Effect of N-terminal amino acid sequence on the protein synthesis using a reconstituted cell-free protein synthesis system



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Abstract

The Escherichia coli (E. coli)-based protein synthesis using recombinant elements (PURE) system is a cell-free protein synthesis system reconstituted from purified factors essential for E. coli translation. The PURE system is widely used for basic and synthetic biology applications. One of the major challenges associated with the PURE system is that the protein yield of the system varies depending on the protein. Studies have reported that the efficiency of ribosomal translation is significantly affected by nucleotide and amino acid sequences, especially in the N-terminal region. Here, we investigated the inherent effect of various N-terminal sequences on protein synthesis using the PURE system. We found that a single amino acid substitution in the N-terminal region significantly altered translation efficiency in the PURE system, especially at low temperatures. This result gives us useful suggestions for the expression of the protein of interest in vitro and in vivo.

1. Introduction

PUREfrex® is based on the PURE system.

The PURE system is a reconstituted cell-free protein synthesis system, which consists of only purified factors necessary for transcription, translation and energy regeneration.

Ref; Shimizu Y. et al. (2001) Nat. Biotechnol., vol. 19, p. 751

One of the challenges;

Differences in the synthesis efficiency depending on the proteins

- · Background;
- The 3rd to 5th amino acid residues in the N-terminal region are important for the efficient translation.
- · Large amino acids, which are encoded by AT-rich codon, facilitate early elongation reaction.
 - Ref; Verma M. et al. (2019) Nat. Commun., Jia B. et al. (2021) Sci. Rep
- · Aim of this study;

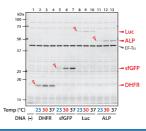
Evaluation of the effect of amino acids in the N-terminal region on the synthesis efficiency at 23, 30 and 37 °C.

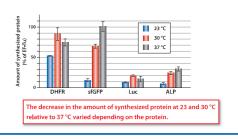
2. Protein synthesis at 23, 30, or 37 °C

< Information of proteins used in this study >

Protein		M.W.	N-terminal AA Seq
DHFR	E. coli dihydrofolate reductase	18.0 kDa	MISLIAALAV
sfGFP	Superfolder GFP	26.8 kDa	MSKGEELFTG
Luc	Firefly luciferase	60.7 kDa	MEDAKNIKKG
ALP	E. coli alkaline phosphatase	47.3 kDa	MRTPEMPVLE



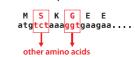




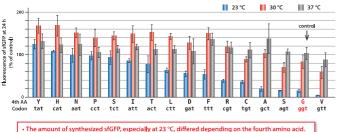
3. Influences of the second and fourth amino acid on sfGFP synthesis



< N-terminal sequence of sfGFP >

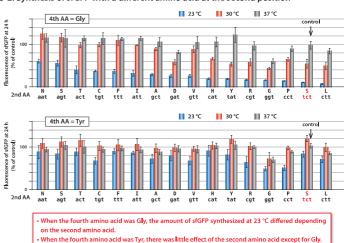


3-1. Synthesis of sfGFP with a different amino acid at the fourth position

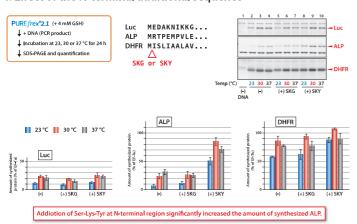


The amount of synthesized sGFP, especially at 23 °C, differed depending on the fourth amino acid.
When the fourth amino acid was a large amino acid such as Tyr or His, the amount of sfGFP was increased compared to Gly.

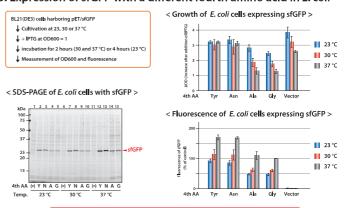
3-2. Synthesis of sfGFP with a different amino acid at the second position



4. Effect of the N-terminal additional sequence



5. Expression of sfGFP with a different fourth amino acid in *E. coli*



Not only Tyr and Asn variants but also Ala and Gly variants were expressed at 23 $^{\circ}\text{C}$

Expression of Ala and Gly variants suppressed E. coli growth

Conclusion

- The efficiency of synthesis especially at low temperature varied from protein to protein.
- The fourth amino acid of sfGFP significantly affected the synthesis efficiency in vitro at 23 °C.
- Addition of Ser-Lys-Tyr to N-terminal region significantly increased the amount of ALP synthesized at low temperatures.
- Ala and Gly variants could be expressed in E. coli even at 23 °C, but suppressed the growth.

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