Defining the metabolic pathway and impact of indole-3-acetic acid on plant-microbe interactions



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Background

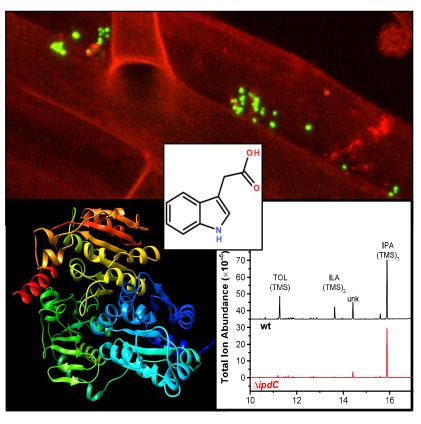
- Many plant-associated microbes, including *Pantoea* sp. YR343, produce the phytohormone indole-3-acetic acid (IAA) which can influence the plant host by induction of plant tissue differentiation, cell division,cell elongation, and lateral root formation.
- Multiple IAA biosynthetic pathways have been described in microbes, but determining which pathway is present in a specific microbe is difficult using genomic analyses alone.

Science

- Through -omics measurements and a targeted gene deletion strategy, we determined the likely IAA biosynthetic pathway in *Pantoea* sp. YR343 and investigated the role of IAA on the physiology and behavior of this microbe.
- Importantly, *Pantoea* sp. YR343 not only synthesizes IAA, but also responds to the presence of IAA by upregulating proteins predicted to function in carbohydrate and amino acid transport and exopolysaccharide (EPS) biosynthesis. Therefore, IAA can act as a signaling molecule in both plants and microbes.

Impact

 Understanding the mechanisms for phytohormone production and its effects on host plants, microbiome organization, and host colonization provides insights into how plants and microbes communicate and informs strategies to influence host performance.



Pantoea sp. YR343 synthesizes IAA using the indole-3pyruvate (IPA) pathway. (Clockwise from top) *Pantoea* sp. YR343 cells expressing GFP (green) colonize plant roots (red). (bottom right) Metabolic profile of wildtype (black) and $\Delta ipdC$ mutant cells (red) showing that disruption of the IPA pathway reduces IAA production. (bottom left) Ribbon structure of indole-3-pyruvate decarboxylase, a key enzyme in the IPA pathway that was deleted in the $\Delta ipdC$ mutant. (center inset) Structure of IAA.



Office of Estenson K, *et al.* 2018. Characterization of indole-3-acetic acid biosynthesis and the effects of this phytohormone on the proteome of the plant-associated microbe *Pantoea* sp. YR343. Journal of Proteome Research 17(4): 1361-1374