Poster Presentation

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T3SS ATPase YsaN. Function and regulation in Yersinia enterocolitica.

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Many Gram negative pathogenic bacteria harbor highly conserved protein export Nano machine known as Type Three secretion system (T3SS). T3SS is essential for interaction with their eukaryotic hosts for establishment of infection. T3SS is composed of approximately 20 different proteins, most of which are present in the inner membrane of the bacteria. Such complex machinery is energized by a unique AAA+ ATPase associated with the cytoplasmic region of T3SS. It is thought that ATPase oligomerization is necessary event for T3SS apparatus formation and activation. So, a complete understanding of T3SS ATPase mechanism and functional insight is required for drug development.

Yersinia enterocolitica has two different T3SSs, one of chromosomal origin and other of plasmidal origin. YsaN, an established ATPase of T3SS (chromosomal origin) from Yersinia enterocolitica is supposed to energize the unfolding and transport of proteins which is yet to be established. YsaN has three domains, the N- terminal domain (probable oligomerization/ regulatory domain), the centrally located ATPase domain and C-terminal domain. The ATPase activity of oligomer (usually hexamer) is greater than its monomeric form. The ATPase activity of YsaN is negatively regulated by dimer of YsaL (a regulator protein) by interaction with its N terminal domain. In this study we are trying to find out the mechanistic insight of YsaN and its regulation by its negative regulator, YsaL.

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