

Molecular and Cristallographyc Analysis of MBP of *Xanthomonas axonopodis* pv
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The maltose/maltodextrin transport system is a member of the ABC-transport family found in different gram-negative bacterial species.. In this work we report the results of crystallization trials, crystal difraction and data processing of *Xac* MBP, previously expressed and purified by our group. Crystals obtained were grown in 12 different conditions. A X-ray diffraction data were collected to a maximum resolution of 2.6 Å. The first attempts to process the diffraction data from crystals refined at 0.1 M Tris-HCl pH 8,0 and 3.5 M sodium formate at 18° C, suggest they belong to the space group P3 with unit-cell parameters a = 68,16, b = 172,21, c = 112,05 ?. The processing is still in progress. In order to obtain crystals from *Xac* MBP without the 6XHis-tag, purified samples of this protein were successfully treated with thermolysin and subtilysin. Bioinformatic analysis also revealed that genes encoding MBPs are found in different bacterial species genomes, including *X. oryzae*, *X. campestris* and *Xac*. The amino acid sequence alignment among *Xanthomonas* MBPs showed identity values above 92%. Circular dicroism assays revealed the *Xac* MBP is stable at different pHs. These data will contribute to understanding of MPB structure and its role on the physiology of *Xac* and other *Xanthomonas* species.

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