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Thesis Title:

"Insight into the structural and functional characterization of T3SS's chaperone PcrG and

stress response protein PspA"

Abstract:

PcrG (in *Pseudomonas*) is a needle-tip protein chaperone that regulates both the secretion activity of the apparatus and the secretion of effectors from the bacterial cytoplasm into the host cytoplasm. The pmf is primarily responsible for energizing effector export through the Type three secretion system (T3SS). T3SS (Ysc-Yop), a component of *Y. enterocolitica* that is also known to transfer pathogenicity into the host cell, during effector export, which causes envelope stress and activates the Phage shock protein (Psp) system. In the event that a secretin component (YscC) is mislocalized, the PspA (PA3731, in Pseudomonas) protein aids in the maintenance of the membrane. The exact structural and functional information of PcrG and PspA protein of the above-mentioned organism is not entirely clear. In this concern, we address the structural view of PcrG as well as conformational change of PspA using in-silico and biophysical methods. First, the dimeric state of PcrG in solution, its specific and overall interface stability, and issues of its most flexible region are shown, and second, at nearneutral pH, CD, FTIR, and MD simulation reveal a \(\theta\)-like conformational change of PspA are shown here for the first time. We also crystallize and resolve the structure of PspA's stable domain. In addition, we also calculate salt-bridge and aromatic-aromatic interaction where

According to Darwin et al., the function of systems required during host infection in particular, as well as bacterial survival in this environment, is linked with T3SS and PSP systems. Therefore, in this section, we addressed the T3SS chaperone PcrG and the stress response protein PspA of *Pseudomonas aeruginosa* and *Yersinia enterocolitica*, respectively. We believe this work has a long-standing effect that would be applicable to other similar systems.

we see salt-bridge play a very crucial role in protein stabilization.

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