Oral presentation

Structural Basis for Regulation of RpoS Turnover by Phosphorylation and ClpXP Anti-Adaptors

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In enterobacteria such as Escherichia coli, the general stress response is mediated by RpoS, the stationary phase dissociable promoter specificity subunit of RNA polymerase. RpoS is degraded by ClpXP during active growth in a process dependent on the RssB adaptor, which is thought to be stimulated by phosphorylation of a conserved aspartate in its N-terminal receiver domain and inhibited by stress-inducible and structurally distinct anti-adaptor proteins, IraD, IraM and IraP. Here we will present the crystal structure of full-length RssB bound to a beryllofluoride phosphomimic as well as structures of IraD:RssB and IraM:RssB complexes together with hydrogen-deuterium exchange and functional data in vitro and in vivo. Strikingly, in all of these three structures, RssB assumes a different conformation, heavily dependent on the plasticity of its inter-domain segmented helical linker. Our study emphasizes the importance of the 4-5-5 face of the RssB receiver domain in binding to RpoS and in serving as a landing platform for the IraD and IraM anti-adaptors, thereby excluding RpoS and inhibiting its delivery to ClpXP.