A LuxR Homolog in a Cottonwood Tree Endophyte That Activates Gene Expression in Response to a Plant Signal or Specific Peptides

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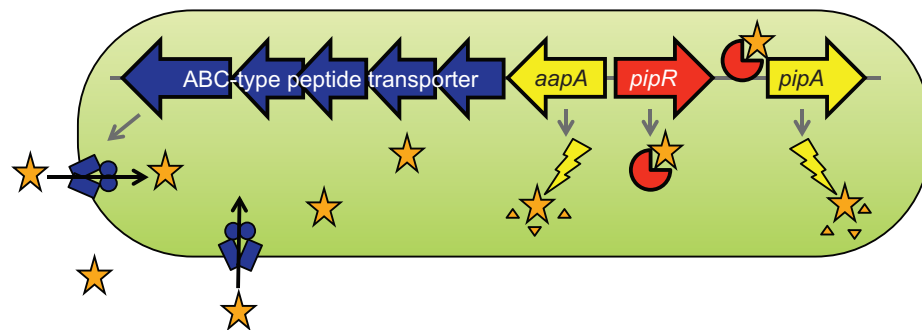
Background

- Many plant-associated bacteria, including those isolated from roots of *Populus*, possess an orphan LuxR homolog (PipR) that responds to an unknown plant signal to control gene expression
- PipR mutants are avirulent in several plant pathogens
- This *pipR* gene is often flanked by predicted peptidase and peptide transporter genes

A model for PipR activation of *pipA* in *Pseudomonas* GM79. The unknown plant/peptone signal(s) (orange stars) are imported via the ABC-type transporter (blue complex). Once in the cell, the signal(s) can bind PipR, converting it to a form capable of binding the *pipA* promoter and activating *pipA,* and possibly *aapA,* resulting in high expression levels of peptidases (yellow bolts). We hypothesize these peptidases act on the signal(s) to reduce activity, thus creating a negative feedback control loop.

Science

- In the *Populus* root endophyte *Pseudomonas* sp GM79, the PipR system is activated by an unknown signal present in plant macerates and peptide-rich material including peptone and a specific tripeptide (ser-his-ser)
- Mutant analyses demonstrated that the *pipR*-linked transporter and peptidases are part of the PipR-signaling system

Significance

- Provides a model integrating how the *pipR*-linked transporter and peptidases contribute to the GM79 PipR-signaling circuit
- Identification of a peptide ligand for GM79 PipR sets the stage to identify plant-derived signals for the PipR family of orphan LuxR receptors, which are present in dozens of bacterial species associated with economically important plants

PMI

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