Poster Presentation

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Structural studies of AraR from B. thetaiotaomicron

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The NrtR family of bacterial transcription factors is characterized by an N-terminal Nudix hydrolase-like effector binding domain and a C-terminal DNA binding domain. A bioinformatics analysis of the NrtR family represented by uncharacterized protein BT0354 in Bacteroides thetaiotaomicron suggests that these regulators control the catabolic pathways for L-arabinose. Many bacteria use L-arabinose as the sole source of carbon energy. The L-arabinose utilization pathway and its transcriptional regulation have been studied for a long time in several model microorganisms. Here we provide biochemical and structural characterization of the novel arabinose-responsive regulator of NrtR family protein BT0354, L-arabinose regulator from B. thetaiotaomicron (BtAraR). The BtAraR DNA binding and the role of effector molecule L-arabinose were confirmed using electrophoretic mobility shift assays. We have solved the crystal structures of BtAraR for two apo forms, and complexes with L-arabinose and double-stranded DNA target. The apo-1 form was solved as two dimers/AU in the R3 space group at 2.35 Å, while the apo-2 form was solved as one monomer/AU in the I213 space group at 2.56 Å resolution. The L-arabinose and DNA complex structures were solved as a dimer/AU in the P21 space group at 1.95 Å resolution and the P23 space group at 3.05 Å resolution, respectively. The biological unit of this protein is a dimer while the N-terminal ligand binding domain of the monomer adopts a Nudix hydrolase-like fold and the C-terminal DNA binding domain is a winged helix-turn-helix. The DNA binding-releasing mechanism can be rationalized through the comparison and analyses of these structures. The apo and DNA bound structures are more similar compared to the L-arabinose-bound structure. The r.m.s. deviation for the apo and DNA bound structures is 1.13 Å, while that for apo and the L-arabinose-bound structures is 4.54 Å. Details about the DNA binding mode, L-arabinose binding and L-arabinose induced structural change will be presented. This work was supported by National Institutes of Health grant GM094585 and by the U. S. Department of Energy, Office of Biological and Environmental Research, under contract DE-AC02-06CH11357.

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