Faculty of Engineering
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Molecular biology of pathogenic streptococci

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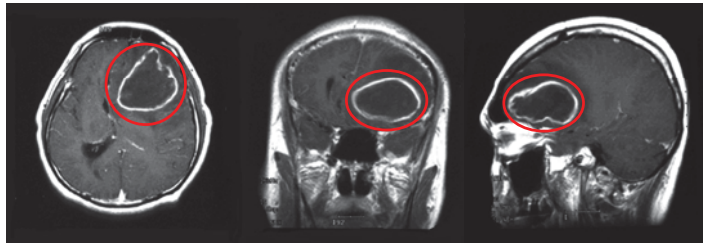

Fig. 1 Brain abscess by *S. intermedius*

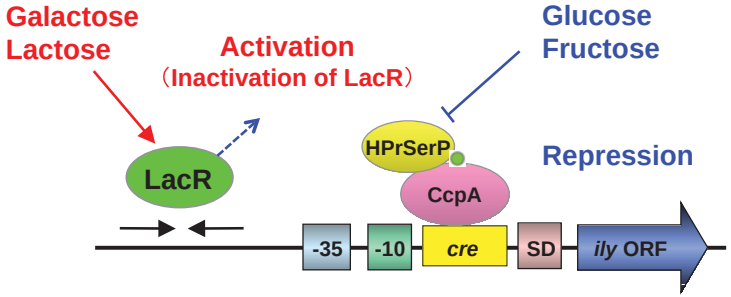

Fig. 2 Transcriptional regulation factors for *ily*

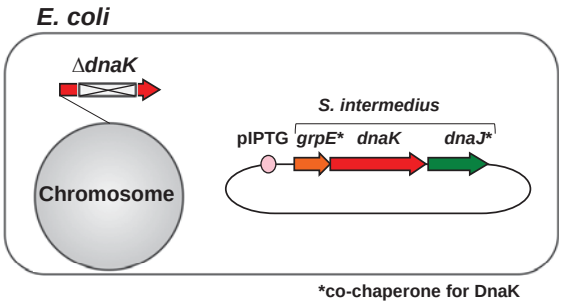

Fig. 3 Analyzing system for chaperone activity of G⁺ DnaK using *E. coli dnaK* knockout (Δ*dnaK*) mutant

Content:

Streptococcus intermedius is a part of the normal flora of the human oral cavity and a leading cause of deep-seated infections, including brain and liver abscesses (Fig. 1). We are investigating the mechanism involved in the regulation of transcription of *ily* (1) that encodes the human-specific cytolysin, intermedilysin, which is the major virulence factor. In addition, we are examining the quality control mechanism for cytosolic proteins by *S. intermedius* DnaK (2).

(1)Transcriptional control mechanism for *ily*

We found two transcriptional regulation factors for *ily*, catabolite control protein (CcpA) and lactose phosphotransferase system repressor (LacR) (Fig. 2). In addition, we reported that ILY-overproducing strains isolated from deep-seated abscesses such as brain and liver abscesses have a loss-of-function mutation in the *lacR*.

(2) Cytosolic protein quality control mechanism

Previous studies have shown that DnaK from gram-positive (G^+) bacteria was unable to show the activity in gram-negative (G^-) *Escherichia coli*, which is the model bacterium for studying the chaperone function. Therefore, many cellular functions of G^+ DnaK remain to be elucidated. We successfully created the system, which could activate the G^+ *S. intermedius* DnaK in *E. coli* (Fig. 3), and thus we have been analyzing the function of G^+ DnaK using our system.

Keywords：Streptococci, Molecular biology, Pathogen, Molecular chaperone

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