MS05 Nucleic acids and their interaction

MS5-02
Structural studies of repressors from SorC/DeoR family
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Abstract
In bacteria, gene expression is controlled at the transcriptional level through interactions between regulatory proteins and DNA operators. Exploration of bacterial genomes led to the discovery of a large number of putative transcriptional regulators with the assignment of new families and subfamilies. One of these is the SorC family that embraces proteins that control the expression of genes and operons involved in the metabolism of sugar substrates. To date hundreds of putative transcriptional regulators have been classified into SorC family with only several members of SorC family functionally characterized: CggR [1] and DeoR [2] from B. subtilis, SorC from Klebsiella pneumonie [3] and LsrR from E. coli [4].
SorC family repressors contain conserved helix-turn-helix domain DNA-binding (DBD) at their N-terminus and an effector-binding domain (EBD) at their C-terminus. The DBD recognizes palindromic operator sequence usually located downstream of the promotor while the EBD (PF04198) has a phosphosugar binding function and plays role in oligomerization.
We performed extensive structural studies of two repressors from B. subtilis: DeoR and CggR [5-7]. By combining techniques of X-ray crystallography and cryo-electron microscopy we explored the mechanism of effector binding and modulation of oligomerization, characterized the DNA recognition and allosteric changes induced by effector binding. Structural studies of these two representatives provided information crucial for understanding the general mechanisms of gene regulation by SorC repressors.

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