LA.P38

Structural studies on oxalate decarboxylase from Photorhabdus luminescens

S. Mathivanan[1], S. Chellappan[1], R. Thippeswamy[2], M. Nagesh[2], H. Savithri[3], M. Murthy[1]

[1]Indian Institute of Science, Molecular Biophysics Unit, Bangalore, India, [2]Indian Council of Agricultural Research, Project Directorate of Biological Control, Bangalore, India, [3]Indian Institute of Science, Department of Biochemistry, Bangalore, India

As a part of exploration of novel bacterial genes coding for insecticidal proteins, we have initiated structural and functional studies on oxalate decarboxylase from Photorhabdus luminescens, a symbiotic bacteria inhabiting guts of nematodes that parasitize insects. Oxalate decarboxylases (OXDC) are enzymes that catalyze the conversion of oxalate to formate and carbondioxide (CO2) in the presence of manganese and dioxygen. Structures of OXDC in complex with ethylene glycol (EDO), EDO/formate (FMT) and FMT/CO2 were determined at resolutions of 1.97Å, 2.36Å and 2.5Å, respectively. The asymmetric unit of these crystals contained a trimeric molecule. A protomer of the enzyme consists of two β-barrel domains belonging to the cupin family of proteins. All the three ligand bound structures of OXDC resemble the closed form of OXDC from B. subtilis reported earlier. Comparison of these structures with the open and closed forms of B. subtilis OXDC indicated that the conformation of Glu166 (corresponding to Glu162 of B. subtilis) in cupin domain I but not in domain II is in a conformation suitable to function as the catalytic base/acid and hence only domain I may be catalytically active. It is observed that the hydrogen bonding interaction between Arg95 and Thr169 of cupin domain I is essential for the positioning of Glu166 for catalysis. A corresponding threonine residue is absent in cupin domain II. An analysis of the similarities and differences between OXDC structures from P. luminescens and other reported bacterial OXDC structures and oxalate oxidase from Hordeum vulgare has been carried out with the view of understanding substrate and functional specificities of these enzymes. The structure provides the molecular framework required to investigate the mode of action of the enzyme, which may be a suitable candidate for developing P. luminescens as a bio-insecticide against plant pests.

Keywords: Oxalate decarboxylase, Photorhabdus luminescens