

Transcriptomic and proteomic approaches to study bacterial wilt

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Ralstonia solanacearum is a β -proteobacterium that causes bacterial wilt on important crops such as tomato and potato. We applied two complementary approaches to study *R. solanacearum* virulence determinants.

First, we carried out transcriptomic to define the genetic programme deployed by the bacterium to infect plants. We detected expression for >90% *R. solanacearum* genes both from isolated bacteria or *in silico* selected transcripts sequenced from infected plant tissues. Global transcriptional profiling provided insight into the intercellular environment encountered by this plant pathogen and the carbon and energy sources it utilizes during plant infection. In addition, we identified several *R. solanacearum* genes that are significantly up-regulated during infection but had not been previously identified as virulence factors.

Second, we applied activity-based protein profiling to dissect changes in protein activity changes that occur in tolerant or susceptible tomato plants in response to *R. solanacearum*. Our work reveals specific activation of papain-like cysteine proteases and serine hydrolases in the leaf apoplast of the tolerant tomato Hawaii 7996 upon *R. solanacearum* infection. In addition, protein network analysis showed that deeper changes in network topology take place in the susceptible tomato variety, suggesting that the tolerant cultivar might be more prepared to face *R. solanacearum* in its basal state.

Our work will help identifying bacterial virulence genes key for successful plant infection, which can be targets for novel antibacterial drugs, and plant response activities that can assist in breeding for disease resistance.