

Bistable expression of relevant genes for *Pseudomonas syringae* virulence

Backgrounds

Heterogeneity or phenotypic variation has been known to take place in microbial clonal populations for decades. Under certain regulatory circuits, heterogeneity in gene expression can be enhanced leading to a bimodal expression profile in homogeneous environments. This process is known as bistability. The relevance of these processes has been demonstrated in *Salmonella enterica* and other human pathogen in the establishment of antibiotic persistence, and it has been shown to affect virulence genes, and to be linked to the establishment of chronic persistence. Nevertheless, little is known about the occurrence or impact of these processes in the adaptation of bacteria to non-animal host.

Objectives

To address the question of whether there is phenotypic heterogeneity in the expression of genes relevant for adaptation to a non-animal host of the model plant pathogen *Pseudomonas syringae*.

Methods

Transcriptional chromosome-located fusion to reporter genes encoding fluorescent protein were constructed in *P. syringae* pv. *phaseolicola*. Genes selected were several encoding different elements of a type III secretion system (T3SS) and flagellin, since motility has been reported as counter-regulated with the T3SS, Expression from these genes was analyzed using single-cell analysis methods, such as flow cytometry and fluorescent microscopy.

Conclusions

We recently showed expression of T3SS genes is phenotypically heterogeneous in planta and becomes bistable under certain laboratory conditions through the action of a double regulatory loop on the transcriptional activator HrpL. We present here single cell analyses of the gene encoding flagellin, as well as its responses to different regulatory proteins.