

Title:

Phenogenomics reveal ecological drivers of the antagonism against fire blight in *Erwinia tasmaniensis*

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Abstract (300 words maximum): :

Manipulation of native microbiomes is a promising tool to help us achieve more sustainable agricultural practices in our fight against crop pests and diseases, one whose success depends on integral understanding of the mechanisms driving ecological interactions. We used genomics, phenomics and competition assays in an integrative approach to understand the mechanisms behind the antagonism between the causative agent of apple fire blight, *Erwinia amylovora*, and strains from the closely related and non-pathogenic species *Erwinia tasmaniensis*, isolated from flowers in an experimental orchard in Wädenswil where it was found to be the dominant member of the flower community.

The pathogen has slightly smaller genomes than the commensal, which has a larger pangenome despite a much narrower sampling range. This was reflected with a larger phenotypic variability in *E. tasmaniensis* than in *E. amylovora*, which might give it a competitive advantage during floral colonization, although only two out of 190 carbon sources evaluated were commonly utilized by all the commensal strains and none of the pathogenic strains. We found evidence supporting different mechanisms of antagonism. Competition assays showed evidence of cell-to-cell killing with outcomes favourable to the commensal, likely the result of a larger number of T6SS. Both species share a central carbon metabolism and thus are expected to compete in the flower for the most abundant sugars and aminoacids. However, we found differences in the rates of utilization of specific resources, suggesting that each species might succeed under different conditions. Unexpectedly, we identified undescribed pathways for the utilization of pectin and arabinogalactans. We delineate four different microbiome interventions that could help protect the plant host against infection.