Poster Presentation

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Structure of pneumococcal GtfA reveals a novel prokaryotic O-GlcNAc transferase

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Protein glycosylation is increasingly recognized as an important process for bacterial physiology and pathophysiology. Glycosylation of serine-rich repeat (SRR) glycoprotein PsrP is essential for the pathogenesis of Streptococcus pneumoniae, one of the most common human pathogens. This glycosylation process is initiated by a glycosyltransferase complex comprising two components, a core enzyme GtfA and a co-activator GtfB. Here we report the 2.0-Å crystal structure of GtfA in complex with GlcNAc and UDP. The structure possesses a core domain of GT-B fold and an unprecedented “add-on” domain of DUF1975, which adopts a β-meander structure. This novel DUF1975 domain is critical for the intact glycosyltransferase activity of GtfA–GtfB complex via mediating their self-recognition and the binding to the acceptor protein PsrP. The glycoproteomic analysis revealed a novel pattern of protein O-linked glycosylation at the serine residue cluster. The findings suggest that GtfA is a new glycosyltransferase and provide a structural basis for the future design of inhibitors against the biogenesis of bacterial SRRPs.

Keywords: O-linked glycosylation, Streptococcus pneumoniae, serine-rich repeat glycoprotein