

BDR SEMINAR in Yokohama

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13:30-15:00, C210-212, Yokohama Central Research Building

Characteristics of bacterial regulatory small RNAs

Summary

Regulation at post-transcriptional steps allows new pathways to cross-regulate genes independently of the transcriptional signals for those genes. Regulatory small RNAs (sRNAs), which act as a post-transcriptional regulator, are transcribed under specific physiological/stress conditions. The sRNAs interact with mRNAs by base-pairing, resulting in changes in the translation and stability of the target mRNAs. In gram-negative bacteria, the base-pairing is facilitated in general by the RNA chaperon Hfq.

E. coli sRNAs are around 100 nucleotides in length, and contain at least two functional regions, an mRNA base-pairing region and an Hfq-binding region essentially overlapping with a Rho-independent terminator sequence. The base-pairing region is partially complementary to the translation initiation region of target mRNAs. The sRNA-mRNA base pairing leads mostly to inhibition of translation of target mRNAs. The Hfq-binding region of the sRNAs consists of a polyU tail and a U-rich sequence immediately upstream of stem loop structure. The polyU tail must be longer than seven for the Hfq-binding. Both the 3'-extended transcripts resulting from read-through and the 3'-shortened transcripts resulting from premature termination no longer function as sRNAs. Discussion will focus on new insights into roles of stem loop structure in Rho-independent terminators of sRNAs.



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