

## Global Regulation in Hyperthermophilic Archaea

Sung-Jae Lee

*Department of Biology, Kyung Hee University*

Sugar sensing transcriptional regulator TrmB family members are distributed in Archaea domain, especially in hyperthermophiles with highly conserved orthologs and acting as the global regulator for sugar transport, metabolism and branched biosynthetic pathways. *Pyrococcus furiosus* genome contained 4 TrmB family member proteins which have only 30% sequence homology in full length of each other. However, they revealed an identical secondary structure of N-terminal DNA binding motif. The TrmB is a main repressor for maltose/trehalose ABC transporter and weak for maltodextrins ABC transporter which was induced by maltose and maltotriose, respectively. The TrmBL1 is a central transcription repressor for the maltodextrins ABC transporter and the glycolytic enzymes which is induced maltotriose and an activator for gluconeogenesis recognizing the TGM sequences. The TrmBL2 is mainly an autoregulator and also regulates maltodextrins ABC transporter. Both TrmB and TrmBL1 bound to upstream region of TrmBL2. The regulational function of TrmBL3 is still unclear. We find a little evidence for regulating of biosynthesis of compatible solutes by the TrmB family members which are generally induced in stress conditions. However, each TrmB member recognized overlapped target promoters with different binding sequences, binding affinity and sugar sensing modulation. Thus, the regulation mechanism of TrmB family members was shown a multi-input motif network regulation. In the future, we will demonstrate that the TrmB family member proteins control more essential metabolic network regulation in direct or indirect manner.

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