**DYNAMICS OF HETEROGENEOUS POPULATUONS OF *PSEUDOMONAS SYRINGAE* WITHIN PLANT TISSUES REVEAL A DIVERSITY OF INTERACTIONS WITH POTENTIAL EVOLUTIONARY IMPLICATIONS**

1Jose S. Rufián, 2Alberto P. Macho, 3David S. Corry, 4John W. Mansfield, 3Dawn L. Arnold, 1Carmen R. Beuzón

1*Instituto de Hortofruticultura Subtropical y Mediterranea, Universidad de Málaga, Consejo Superior de Investigaciones Científicas (IHSM-UMA-CSIC), Departamento Biología Celular, Genética y Fisiología, Campus de Teatinos, Málaga E-29071. cbl@uma.es*

2*The Sainsbury Laboratory, Norwich Research Park, Norwich NR4 7UH, United Kingdom*

3*University of the West of England. Faculty of Health and Life Sciences. Frenchay Campus, Coldharbour Lane, Bristol BS16 1QY.*

4*Imperial College London. Department of Life Sciences. South Kesington Campus, London SW72AZ*

Bacterial populations have been traditionally assumed to be clonal, and as such, genetically and phenotipically identical. However, research carried out in the last few decades has proven this view naïve. Formation of distinct bacterial subpopulations has been seen to take place under stressing conditions, such as those encountered by pathogenic bacteria within the host, and is often associated to epigenetic changes that give rise to phenotypic heterogeneity without altering the genotype (Casadesús and Low, 2013). A somewhat different example of reversible genomic changes that can affect virulence can be found in *Pseudomonas syringae* pv*. phaseolicola*, the causing agent of halo blight in bean. Inoculation of this bacterium into resistant plants triggers the excision of PPHGI-1, a genomic island encoding the effector that causes the resistance, AvrPphB, from the chromosome (Pitman et al, 2005). In recent years, extensive research has focused on the interaction between individual bacterial strains and the plant host (Dodds & Rathjen, 2010), although little is known about how heterogeneous (or mixed isogenic) bacterial populations of a given pathogen interact and develop with the host plant. In this work, we aimed to analyse how mixed isogenic populations, varying in their virulence, develop within the plant host. Using confocal microscopy, we investigate the cellular basis that determine whether co-existing *P. syringae* bacteria with different virulence capabilities interfere with the growth of each other. Moreover, we analyse the consequences of such interferences on the development of disease and the activation of a defence response.