

CRYSTALLOGRAPHIC STRUCTURE AND ANALYSIS OF THE MOLYBDATE-BINDING PROTEIN (MODA) FROM XANTHOMONAS AXONOPODIS PV. CITRI

Santacruz, C. P.¹, Balan, A.¹, Moutran, A.¹, Neshich G.², Ferreira, L.C.S.¹ and Barbosa, J.A.R.G.³

¹USP, São Paulo; ²EMBRAPA, Campinas; ³LNLS, Campinas.

Molybdenum is an essential nutrient required for most bacteria as well as for plants and animals. High affinity uptake of molybdate in gram-negative bacteria occurs via a specific ABC transport system and involves a periplasmic molybdate-binding protein, (ModA), a permease protein (ModB) and an ATPase-binding protein (ModC) that interact to transport this ion. The crystal structure of the periplasmic molybdate-binding protein (ModA) of the plant pathogen *Xanthomonas citri*, responsible for the citrus canker, was solved by X-ray crystallography. Diffraction data were collected at the D03B-MX1 beamline of the LNLS to a maximum resolution of 1.75 Å. The structure was solved by molecular replacement, using the *Escherichia coli* ortholog as a template. The *Xac* ModA structure is ellipsoidal, composed of two nearly symmetrical domains separated by a hinge region where the substrate-binding site lies. ModA sequences of *Xac*, *Eco* and *Azotobacter vinelandii* revealed three distinct groups of molybdate-binding proteins described as phytopathogens, enterobacteria and soil bacteria, respectively. The conserved common patterns and specific divergences between the three groups are discussed in light of the atomic structures. The homology modelling of ModB and ModC *Xac* structures is being conducted to try to define the interacting regions between the proteins of this ABC system.

Key Words: molybdate-binding protein, ModA, *Xanthomonas citri*, crystallographic structure.

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