incorporating phosphoserine at engineered UAG codons.

In this study, we present a strategy for enhanced translational insertion of Sep by the SEP-system. A derivative of the MG1655 *E. coli* strain harboring TAG-to-TAA genomic recoding at seven essential TAG-terminating genes (*hda*, *lolA*, *lpxK*, *coaD*, *mreC*, *murF*, and *hemaA*) was constructed to permit the deletion of the *prfA* gene [9]. In this new genetic context, genetically encoded Sep insertion was significantly enhanced by converting the UAG stop codon to a sense codon for phosphoserine.

2. Materials and methods

2.1. Generation of a partially recoded RF-1 knockout strain

The sequences of oligonucleotides used in this study are listed in the supplementary material (Table S1). The strains in this study were generated from a modified *E. coli* MG1655 strain (EcNR2: *E. coli* MG1655 Δ mutS:cat(*ybhB*-*bioAB*):[*cl857* Δ (*cro*-*ea59*):*tetR*-*bla*)] [12]. The following modifications were made to EcNR2 and are described in greater detail in the Supplementary material. The TAG stop codons terminating seven essential genes were recoded to TAA in EcNR2 with mutagenic oligonucleotides by multiplex automated genome engineering (MAGE) [12]. The gene encoding RF-1 (*prfA*) was replaced by the spectinomycin resistance gene (*spec^{ck}*) to generate rEc7 Δ *prfA*. The native *tolC* gene [13] was deleted to generate rEc7 Δ *prfA* Δ *tolC* and subsequently reintroduced within the *bla* locus to generate rEc7 Δ *prfA* Δ *tolC*:*bla*:*tolC*. A cassette encoding T7 polymerase was integrated within the *bla* locus, replacing *tolC* to create rEc7 Δ *prfA* Δ *tolC*:*bla*:T7. Phosphoserine phosphatase (*serB*) was disrupted with a premature stop codon [2]. The SEP-system was introduced to generate EcAR7.SEP [2] (Table S2). Alternatively, suppression of TAG codons with glutamine was enabled by transformation of EcAR7 with pGFIb-supE to generate EcAR7.supE.

Growth curves were obtained using a Biotek Synergy HT Plate reader. All strains were grown at 34 °C in 150 μ L of LB medium supplemented with 2 mM Sep, 50 μ L IPTG and antibiotics for plasmid maintenance where indicated. Growth media was inoculated with pre-cultures to an initial A_{600} of \sim 0.1 and A_{600} was measured at 10-min intervals for 27 h. All data were obtained in triplicate and averaged to construct a representative growth curve for each strain. Doubling times were calculated in triplicate and averaged to obtain representative values for each strain.

2.2. Plasmids and strains for incorporation of Sep

Plasmids and methods for Sep incorporation have been described previously [2]. Sep incorporation into recombinant reporter proteins green fluorescent protein (GFP) and mouse serine/threonine protein kinase (WNK4) was monitored in the newly created strain EcAR7, as well as the previously published strains of *E. coli* BL21 (Table S2) [2].

C-terminally His-tagged GFP under the control the P_{LtetO} promoter was subcloned from pZE21G [14] and blunt-end cloned into pCR[®]-Blunt II-TOPO (Invitrogen). The kanamycin resistance cassette was deleted from the resulting construct by digestion with *BsaI* and *RsrII* followed by blunting of the sticky ends and religation. Codons encoding residues E17, Y66, Q94, E132, E142, Q157, S202, S205, E213 and E222 were mutated to TAG using the QuikChange site-directed mutagenesis kit (Agilent) to yield single or double TAG sites within the protein.

The C-terminal regulatory domain (amino acids 1000–1222) of mouse WNK4 was used to test translational phosphoserine incorporation in a mammalian protein. The vector PCR T7/NT-TOPO was modified by replacing the multicloning site with P_{LtetO} -GFP from pZE21G [14]. An extra copy of the Tet-repressor was also introduced [14,15]. The P_{LtetO} -GFP *KpnI* and *HindIII* were used to replace GFP with the WNK4 construct. The corresponding serine codons, S172 and S199, were reassigned to TAG by QuikChange to create coding sequences for mutants containing one or two TAG codons, respectively. Detailed methods can be found in Supplementary materials.

3. Results

3.1. Phosphoserine incorporation imposes a severe growth phenotype in wild type and RF-1 deletion strains

In this study, we sought to identify important factors that enable enhanced production of site-specific phosphorylated proteins in engineered strains of *E. coli*. We hypothesized that several classes of modifications would collectively increase the efficiency of site-specific phosphoserine incorporation in the EcNR2 strain of *E. coli* [12,16]. First, we performed targeted TAG codon reassignment to the synonymous TAA codon across seven annotated essential genes [9,17]. EcNR2 was used as the parent strain because it allows the use of MAGE for targeted, seamless and efficient genetic modifications directly at each genomic locus (Fig. 1A and B) [12,16]. Seven codon reassignments were performed at their natural positions of seven essential ORFs (*coaD*, *hda*, *hemaA*, *mreC*, *murF*, *lolA*, and *lpxK*) via MAGE and verified by MASC-PCR as described previously (Fig. 1B) [16]. These seven TAG-to-TAA codon reassignments were introduced to re-direct chain termination of these stop codons from RF-1 to RF-2. Consistent with prior work, we sought to determine if these seven reassigned codons enabled us to delete the *prfA* gene, which encodes for the release factor 1 protein (RF-1) [9]. Specifically, these modifications allowed for the replacement of *prfA* by a spectinomycin resistance gene (*spec^{ck}*). Successful replacement was demonstrated by PCR with primers binding within and adjacent to the *prfA* site (Fig. 1C and D). Prior studies have shown that the RF-1 deletion either requires reassignment of at least seven TAG codons to TAA stop codons and [10,11,18] modifications to RF-2 [7,8]. Since mutations to RF-2 could have unexpected secondary effects, we focused on the recoding of TAG codons to TAA codons in the genome to delete RF-1.

Next, we introduced a series of genetic and translational modifications (Supplementary Figs. S1–S4) to permit site-specific incorporation of phosphoserine at in-frame TAG codons [2] (Fig. 1A). These modifications included introduction of a non-sense mutation in the phosphoserine phosphatase gene (*serB*) by a mutagenic oligonucleotide. All genomic alterations were verified by PCR amplification at the genetic locus for each modification and are depicted in Fig. 1A. The resulting strain was termed EcAR7 and was transformed with either a plasmid containing a natural suppressor tRNA *supE* [18] or the phosphoserine incorporation system (SEP-system) [2] to yield EcAR7.*supE* or EcAR7.SEP, respectively.

To investigate the cellular fitness of the recoded *E. coli* strains, we obtained growth curves for all of the strains and calculated their respective doubling times (Table 1 and Fig. 2). While recoding of seven TAG stop codons to TAA had no effect on the growth phenotype (79 min (EcNR2) and 82 min (rEc7) doubling time), the RF-1 knockout (rEc7. Δ *prfA*) strain showed a 1.6-fold increase in doubling time to 134 min. All further modifications did not have an impact on the growth phenotype (Fig. 2 and Table 1).

We next investigated whether the growth defect imposed by RF-1 deletion can be restored by introducing the suppressor tRNA

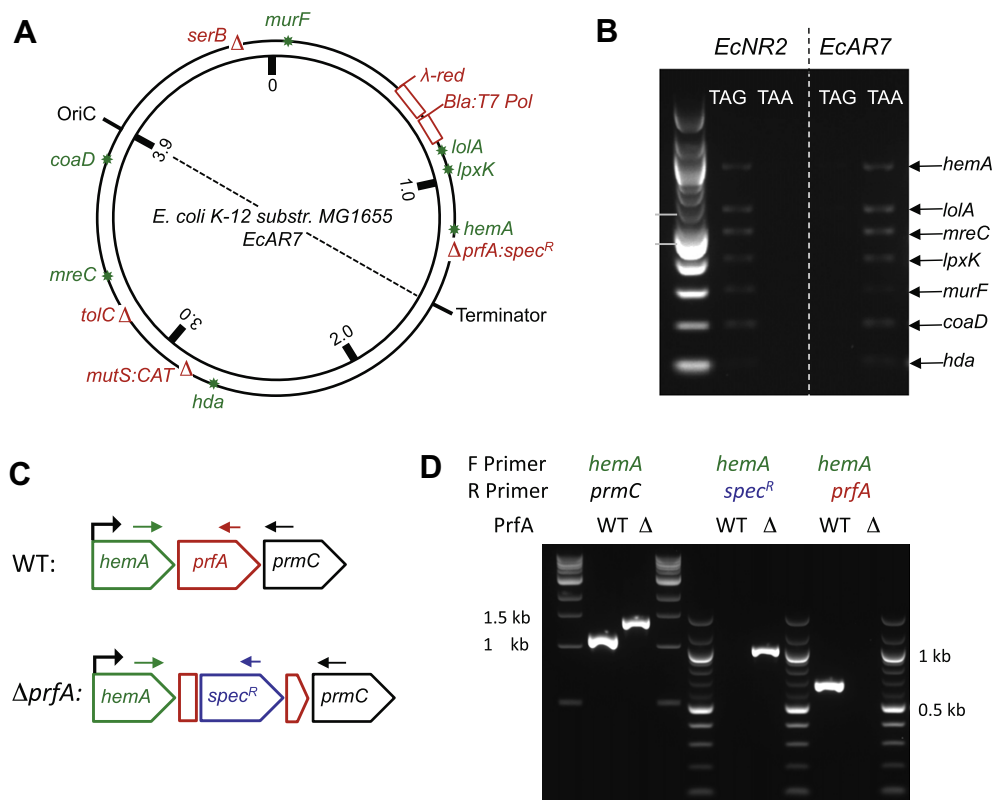


Fig. 1. Construction of EcAR7. (A) Genomic locations of seven essential genes where the stop codons were recoded from TAG to TAA (green). Additional genomic modifications are shown in red. (B) Verification of TAG-to-TAA recoding at seven essential genes, using multiplex allele specific PCR. (C) Illustration of the genomic context of *prfA* and its replacement with a gene that confers resistance to spectinomycin. Primers that were used to scrutinize *prfA* for successful integration of *spec^R* are indicated with arrows and color-coded for reference in (D). (D) Replacement of *prfA* with *spec^R*. Three unique primer pairs were used to verify successful *spec^R* integration at the *prfA* locus by PCR. All reactions were performed using a forward primer that anneals upstream of *prfA* (within *hemA*), and are distinguished by the use of a unique reverse primer depicted above the image and color-coded for reference in (C).

Table 1

Doubling times and maximum optical density of various strains grown in LB supplemented with 2 mM phosphoserine, 50 μM IPTG and required antibiotics. Doubling times and standard deviations were obtained from at least three independent growth curves.

Strain	Doubling time (min)	Maximal A_{600}
MG1655	71.06 ± 0.74	1.90 ± 0.06
EcNR2	79.37 ± 0.80	1.72 ± 0.08
rEc7	82.29 ± 2.53	1.92 ± 0.06
rEc7.ΔprfA	134.44 ± 2.59	0.77 ± 0.03
EcAR7	136.75 ± 2.06	0.56 ± 0.02
EcAR7.SEP	379.41 ± 3.43	0.30 ± 0.01
EcAR7.supE	132.38 ± 0.52	1.16 ± 0.04
BL21.WT	81.81 ± 1.38	1.81 ± 0.03
BL21.SEP	114.11 ± 2.85	1.34 ± 0.04
BL21.L11C.SEP	104.66 ± 5.34	1.66 ± 0.03

supE, as described previously [11]. We used tRNA-scanSE [19] to verify that EcAR7 does not encode an annotated natural amber suppressor tRNA [20]. When the suppressor tRNA *supE* was supplied *in trans*, EcAR7.*supE* displayed a similar doubling time but demonstrated enhanced viability by reaching a higher final OD (Table 1 and Fig. 2). These results indicate that a suppression system for glutamine can partially rescue the RF-1 induced phenotype. These results suggest that *supE* permits glutamine incorporation at a subset of natural TAG stop codons that relieves ribosomal stalling and results in the production of elongated proteins, which we posit maintain function.

Next, we investigated fitness and viability of EcAR7.SEP and two BL21-derived strains (BL21.SEP and BL21.L11C.SEP) upon introduc-

tion of the SEP-system. Overexpression of the L11C mutant ribosomal subunit has been shown to decrease RF-1 activity [21]. A striking reduction in fitness and cell viability were observed (Table 1 and Fig. 2). The doubling time for EcAR7.SEP was reduced 2.8-fold to 379 min. The maximum optical density reached under these conditions was $A_{600} = 0.3$, which is a 2.6-fold decrease compared to EcAR7. Thus, while the pleiotropic effects associated with RF-1 deletion can be compensated by suppression of TAG with glutamine, Sep incorporation places an additional burden on the cell. We observed a similar phenomenon for BL21.SEP and BL21.L11C.SEP, where doubling times increased upon induction by 1.33- and 1.4-fold respectively, and final cell densities decreased (Table 1).

3.2. Phosphoserine is incorporated into the proteome in response to native UAG codons

While the incorporation of unnatural amino acids into recombinant proteins has been widely studied [22], the global effect of an amber suppressor system on the host proteome has only been considered recently [7,11,16]. Here, we observe that EcAR7.SEP has a significant growth defect upon induction of the Sep expression system. We hypothesize that widespread Sep incorporation at endogenous TAG codons partially explains the reduced phenotype. Total proteins from IPTG-induced EcAR7.SEP strains were isolated, digested with trypsin, subjected to large scale phosphopeptide enrichment, and analyzed with LC-MS to directly measure Sep incorporation in the natural proteome. Analysis of both phosphopeptide and non-phosphopeptide fractions of the EcAR7.SEP prote-

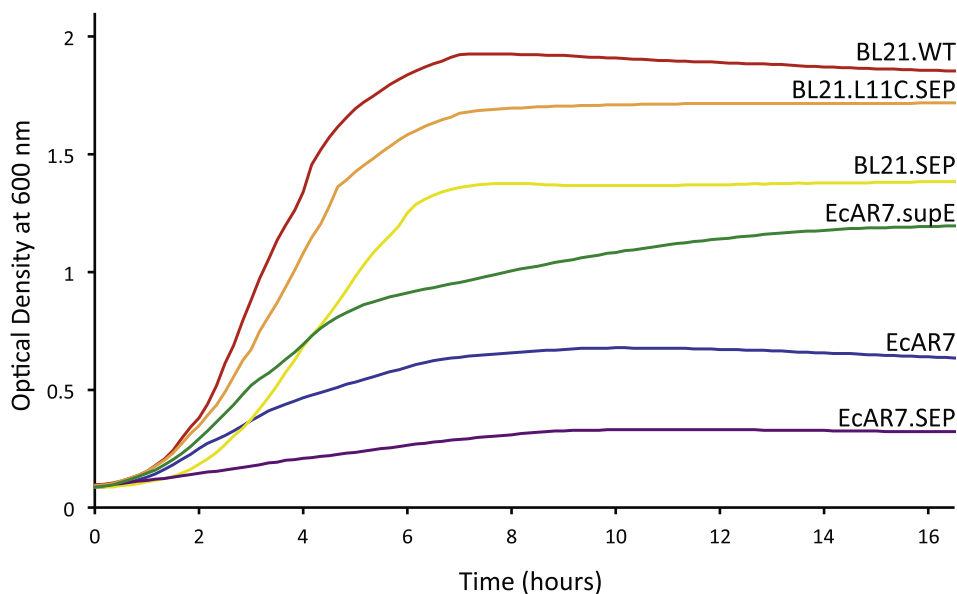


Fig. 2. Cellular fitness. Growth curves were obtained in triplicate in LB-medium containing 2 mM phosphoserine and 50 μ M IPTG. A representative growth curve is depicted.

ome identified approximately 1100 *E. coli* proteins with 82 TAG [16] containing open reading frames identified. We investigated the genomic context of several of the most abundant TAG containing ORFs in our proteome data and identified a region of the *luxS* gene (encoding S-ribosylhomocysteine lyase) that could produce a detectable tryptic phosphopeptide upon TAG suppression with Sep (Fig. 3A). We predicted that the LuxS protein would be extended by a total of eight amino acids followed by natural termination at a second downstream TAA stop codon (Fig. 3A). The peptide LGELHIS^PSVNYLHN was indeed observed and phosphoserine insertion at the amber codon was unambiguously identified in the enriched phosphopeptide fractions of the *E. coli* proteome (Fig. 3B). We then repeated this experiment and used label free quantitation to examine the abundance of the Sep-extended LuxS peptide in strains BL21, BL21.SEP, BL21.L11C.SEP, and EcAR7.SEP. As expected, no Sep-extended LuxS peptide was detected in BL21. WT cells without the SEP-system (Fig. 3C, blue). However, the peptide was readily detected in both BL21.SEP (red) and BL21.L11C.SEP (pink) with the total peptide yields slightly increased by the overexpression of the ribosomal subunit L11C. L11C overexpression was previously shown to quantitatively enhance recombinant Sep protein production [2]. We also observed a striking increase of Sep-mediated *luxS* suppression in the EcAR7.SEP strain (Fig. 3C, black). These results provide direct evidence of Sep insertion at a native TAG site in an unmodified *E. coli* locus and suggest that other sites are open to Sep suppression and global proteome extension. Furthermore, the dramatic increase in Sep-extended LuxS protein production showed that our engineering strategy had indeed boosted the efficiency of genetically encoded Sep insertion at amber codons.

3.3. Phosphoserine incorporation is enhanced in a RF-1 deletion strain

We investigated the efficiency of Sep incorporation in the EcAR7.SEP strain in detail by examining the efficiency of UAG read-through directly compared to our previously reported BL21 strains [2]. We introduced TAG codons in various positions in plasmid-encoded GFP (Fig. 4). These constructs were then transformed into EcAR7.SEP, EcAR7.supE, BL21 and BL21.L11C.supE. Western blot analysis of GFP with an N-terminal antibody enabled analysis of read-through of the UAG codons. As depicted in Fig. 4A, panel 1, no full length GFP is detected in BL21 without a functional UAG suppressor system. The combination of *supE* and Q94TAG or

Q157TAG was selected to examine UAG suppression without changing the amino acid at the position of the UAG in GFP. Using this strategy we clearly showed that while *supE* can function effectively in BL21, the suppression efficiency is dramatically enhanced in the EcAR7 background (Fig. 4A). After confirming that UAG codons were converted to sense codons in EcAR7 we next examined the efficiency of Sep insertion in this strain. The same GFP variants were expressed in EcAR7.SEP and, while Sep insertion at Q157 was equivalent in expression to WT GFP, Q94TAG was non-permissive to Sep insertion. These results contrast the expression of the same constructs in BL21.L11C.SEP. While Q157TAG was more permissive than Q94TAG in BL21.L11C.SEP, the efficiency of Sep insertion was dramatically reduced and truncated products could easily be detected. These data demonstrate that Sep insertion is competing with RF-1 in BL21.L11C.SEP and enhanced in the RF-1 deficient background of EcAR7.SEP. These data suggest that Sep insertion at Q94TAG might destabilize GFP and result in protein degradation. Similar results have been described in studies that have aimed to introduce unnatural amino acids into GFP [7].

Next, we expanded our screen to find other Sep-permissive sites in GFP (Fig. 4B). We reasoned that glutamate residues in GFP might be more permissive to Sep insertion, but surprisingly found only two of the five glutamate positions tested (E17 and E142) tolerated Sep insertion (Fig. 4B). This result was interesting since glutamate is often used as a phosphoserine mimetic [2], however, we observed glutamate sites that did not permit phosphoserine insertion (E132, E213, and E222). This will be investigated in future studies and could be due to a number of factors that include, protein instability, steric hindrance, or charge incompatibility. Our small scale screen identified 3 out of 10 amino acid positions in GFP that can be efficiently replaced with Sep. Identifying several permissive Sep sites in GFP allowed us to further examine the production of recombinant phosphoproteins in the EcAR7.SEP strain.

Our previous work demonstrated that multiply phosphorylated proteins had extremely low yields (~ 1 μ g/L) in the BL21.L11C.SEP strains [2]. In contrast, the EcAR7.supE strain showed highly efficient suppression of two in frame UAG codons (Fig. 4A). This suggested that multiply phosphorylated proteins might show a similar translational efficiency in EcAR7. We found that the combination of two permissible Sep sites (Q157 and E17) was efficiently translated to produce a doubly phosphorylated GFP protein (Fig. 4B). This result was in stark contrast to the very low level of Q157/E17TAG

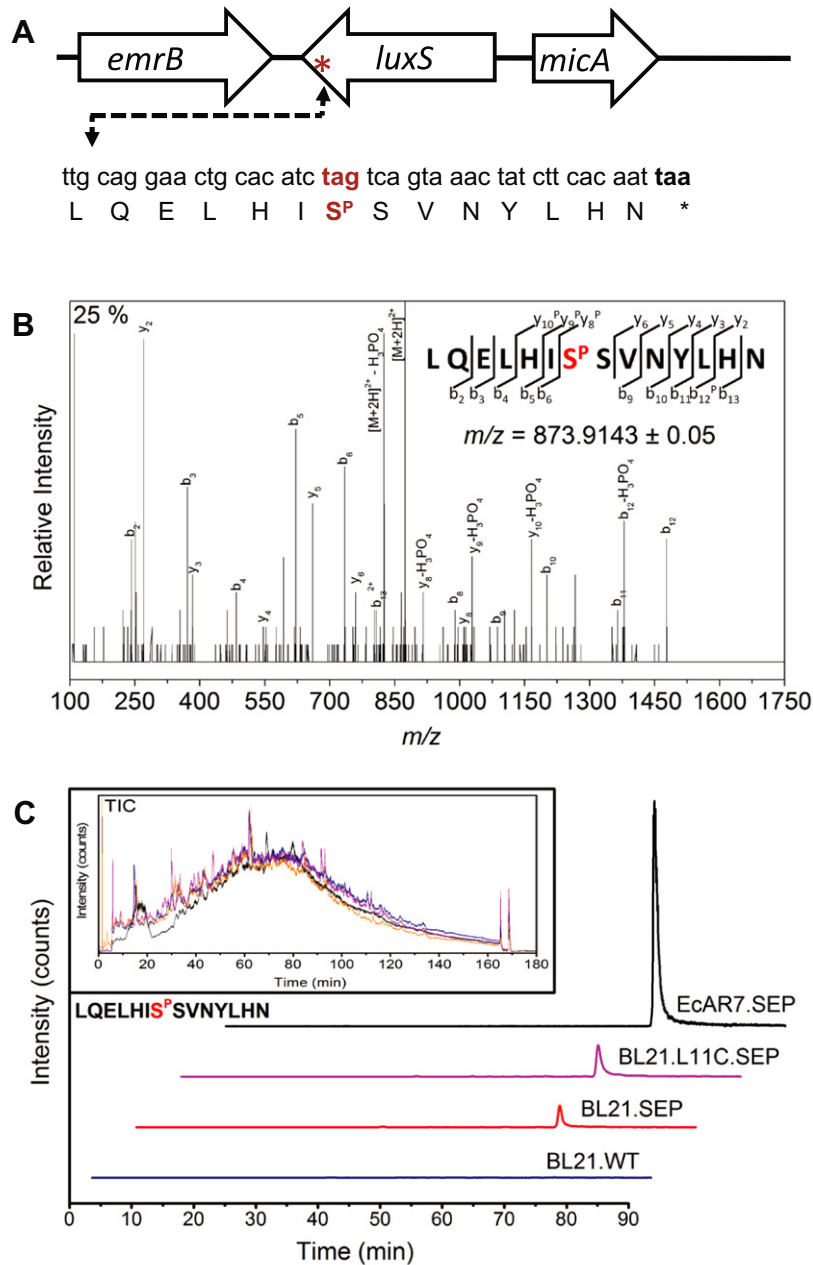


Fig. 3. Natural UAG codon suppression in *luxS* monitored by mass spectrometry. (A) The genetic context of the *luxS* gene is shown. Suppression of the natural amber stop codon (tag = red) with phosphoserine (S^P) is predicted to extend protein synthesis to the next in-frame non-amber stop codon (taa). (B) Annotated tandem MS spectra and sequence coverage (y and b ions) for the predicted phosphopeptide LQELHIS^PSVNYLHN from *LuxS* detected in EcAR7.SEP. Fragment ions ($[M+2H]^{2+}$ precursor = 873.914) showing neutral losses consistent with phosphorylation are indicated with a P in the sequence coverage map. (C) Extracted ion chromatograms of the same peptide across multiple *E. coli* strains demonstrating improved suppression in the recoded strain. Total ion chromatograms of each experiment demonstrate equal loading (inset).

expression in BL21.L11C.SEP. Interestingly, the combination of the non-permissible Y66 and E213 sites with Q157 rendered the entire GFP unstable. We overexpressed and purified various phosphoserine containing GFPs on a larger scale and found the yield was approximately 0.23 g/L culture for E213TAG, 1.1 g/L for E17TAG, 6.6 g/L for E17/Q157TAG and 31 g/L for WT. In general, yields for singly and doubly phosphorylated GFP proteins were 10-fold greater in EcAR7.SEP when compared to yields from the BL21.L11C.SEP strain. Finally, we validated Sep insertion at GFP Q157TAG, E142TAG, and E17TAG (Fig. 4C) with mass spectrometry. Sep insertions at all three sites could be unambiguously identified.

One important application of our Sep-expression system is to study physiologically relevant protein phosphorylation [2]. Furthermore, we wondered if phosphoserine insertions at naturally

phosphorylated sites might be more permissible and contrast to the general impermissibility of phosphoserine insertion across GFP (Fig. 4A and B). To examine this directly we expressed an important switch domain of the mouse serine/threonine kinase WNK4. WNK4 acts as a molecular switch that can vary the balance between NaCl reabsorption and K^+ secretion to control blood pressure in humans [23–26]. Two phosphoserine residues have been implicated in the physiological regulation of WNK4 and a system to produce this phosphoprotein could enable new types of research into its function. We expressed recombinant WNK4 proteins containing either one or two phosphoserine sites and observed variable expression levels in BL21.SEP and very low levels of multiply phosphorylated protein (Fig. 4C). In contrast, singly and multiply phosphorylated proteins were produced at very similar

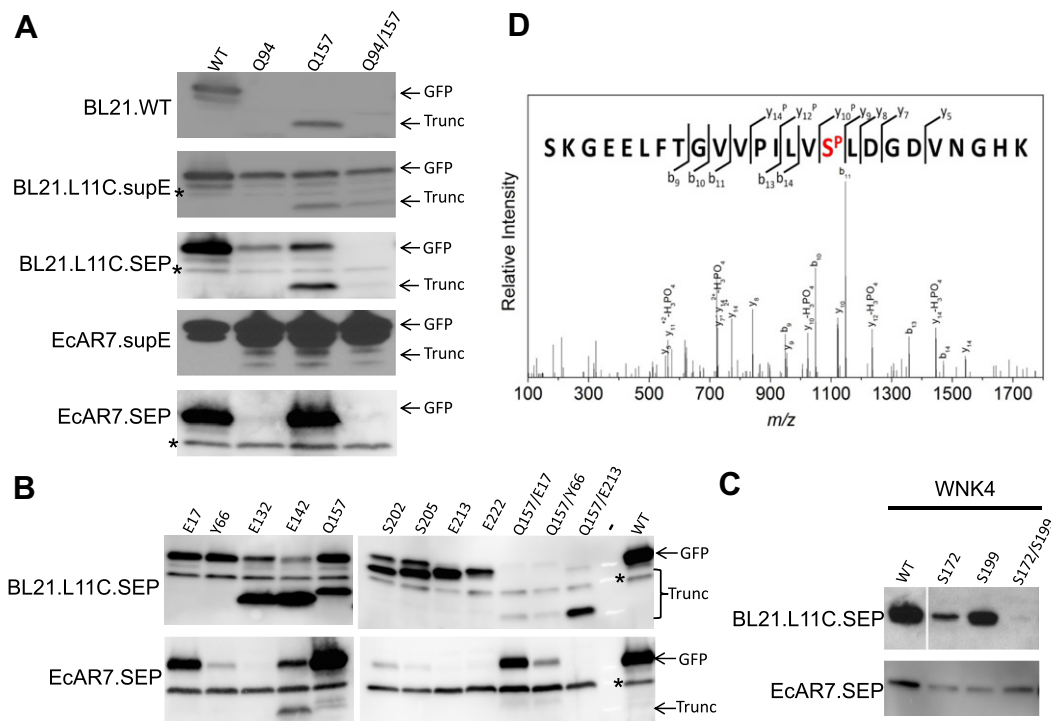


Fig. 4. Recoding of TAG to a sense codon. (A) BL21 and EcAR7 strains containing either a suppressor tRNA (*supE*) or the SEP-system (SEP) were transformed with plasmids encoding WT GFP, GFPQ94TAG, GFPQ157TAG or GFPQ94/Q157TAG, respectively. Western blots using the antibody against the N-terminus of GFP are shown (*indicates a non-specific band). (B) EcAR7.SEP and BL21.L11C.SEP were transformed with plasmids containing GFP-variants encoding TAG at the various positions indicated. A range of site specific truncations that accumulate in BL21.L11C.SEP are indicated by a bracket (* indicates a non-specific band). (C) EcAR7.SEP and BL21.L11C.SEP were transformed with plasmids harboring WNK4-WT and WNK4-TAG-containing variants as indicated. Western blot against the C-terminal His-tag are shown. (D) MS/MS validation of Sep insertion at E17TAG. Fragment ion spectra ($[M+3H]^{3+}$ precursor = 897.452) showing characteristic neutral losses consistent with phosphoserine (S^P) allowed unambiguous assignment of phosphoserine at position 17 in GFP.

levels in EcAR7.SEP. However, expression of the WT protein was higher in BL21.SEP and, in general, the level of phosphoserine containing protein was lower. This shows that addition of chaperones or further genetic modifications to increase fitness might be required for some recombinant proteins.

4. Discussion

4.1. Efficiency of phosphoserine incorporation increases in a RF-1 knockout strain

In this study we aimed to enhance the incorporation efficiency of phosphoprotein production. Several methods for RF-1 knockout have been published recently [7,8,10,11] and we sought to combine these advances with newly developed methods of genome engineering (i.e., MAGE) to reassign the previously described essential TAG stop codons to synonymous TAA codons [10,12]. Our results show that a RF-1 deletion strain prevents premature stopping at the TAG codon and improves yields of phosphoprotein production in strains that harbor deficiencies in both fitness and viability.

In the resulting strain EcAR7 we were able to produce large amounts of phosphoprotein in GFP and the eukaryotic WNK4 phosphoprotein compared to the previously used strains BL21.SEP and BL21.L11C.SEP. Specifically, phosphoserine incorporation at a single TAG site yielded a 48-fold increase in protein yield (e.g. 1.2 mg/L culture for GFP E17TAG compared to 25 μ g MEK1SEP/Liter culture in BL21.L11C.SEP) [2]. In WNK4, no reduction in protein yield was observed upon introduction of one or two TAG sites, respectively. The newly created strain EcAR7.SEP is thus a highly useful tool in phosphoprotein production and could be employed to investigate the function of single phosphoserine sites (e.g., WNK4) as well as other unnatural amino acids [22].

4.2. Phosphoserine is incorporated into the natural proteome and leads to reduced cell fitness and viability

While we were able to improve overall phosphoprotein yield up to 120-fold, the deletion of RF-1 and especially the introduction of our phosphoserine incorporation system had a major effect on strain viability (see Fig. 2). Interestingly, some of the growth phenotype of the release factor deletion could be rescued upon introduction of a natural suppressor tRNA, which allows for incorporation of glutamine in response to UAG, as previously described [11]. However, Sep incorporation had a deleterious effect on the host cell. Taken together, these results suggest that the striking loss in cell fitness is most likely the result of Sep-induced synthetic peptide chain extension at native UAG sites, as demonstrated by the incorporation of phosphoserine into the final peptide of LuxS. It is possible that some proteins may be able to tolerate extensions with glutamine incorporation, while the significant negative charge that accompanies phosphoserine may lead to misfolded or dysfunctional proteins. While the reassignment of seven TAG stop codons to TAA codons permitted the deletion of RF-1, more codon reassignments will be required to further increase phosphoserine incorporation and to compensate for the introduction of an unnatural amino acid (e.g., highly negatively charged phosphoserine) at a dedicated TAG sense codon without suffering loss of cellular fitness [16].

Acknowledgments

This work was supported by grants from the National Institute of General Medical Sciences and the National Science Foundation (to D.S.), DARPA CLIO Contract No. N66001-12C-4020 (to F.I.), and NIDDK (K01DK089006) (to J.R.). I.U.H. was supported from

the Deutsche Forschungsgemeinschaft (HE5802/1-1). We thank Patrick O'Donoghue and Laure Prat for helpful discussions.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.febslet.2012.08.031>.

References

- [1] Tarrant, M.K. and Cole, P.A. (2009) The chemical biology of protein phosphorylation. *Annu. Rev. Biochem.* 78, 797–825.
- [2] Park, H.S. et al. (2011) Expanding the genetic code of *Escherichia coli* with phosphoserine. *Science* 333, 1151–1154.
- [3] Eggertsson, G. and Söll, D. (1988) Transfer ribonucleic acid-mediated suppression of termination codons in *Escherichia coli*. *Microbiol. Rev.* 52, 354–374.
- [4] Wang, L., Brock, A., Herberich, B. and Schultz, P.G. (2001) Expanding the genetic code of *Escherichia coli*. *Science* 292, 498–500.
- [5] Ryden, S.M. and Isaksson, L.A. (1984) A temperature-sensitive mutant of *Escherichia coli* that shows enhanced misreading of UAG/A and increased efficiency for some tRNA nonsense suppressors. *Mol. Gen. Genet.* 193, 38–45.
- [6] Gerdes, S.Y. et al. (2003) Experimental determination and system level analysis of essential genes in *Escherichia coli* MG1655. *J. Bacteriol.* 185, 5673–5684.
- [7] Johnson, D.B. et al. (2011) RF1 knockout allows ribosomal incorporation of unnatural amino acids at multiple sites. *Nat. Chem. Biol.* 7, 779–786.
- [8] Johnson, D.B., Wang, C., Xu, J., Schultz, M.D., Schmitz, R.J., Ecker, J.R. and Wang, L. (2012) Release factor one is nonessential in *Escherichia coli*. *ACS Chem. Biol.* 7, 1337–1344.
- [9] Mukai, T., Hayashi, A., Iraha, F., Sato, A., Ohtake, K., Yokoyama, S. and Sakamoto, K. (2010) Codon reassignment in the *Escherichia coli* genetic code. *Nucleic Acids Res.* 38, 8188–8195.
- [10] Mukai, T. et al. (2011) Genetic-code evolution for protein synthesis with non-natural amino acids. *Biochem. Biophys. Res. Commun.* 411, 757–761.
- [11] Ohtake, K., Sato, A., Mukai, T., Hino, N., Yokoyama, S. and Sakamoto, K. (2012) Efficient decoding of the UAG triplet as a full-fledged sense codon enhances the growth of a *prfA*-deficient strain of *Escherichia coli*. *J. Bacteriol.* 194, 2606–2613.
- [12] Wang, H.H., Isaacs, F.J., Carr, P.A., Sun, Z.Z., Xu, G., Forest, C.R. and Church, G.M. (2009) Programming cells by multiplex genome engineering and accelerated evolution. *Nature* 460, 894–898.
- [13] DeVito, J.A. (2008) Recombineering with *tolC* as a selectable/counter-selectable marker: remodeling the rRNA operons of *Escherichia coli*. *Nucleic Acids Res.* 36, e4.
- [14] Isaacs, F.J., Dwyer, D.J., Ding, C., Pervouchine, D.D., Cantor, C.R. and Collins, J.J. (2004) Engineered riboregulators enable post-transcriptional control of gene expression. *Nat. Biotechnol.* 22, 841–847.
- [15] Lutz, R. and Bujard, H. (1997) Independent and tight regulation of transcriptional units in *Escherichia coli* via the LacR/O, the TetR/O and AraC/I1-12 regulatory elements. *Nucleic Acids Res.* 25, 1203–1210.
- [16] Isaacs, F.J. et al. (2011) Precise manipulation of chromosomes *in vivo* enables genome-wide codon replacement. *Science* 333, 348–353.
- [17] Baba, T. et al. (2006) Construction of *Escherichia coli* K-12 in-frame, single-gene knockout mutants: the Keio collection. *Mol. Syst. Biol.* 2, 2006.0008.
- [18] Jahn, M., Rogers, M.J. and Söll, D. (1991) Anticodon and acceptor stem nucleotides in tRNA(Gln) are major recognition elements for *E. coli* glutamyl-tRNA synthetase. *Nature* 352, 258–260.
- [19] Schattner, P., Brooks, A.N. and Lowe, T.M. (2005) The tRNAscan-SE, snoscan and snoGPS web servers for the detection of tRNAs and snoRNAs. *Nucleic Acids Res.* 33, W686–W689.
- [20] Hayashi, K. et al. (2006) Highly accurate genome sequences of *Escherichia coli* K-12 strains MG1655 and W3110. *Mol. Syst. Biol.* 2, 2006.0007.
- [21] Huang, Y., Russell, W.K., Wan, W., Pai, P.J., Russell, D.H. and Liu, W. (2010) A convenient method for genetic incorporation of multiple noncanonical amino acids into one protein in *Escherichia coli*. *Mol. Biosyst.* 6, 683–686.
- [22] Neumann, H. (2012) Rewiring translation – genetic code expansion and its applications. *FEBS Lett.* 586, 2057–2064.
- [23] Yang, C.L., Zhu, X., Wang, Z., Subramanya, A.R. and Ellison, D.H. (2005) Mechanisms of WNK1 and WNK4 interaction in the regulation of thiazide-sensitive NaCl cotransport. *J. Clin. Invest.* 115, 1379–1387.
- [24] Rozansky, D.J. et al. (2009) Aldosterone mediates activation of the thiazide-sensitive Na–Cl cotransporter through an SGK1 and WNK4 signaling pathway. *J. Clin. Invest.* 119, 2601–2612.
- [25] Ring, A.M., Leng, Q., Rinehart, J., Wilson, F.H., Kahle, K.T., Hebert, S.C. and Lifton, R.P. (2007) An SGK1 site in WNK4 regulates Na⁺ channel and K⁺ channel activity and has implications for aldosterone signaling and K⁺ homeostasis. *Proc. Natl. Acad. Sci. USA* 104, 4025–4029.
- [26] Lin, D.H., Yue, P., Rinehart, J., Sun, P., Wang, Z., Lifton, R. and Wang, W.H. (2012) Protein phosphatase 1 modulates the inhibitory effect of With-no-lysine kinase 4 on ROMK channels. *Am. J. Physiol. Renal Physiol.* 303, F110–F119.