Poster Presentation

Crystal structure of isocitrate lyase from Magnaporthe grisea

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Glyoxylate cycle is a branched metabolic pathway in the TCA cycle that was initially discovered in microorganisms. The branched cycle plays an essential role in those organisms by providing the means for microorganisms to utilize acetate, ethanol, or fatty acids as carbon sources. In fact, pathogenic microorganisms rely on the glyoxylate cycle, rather than the TCA cycle, during infection. Therefore, the enzymes in the glyoxylate cycle of pathogens were suggested to be one of drug target molecules. Magnaporthe grisea isocitrate lyase (MgICL), a key enzyme in the cycle, is highly expressed during appressorium-mediated plant infection. In order to characterize the structural and functional features of MgICL, a structure of MgICL was determined at 2.7 Å resolution by X-ray crystallography. Recently, we are carrying out structure determination of MgICL in complex with a possible candidate for inhibitors. Our study could provide detailed structural features of MgICL and the binding mode of an inhibitor. This work was supported by a grant from Center for Fungal Pathogenesis by National Research Foundation, Republic of Korea.

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