Phenotypically heterogeneous loci in the plant pathogen *Pseudomonas syringae*

Laura Mancera-Miranda, Nieves López-Pagán, José S. Rufián, María Antonia Sánchez-Romero, Gabriel Gutiérrez-Pozo, Cathrin Spröer, Boyke Bunk, Javier Ruiz-Albert and Carmen R. Beuzón

[1]Instituto de Hortofruticultura Subtropical y Mediterránea, University of Málaga, Consejo superior de Investigaciones Científicas, HSM-UMA-CSIC, Málaga, Spain

[2]Departamento de Microbiología, Facultad de Farmacia, Universidad de Sevilla, Sevilla, Spain

[3]Departamento de Genética, Facultad de Biología, Universidad de Sevilla, Sevilla, Spain

[4]Leibniz Institute DSMZ-German Collection of Microorganisms and Cell Cultures, Braunschweig, Germany

Phenotypic heterogeneity usually refers to the co-existance of different phenotypes within a population. Phenotypic differences may arise through genetic variation (genomic rearrangements or mutations) or through the response to differences in the stimuli as encountered within the microenvironment. But also, sometimes, the sources of variation may not be deterministic, *i.e*. directly related to stimuli, but a consequence of molecular noise in gene expression and/or a programmed event under genetic or epigenetic control. A particular example of phenotypic heterogeneity is bistability. Bistability occurs when a bacterial clonal population splits into two subpopulations showing distinct phenotypes. Phenotypic heterogeneity can be beneficial in fluctuating environments by allowing some individuals within the clonal population to survive sudden changes (risk-spreading). It can also benefit the entire population through cooperation between individuals displaying phenotypic differences (division of labour). These processes and their biological relevance have been described in some animal pathogens, but little is known about them in plant-pathosystems.

Pseudomonas syringae is a plant-pathogenic bacterium whose virulence depends on the expression of a type III secretion system (T3SS). Our team has previously reported that T3SS expression is bistable under inducing conditions, generating two subpopulations ($T3SS^{ON}$/$T3SS^{OFF}$) that show differences in virulence. We have identified other loci including genes related to motility, biofilm formation and DNA methylation that also display phenotypic heterogeneity to very different degrees and with different dynamics and are at different stages on their molecular and biological characterization. Our latest advances on this front will be presented and discussed.