Pathogens modify host cell responses through a paradigm of proteins delivered into the host through a conserved bacterial secretion system. One of the ways cell responses are modified to assure pathogen-specific bacterial protein activation is by the diacylglycerol kinase (DGK) family. DGKs are among the best-studied bacterial effectors and represent broad specificity kinase families that play a role in the development of bacterial infections. The biophysical and structural analysis of the Opg sensor protein from Bacillus subtilis has been performed to better understand the role of this protein in bacterial infection. The structure of Opg from Bacillus subtilis has been solved by X-ray crystallography and the crystal structure reveals that Opg is a typical DGK with a CDP(3')-diacylglycerol binding pocket. The Opg structure provides insights into the mechanism of Opg activation and suggests that Opg interacts with the NefA pathway. Both NefA and Opg exhibit the NEAT pathway, however, their substrates are yet unknown.

Keywords: host-pathogen interactions, bacterial effector kinases

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