Structural characterization of seven-bladed beta-propeller lectin family from *Photorhabdus laumondii*

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Lectins, carbohydrate recognizing proteins, play an important role in various physiological and pathophysiological processes as well as both mutualistic and parasitic interactions between microorganisms and hosts [1]. In connection with the last-mentioned process, lectins from pathogenic bacteria can mediate the first step of infection and they are considered an important virulence factor.

Photorhabdus laumondii is an entomopathogenic bacterium, which is known for its complicated life cycle, including mutualism and pathogenicity towards two different invertebrate hosts [2]. This contribution is focused on the newly described PLL lectin family, which shares a seven-bladed beta-propeller fold. All five members of this family are highly similar to each other in primary, secondary, and tertiary structure. However, the oligomeric state of these lectins differs significantly. Members of the PLL family have been confirmed to bind multiple monosaccharides, including L-fucose and *O*-methylated saccharides. X-ray structures of PLL family discovered two sets of binding sites with different ligand specificity per monomer, "polar" sites and "hydrophobic" sites. Amino acids involved in the ligand-binding are highly conserved within the lectin molecule. Ligands are bound in both types of binding sites via hydrogen bonds and via CH-π interaction with aromatic residues. Lectin/saccharide interaction is mostly mediated via hydrogen bonds. However, hydrophobic sites are deepened with a hydrophobic pocket. The importance of non-polar interactions, such as CH-π interactions between aromatic amino acids and apolar part of carbohydrate molecules, was shown recently [3].

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