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枯草菌の一般ストレス応答機構に関する構造研究

Structural Studies on General Stress Response Mechanism in *Bacillus subtilis*

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Microorganisms experiencing a fluctuating environment commonly exhibit a short-lived and reversible response that allows survival and recovery of the cell. In Gram-positive bacteria such as *Bacillus subtilis*, a range of stress and starvation stimuli causes the dramatic induction of above 100 σ^B-dependent general stress genes. The activity of σ^B in forming the complete transcriptional complex is governed by the signaling cascade with two distinct branches, which are composed of a set of signal transduction proteins termed *r*egulators of *s*igma *B* (Rsb).

One branch is specific for energy stresses, such as carbon, phosphate, or oxygen limitation. Once exposing the stresses, an α/β hydrolase RsbQ likely provides a hydrophobic small compound as an essential cofactor to RsbP. The other is specific for environmental stresses which trigger activation of the supermolecular protein-complex stressosome composed of RsbR, RsbS, and RsbT proteins. Upon the stresses, RsbR and RsbS are completely phosphorylated by RsbT, thereby inactivating RsbS and releasing RsbT from stressosome, following RsbT interacts with and activates RsbU. Each branch terminates with two serine phosphatases, RsbP and RsbU. Both of them dephosphorylate the common downstream factor, RsbV. Depending on the phosphorylation state of RsbV, RsbW regulates σ^B activity *via* a partner-switching mechanism.

A comprehensive understanding of this crucial stress response is essential not only for bacterial physiology but also for applied microbiology, including pathogenicity and pathogen control. To elucidate the structural and functional relationship between these proteins, we have determined crystal structures of RsbQ, RsbX and domain structures of RsbP. Further structural analysis is under way. We will present our structal studies of these proteins.

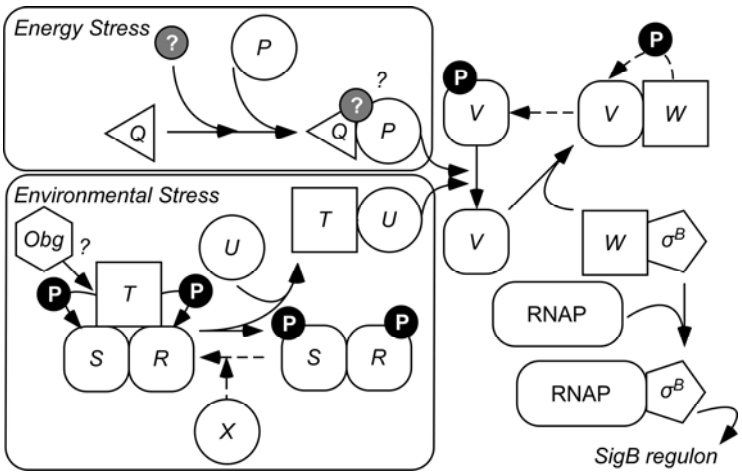

Figure. Regulational cascade of σ^B.