

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

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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 subsequent 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.

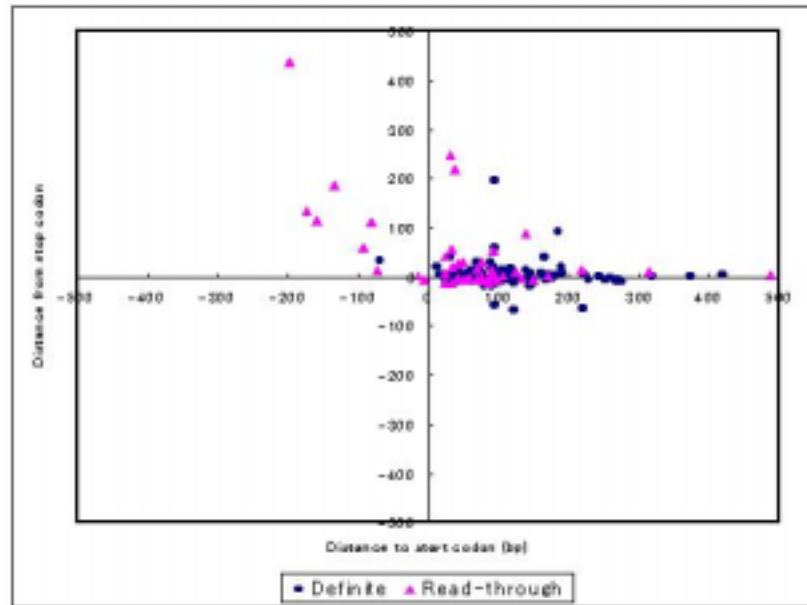


Figure 1: Location of terminator sequences.

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