Ebb and flow of vascular pathogenesis through gain and loss of a molecular switch

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1. We downloaded 86 complete genomes of beta- and gamma-proteobacteria, focusing on the Xanthomonadaceae
2. We tested for associations between vascular lifestyle and gene family (i.e., orthogroup) presence using BayesTraits
3. We determined the genomic contexts of genes in the most significant orthogroup using bespoke bioinformatic scripts
4. We identified duplications, losses, and horizontal gene transfers (HGTs) affecting the most significant orthogroup using phylogeny and tree reconciliation and hypothesis testing
5. We evaluated pathogenicity of two non-vascular pathogens transformed with genes from the top orthogroup that originated from vascular pathogens

Results

- **celA** is a celllobiohydrolase that is significantly associated with transitions to vascular lifestyles
- **celA** is conserved in vascular pathogens from three distinct genera: Xanthomonas, Xylella, and Ralstonia.
- **celA** is found in 4 distinct genomic contexts
- **celA** has been transferred at least 4 times to what are now vascular pathogens through recombination-mediated HGT
- **celA** has been lost at least 10 times in non-vascular pathogens through TE insertions and sequence deletions
- Heterologous expression of CelA changed tissue-specificity, converting two non-vascular Xanthomonas strains to xylem-colonizing vascular pathogens

Methods

Introduction

- Vascular pathogens of plants and animals move long distances through host veins, leading to systemic infection
- Non-vascular pathogens remain restricted to the site of infection, triggering localized symptom development
- Differences between these modes of infection have important ecological and economic consequences, yet their genetic and biological bases are unclear.
- We aimed to determine the origins of vascular pathogenesis in Xanthomonas, a diverse genus of Gram-negative bacteria that cause vascular and non-vascular diseases in over 200 monocot and dicot plants.

Results

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Discussion

- Rather than representing evolutionary endpoints, our results suggest that Xanthomonadaceae rapidly modulate between vascular and non-vascular lifestyles through gene gain and loss

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Supporting Data

Figure 2. Horizontal gene transfer and loss drive the distribution of celA in vascular and non-vascular bacterial pathogens. Shown to the left is a majority rule consensus tree based on 81 maximum likelihood trees of single copy orthologs that summarizes species relationships among bacteria included in this study. To the right of the tree is a graphic summarizing the presence/absence of the four distinct neighborhoods in which celA is found across each genome, in all cases whether celA is present or not. Transpositions, gains, and losses are numbered and summarized below.

Figure 3: Convergent inactivation of celA in non-vascular pathogens through sequence deletions and transposable element (TE) insertions. Multiple sequence alignment of celA CDS from vascular and non-vascular X. oryzae strains (left) and X. translucens strains (right). SNPs shown in red.

Figure 4: Homologous recombination mediates the insertion of horizontally-acquired celA sequences through TE insertions. Shown above are two maximum likelihood trees with bootstrap support depicting the phylogenetic relationships of sequence flanking an intragenic recombination breakpoint in X. campestris p.v. campestris (vascular)

Check out Poster 192 “A single celllobiohydrolase is required for barley hydathode and xylem colonization by Xanthomonas translucens” presented by Jonathan M. Jacobs for more on celA