Session 1 – Oral presentation

Features associated to woody hosts in the bacterial pathogen of olive plants *Pseudomonas savastanoi* pv. savastanoi

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Abstract: The causal agent of olive knot disease, *Pseudomonas savastanoi* pv. savastanoi, belongs to the *Pseudomonas syringae* complex, a bacterial group causing diseases in a broad variety of both woody and herbaceous plant species. Here we summarize our results regarding a set of *P. savastanoi* pv. savastanoi features exclusively found in the genomes of bacteria from the *P. syringae* complex isolated from woody hosts. Comparative genomics and evolutionary studies allowed us to identify a 15 kb genomic island (WHOP, from woody host and *Pseudomonas*), carrying a set of genes involved in degradation of phenolic compounds and exclusively found in bacterial pathogens of woody hosts. Deletion of several WHOP-encoded genes in *Pseudomonas savastanoi* pv. savastanoi NCPPB 3335 revealed that they play a role in the virulence of the strain in woody olive plants but not in *in vitro*-grown (nonwoody) plants. In addition, several type III secretion system effectors belonging to the HopAF, HopAO and HopBL families were shown to be clustered across the *P. syringae* complex according to the woody/herbaceous nature of their host of isolation. Further functional analyses of these virulence factors are needed to facilitate the design of novel strategies directed to control bacterial pathogens of woody hosts.