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X-ray Crystallographic Study of Glucodextranase from a Gram-positive Bacterium, *Arthrobacter globiformis* I42

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Glucodextranase (GDase) hydrolyzes α-1,6-glucosidic linkages of dextran from the non-reducing end to produce β-D-glucose. GDase is classified under GH15, whose major member is glucoamylase (GA) that hydrolyzes α-1,4-glucosidic linkages of starch. We have cloned a GDase gene from the Gram-positive bacterium *Arthrobacter globiformis* I42 and determined the crystal structure at 2.42-Å resolution. The structure of GDase is composed of four domains N, A, B and C. Domain N consists of 17 antiparallel β-strands and domain A forms an $(\alpha/\alpha)_6$ barrel structure, which is conserved between GAs. Furthermore, the complex structure with acarbose was also determined at 2.42-Å resolution. The structure of GDase complexed with acarbose revealed that the positions and orientations of the residues at subsites -1 and +1 are nearly identical for GDase and GA; however, Glu380 and Trp582 located at subsite +2, which form the entrance of the catalytic pocket, and the position of the open space and constriction of GDase are different from those of GAs. On the other hand, domains B and C are not found in GAs. The primary structure of domain C is homologous with the surface layer homology (SLH) of pullulanases from Gram-positive bacteria, and the three-dimensional structure of domain C resembles the carbohydrate-binding domain of some glycohydrolases. The hydrophobicity of domain B is higher than that of the other three domains. These findings suggest that domains B and C serve as cell

wall anchors and contribute to the effective degradation of dextran at the cell surface.

Key words: glucodextranase, glucoamylase, glycoside hydrolase family 15, X-ray crystallography, S-layer homology

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