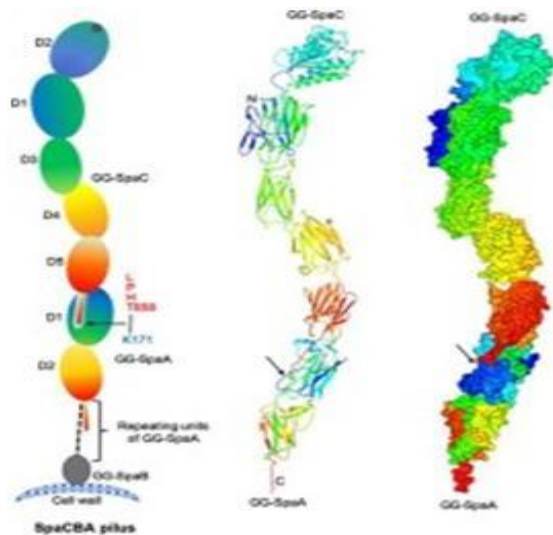


Crystal structure of lactobacillar SpaC reveals an atypical five-domain pilus tip adhesin

In the current study, scientists at DBT's Regional Centre for Biotechnology (RCB), Faridabad revealed full-length high-resolution (1.9 Å) crystal structure of SpaC, a first for a sortase-dependent pilus-bearing commensal. The SpaC structure, unlike the representative four-domain architecture of other Gram-positive tip pilins, espouses an atypically longer five-domain arrangement that includes N-terminal 'binding' and C-terminal 'stalk' regions of two and three domains, respectively. With the prospect of establishing new mechanistic insights, a structural basis for the multi-substrate binding nature of SpaC, as well as a structural model that reconciles its exclusive localization at the SpaCBA pilus tip has been provided.



Adhesion to cell surfaces is an essential and early prerequisite for successful host colonization by bacteria, and in most instances involves the specificities of various adhesins. Among bacterial Gram-positives, some genera and species mediate attachment to host cells by using long non-flagellar appendages called sortase-dependent pili. A case in point is the beneficial *Lactobacillus rhamnosus* GG gut-adapted strain that produces the so-called SpaCBA pilus, a structure noted for its promiscuous binding to intestinal mucus and collagen. Structurally, SpaCBA pili are heteropolymers of three different pilin-protein subunits, each with its own location and function in the pilus: backbone SpaA for length, basal SpaB for anchoring, and tip SpaC for adhesion. Previously, this research group solved the SpaA tertiary structure by X-ray crystallography and also reported on the crystallization of SpaB and SpaC.

Dr. Vengadesan Krishnan, Associate Professor of Regional Centre for Biotechnology, published a research article with his group on “*Crystal structure of lactobacillar SpaC reveals an atypical five-domain pilus tip adhesin: Exposing its substrate-binding and assembly in SpaCBA pili*”.

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