

GENOMICS AND PLANT/MICROBE INTERACTIONS

Dynamics of plant pathogen infections.

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Plant diseases are generally rare, however when pathogens breach plant constitutive and inducible defences, the consequences can be devastating. We are interested in how pathogens successfully evade plant defences and redirect host metabolism for nutrition. To this end we are taking an integrated systems approach using *Arabidopsis thaliana* and variants of the highly virulent *Pseudomonas syringae* pv. *tomato* strain DC3000 to study the transition from health to disease. Initial studies using time delimited comparative global transcript profiling of basal defence and disease revealed the compendium of genes associated with basal defence responses and those modified by delivery of bacterial effector proteins and associated virulence factors (Truman *et al.* 2006). This unbiased approach unexpectedly revealed a crucial role for abscisic acid (ABA) in pathogenicity. Moreover we were able to show conditional expression of a single bacterial effector, AvrPtoB, was able to activate ABA biosynthesis and suppress genes associated with basal defence (de Torres *et al.* 2007). The role of ABA in plant defence and its interaction with other hormonal signalling pathways will be discussed.

In addition, transcript profiling revealed likely effector driven perturbations in primary and secondary metabolism. We hypothesise that these changes are fundamental to pathogen nutrition during pathogenesis and are currently exploring the transitions in metabolite profiles using a combination of targeted and global (GC & LC-MS/MS, NMR) metabolomic approaches.

Truman *et al.* (2006). Type III effectors orchestrate a complex interplay between transcriptional networks to modify basal defence responses during pathogenesis and resistance. *Plant J.* 46: 14-33.

de Torres-Zabala *et al.* (2007). *Pseudomonas syringae* pv. *tomato* hijacks the *Arabidopsis* abscisic acid signalling pathway to cause disease. *EMBO*, 26, 1434–1443.