

Know the enemy - deciphering virulence and pathogenicity determinants of the plant pathogenic bacterium *Acidovorax citrulli*

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Acidovorax citrulli (Ac) is a Gram-negative bacterium that cause bacterial fruit blotch (BFB) of cucurbits, a threatening disease of watermelon and melon industries worldwide. Despite the economic importance of BFB, still little is known about basic aspects of Ac-host interactions. Understanding such aspects is one the main topics of research in our lab. Based on biochemical and genetic features, most Ac strains can be divided into two major groups: group I includes strains that were mainly isolated from melon and other non-watermelon hosts, while group II includes strains that were mostly isolated from diseased watermelon. As similar as several other Gram-negative pathogenic bacteria, Ac requires a functional type III secretion system (T3SS) for pathogenicity. The T3SS injects protein effectors into the plant cells, which collectively manipulate host cellular activities to the pathogen benefit. Due to the crucial role of type III secretion in Ac pathogenicity, we hypothesized that the distinguished host preferential association among group I and II strains, is associated with differences in the repertoire of type III-secreted effectors (T3Es). Indeed comparative analyses of T3E genes from Ac strains isolated from various hosts and geographic locations revealed that overall, T3E genes cluster according to the group I/II classification. These analyses also revealed the existence of a third group of *A. citrulli* strains, which also differed from group I and II strains in other features. We are currently using marker exchange mutagenesis combined with virulence assays, as well as heterologous expression in yeast to assess the role of individual effectors in virulence of Ac. Bioinformatics approaches are also being employed to identify novel putative effectors of this pathogen, and to identify the genetic differences distinguishing between the different groups of Ac by comparative genome analyses. We are also investigating the contribution of other virulence determinants, eg., polar flagella and type IV pili, as well as the phenomenon of phenotypic variation in pathogenicity of Ac.