

Structure of a 1.5-MDa bacterial adhesin reveals its role in the mixed-species biofilm formation with diatoms on ice

Shuaiqi Guo^{#†}, Ilja K. Voets[#] and Peter L. Davies[†].

[†]Protein Function Discovery Group and the Department of Biomedical and Molecular Sciences, Queen's University, Kingston, Ontario K7L 3N6, Canada

[#]Institute for Complex Molecular Systems, Laboratory of Macromolecular and Organic Chemistry, and Laboratory of Physical Chemistry, Department of Chemical Engineering and Chemistry, Eindhoven University of Technology, Eindhoven, 5600MD the Netherlands

Abstract

Bacterial adhesins are modular cell-surface proteins that mediate adherence to other cells, surfaces and ligands. The Antarctic bacterium *Marinomonas primoryensis* uses a 1.5-MDa adhesin comprising over 130 domains to position it on ice at the top of the water column for better access to oxygen and nutrients. We have reconstructed this 0.6 μm -long adhesin using a 'dissect and build' structural biology approach and have established complementary roles for its five distinct Regions. Domains in Region I (RI) tether the adhesin to the Type I secretion machinery in the periplasm of the bacterium and pass it through the outer membrane. RII comprises ~ 120 identical Ig-like β -sandwich domains that rigidify on binding Ca^{2+} to project the adhesion regions RIII and RIV into the medium. RIII contains ligand-binding domains that join diatoms and bacteria together in a mixed species community on the underside of sea ice where incident light is maximal. RIV is the ice-binding domain; and the terminal RV domain contains several 'Repeats-in-Toxin' motifs and a non-cleavable signal sequence that target proteins for export via the Type I secretion system. Similar structural architecture is present in the adhesins of many pathogenic bacteria and provides a guide to finding and blocking binding domains to weaken infectivity

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