

Functional Surprises from the Structures of some *Xanthomonas* Proteins

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Over the past few years, we have determined the structures of a few proteins from the phytopathogen *Xanthomonas axonopodis* pv *citri* (*Xac*). In this short presentation, I will quickly highlight three cases; in two of which the structures revealed details that could not have been predicted from the sequence alone and a third in which significant secondary and tertiary structure differences were observed when compared to the previously determined structures of homologs.

1) *YaeQ* is a well-conserved bacterial protein of unknown function whose crystal structure determined by MAD phasing revealed it to belong to a the PD-(D/E)XK family of metal-dependent nucleases. This finding led us to propose specific hypotheses regarding *YaeQ* function which have found some support from preliminary experimental results.

2) *VirB7* is a hypervariable periplasmic lipoprotein and component of the Type IV secretion system, a machine that transports bacterial macromolecules to the host cell. *Xac* *VirB7* is particularly large, approximately twice as large as *VirB7* subunits from other organisms. Its NMR structure revealed an extra domain that may be involved in intracellular signaling.

3) *PilZ* is a member of a highly variable superfamily of proteins implicated in the binding of cyclic diGMP. The *Xac* *PilZ* protein however shows structural features that set it apart from other *PilZ* proteins of known structure and suggest that the paralogous group to which it pertains may in fact carry out previously non-contemplated functions.