

Infections & Host-Pathogen Interactions

P167

Comparative Analysis of the Type III Secretion System Effector Repertoires of *Pseudomonas savastanoi* Pathovars Pathogenic on Woody Hosts

Alba Moreno-Pérez¹, M. Pilar Castañeda-Ojeda¹, Jesús Murillo², Emilia López-Solanilla³, Pablo Rodríguez-Palenzuela³, Cayo Ramos¹

¹Instituto de Hortofruticultura Subtropical y Mediterránea «La Mayora», Universidad de Málaga-CSIC, Área de Genética, Universidad de Málaga, Malaga, Spain, ²Departamento de Producción Agraria, ETS de Ingenieros Agrónomos, Universidad Pública de Navarra, Pamplona, Spain, ³Centro de Biotecnología y Genómica de Plantas, Universidad Politécnica de Madrid – Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Parque Científico y Tecnológico de la UPM, Madrid, Spain

The species *Pseudomonas savastanoi*, a member of the *Pseudomonas syringae* complex, includes four pathovars causing knots or excrescences in woody hosts: *P. savastanoi* pv. *savastanoi* (Psv), pv. *fraxini* (Psf), pv. *nerii* (Psn) and pv. *retacarpa* (Psr), comprising isolates from olive, ash, oleander and broom plants, respectively. Pathogenicity of *P. savastanoi* is dependent, among other factors, on the type III secretion system (T3SS) and its effector (T3E) repertoire. Furthermore, a putative role in the interaction with woody hosts has been suggested for several of these T3E. The recent availability of the genome sequences of several *P. savastanoi* strains isolated from different hosts has facilitated bioinformatics predictions of their T3SS genes and T3E pools, the study of their distribution in other strains of the *P. syringae* complex isolated from woody hosts and the functional analysis of several of these secreted proteins. As previously reported for Psv, Psn and Psf, here we show that pathogenicity of Psr ICMP16945, is also dependent on the T3SS. Psv strains NCPPB 3335, ICMP4352 and PseNe107 share a core set of at least 22 T3E, 18 of which are also encoded in Psn ICMP16943, Psf ICMP7711 and Psr ICMP16945. However, these three strains encode truncated versions of 1-2 of these 18 T3E and, Psr ICMP16945 contains three pathovar-specific T3E. Our results also show that several T3E, including HopAO1, are phylogenetically clustered across the *P. syringae* complex according to the woody/herbaceous nature of their host of isolation, suggesting host specialization of these effectors in this complex.