Stem Loop Structures in the *B. subtilis* Genome and Their Roles in the Transcription Machinery

Takanori Washio[1] washy@sfc.keio.ac.jp
Kei Asai[2] asai@bs.aist-nara.ac.jp
Kazuo Kobayashi[2] kazuok@bs.aist-nara.ac.jp
Naotake Ogasawara[2] nogasawa@bs.aist-nara.ac.jp
Hiroki Yamamoto[3] ymmthrk@giptc.shinshu-u.ac.jp
Jun-ichi Sekiguchi[3] jsekigu@giptc.shinshu-u.ac.jp
Ken-ichi Yoshida[4] kyoshida@bt.fubt.fukuyama-u.ac.jp
Yasutaro Fujita[4] yfujita@bt.fubt.fukuyama-u.ac.jp
Masaru Tomita[1] mt@sfc.keio.ac.jp

[1] Laboratory of Bioinformatics., Keio University 5322 Endo, Fujisawa 252, Japan
[2] Graduate School of Biological Sciences, Nara Institue of Science and Technology, Nara, 630-0101, Japan
[3] Department of Applied Biology, Faculty of Textile Science and Technology, Shinshu University, Nagano, Japan
[4] Faculty of Engineering, Fukuyama University, Fukuyama, 729-0292, Japan

Keywords: *B. subtilis*, transcription termination, stem loop, hairpin formation

1 Introduction

In the rho-independent mechanism of transcription termination, the elongation process of RNA polymerase is believed to be terminated by a stem loop in the secondary structure of the mRNA followed by a polyU signal. On the other hand, Northern hybridization experiments recently revealed that many termination sites are "indefinite", due to the fact that RNA polymerases of *B. subtilis* sometimes "read-through" the termination sites. In this study, we analyzed the nucleotide sequences of all termination sites of *B. subtilis* that could be identified by Northern hybridization.

2 Method and Results

We systematically computed the free energy values of mRNA secondary structures at those sites in order to detect stem-loop structures for rho-independent termination. No apparent difference in nucleotide sequence was found between "definite" and "read-through" terminators. However, we did find that some of the "read-through" terminator sequences were located near the start codon of the subsequent gene (Fig. 1). This finding suggests that these terminator sequences may have a role in the transcription initiation of the subsequence gene, since stem loop structures are known to act as regulators of transcription initiation for some genes, such as bglP [1] and S-box [2] and T-box families [3, 4]. Based on these results, we concluded that some of the "read-through" events result from the stem loop acting as initiator of transcription.

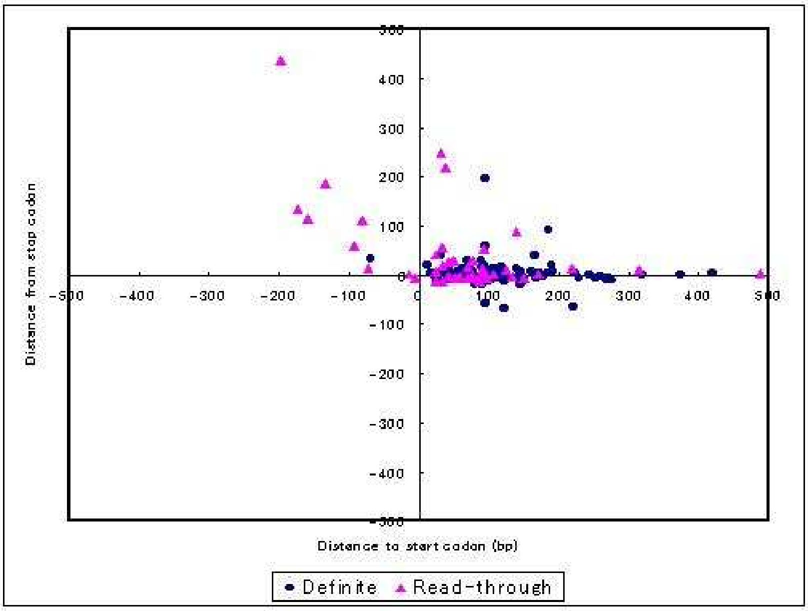

Figure 1: Location of terminator sequences.

References

[1] Kruger, S., Gertz, S. and Hecker, M., Transcriptional analysis of bglPH expression in *Bacillus subtilis*: evidence for two distinct pathways mediating carbon catabolite repression, *J. Bacteriol*, 178(9):2637-44, 1996.

[2] Frank, J.G. and Tina, M.H., The S box regulon: a new global transcription termination control system for methionine and cysteine biosynthesis genes in Gram-positive bacteria, *Mol. Microbiol.*, 30(4):737–49, 1998.

[3] Grundy, F.J. and Henkin, T.M., Conservation of a transcription antitermination mechanism in aminoacyl-tRNA synthetase and amino acid biosynthesis genes in gram-positive bacteria, *J. Mol. Biol.*, 235(2):798–804, 1994.

[4] Grundy, F.J. and Henkin, T.M., tRNA as a positive regulator of transcription antitermination in *B. subtilis*, *Cell*, 74(3):475–82, 1993.