

Poster Presentation

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Structural Insights into Regulation of Quinate Degradation in Bacteria

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The shikimate pathway is an essential metabolic pathway in bacteria, as well as plants and fungi, which ultimately leads to the synthesis of three aromatic amino acids among other important aromatic compounds. The fourth step in the pathway is the reduction of dehydroshikimate to shikimate, catalyzed by shikimate dehydrogenase (SDH/AroE). In addition to AroE, at least four functionally distinct SDH homologs exist in bacteria. The structure and catalytic residues of the SDH enzyme family are highly conserved, however the key residues for substrate binding vary among the different homologs. Together, these data suggest that the catalytic mechanism is maintained among homologs, yet each may bind a different substrate. The YdiB homolog catalyzes the first step in the quinate degradation pathway, which is a branch of the shikimate pathway. In various species, the operons containing the *ydiB* gene are predicted to be controlled by one of two different transcriptional regulators belonging to either the TetR or LysR family. In both cases, these regulators are predicted to be activated or repressed by intermediates of the quinate degradation pathway. We will be using structural biology to determine how these regulators recognize pathway intermediates, and to understand the structural basis of how two distinct regulators can control transcription of the equivalent operon in different species.

Keywords: Transcriptional Regulator, Bacteria, Quinate