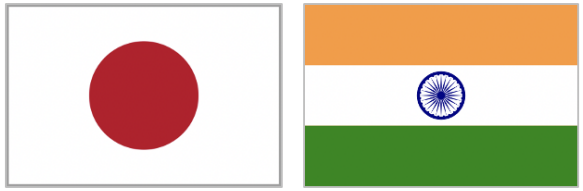

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SERIES 71 (2022-03-30)

Dr. Shantanu Shukla, Postdoctoral Fellow
Feinberg School of Medicine,
Northwestern University, Chicago, IL, USA

Series – 71

Date & Time - March 30, 2022 (01:30-02:30 JST | 10:00-11:00 IST)
Venue - Zoom
Speaker - Dr. Shantanu Shukla
Affiliation - Center for Structural Genomics of Infectious Diseases (CSGID), Northwestern University, Feinberg School of Medicine Chicago, IL 60611
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Deciphering the functional difference in structurally related proteins in bacteria

Evolution has molded bacteria to maintain a genome which discourages redundancy due to a negative selection pressure. Moreover, bacterial genomes have an increased plasticity when it comes to adjusting in environments with dwindling resources. However, contrary to our intuition, several bacteria possess structurally similar isoforms of the same protein or structurally similar homologous proteins. For example, there are three isoforms of the maltose-binding protein in *Thermotoga maritima* that are all associated with a single maltose-ABC transporter system. Additionally, *Vibrio cholerae* has two homologous retraction ATPases in their type IVa pili that are structurally very similar. It can be hypothesized that these redundant proteins are possibly required for key cellular processes that are essential for cellular physiology and bacterial survival. Therefore, to understand this phenomenon of redundancy, we need to identify key structural and functional features that differentiates these proteins. Using X-ray-, electron-, and neutron-based structural and biophysical methods, in tandem with computational molecular dynamics, I have characterized the determining factors that shape important cellular events like substrate binding and pilus retraction in bacteria and how redundant structurally similar proteins are important to sustain bacterial growth. My study revealed that there is an intricate link between the structural and dynamical changes in proteins that shapes their function and allow them to take tangential roles that substantiate their place in the bacterial genome.