

Tiyakhon Chatnaparat 2012: The Role of *luxR* Homolog of *Xanthomonas axonopodis* pv. *glycines* is Important for Virulent in Soybean. Doctor of Philosophy (Plant Pathology), Major Field: Plant Pathology, Department of Plant Pathology. Thesis Advisor: Associate Professor Sutruedee Prathuangwong, Ph.D. 176 pages.

This study reports the role of a novel *luxR* homolog, *XagR*, in *Xanthomonas axonopodis* pv. *glycines* strain 12-2 (*Xag*), the cause of soybean pustule disease. *XagR* controlled expression of *pip*, proline iminopeptidase; *yapH*, a homolog of *Yersinia* auto- transporter-like protein H; and at least 77 other genes. *XagR* and *Pip* were required for full virulence of *Xag* to soybean while constitutive over-production of *XagR* suppressed infection. The *xagR*-dependent induction of *pip* occurred *in planta* only 2 days or more after inoculation. While the transcription of *xagR* appeared constitutive, *XagR* accumulated only in cells that had colonized soybean plants for more than 2 days. This event suggested that some component(s) produced during the infection process mediated post-transcriptional control, likely by protecting *XagR* from proteolytic degradation. *XagR* modulated the adhesiveness of the pathogen during the infection process by suppressing the adhesin *YapH*. The *yapH* mutant incited more infections of soybean leaves than the wild type strain when topically applied under dry conditions, while it caused fewer infections when leaves were subject to simulated rain events after inoculation. Likewise, *yapH* mutant and strain in which *XagR* was over-expressed exhibited much more egress from infected leaves than the wild type strain. Thus *XagR* differentially modulates expression of a variety of genes during the infection process in response to feedback from plant molecules elaborated during infection to coordinate processes such as invasion, infection, and cell egress needed to complete the disease cycle.

To identify the genes in *Xag*12-2 that are altered in expression during infection of soybean plants compared to growth in a minimal medium *in vitro*, *Xag* draft genome was developed and transcriptome analysis using deep RNA sequencing of mRNA was performed. Of 5062 predicted genes in the *Xag* draft genome, 534 genes were identified as being up-regulated in the plant while 289 were down-regulated. Plant up-regulated genes included the *hrp* cluster, and genes encoding avirulence and type III effector proteins, extracellular enzymes, chemotaxis components, and several other known or new putative virulence factors. Plant down-regulated genes included those involved in attachment and the movement process. This study is the first to report on *Xag* gene expression during infection of soybean and the insights into the behavior of the pathogen should prove useful for developing strategies for controlling disease in this important agricultural crop.

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Thesis Advisor's signature