

植物ゲノム・遺伝子源解析センター 月例セミナー

とき 平成29年7月21日（金）16時～17時
ところ 農学部 DS304講義室



Dr. Marc Valls

題目「Transcriptomic and Genetic Approaches to Study *Ralstonia solanacearum* Virulence on Plants」

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概略

Ralstonia solanacearum is a β -proteobacterium that causes bacterial wilt on important crops such as tomato and potato. This bacterium survives in soil and waterways, infects plants through the roots, and finally colonises and multiplies extensively in the xylem vessels causing plant death. I will present two complementary approaches that we applied to study *R. solanacearum* virulence determinants.

First, I will describe the characterisation of AWR5, a type III effector secreted by *R. solanacearum*. We found that this effector is an inhibitor of TOR, a central regulator in eukaryotes that controls the switch between cell growth and stress responses in response to nutrient availability. Heterologous expression of AWR5 in yeast caused growth inhibition and autophagy induction coupled to massive transcriptomic changes, unmistakably reminiscent of TOR inhibition by rapamycin or by nitrogen starvation. Detailed genetic analysis of these phenotypes in yeast, including suppression of AWR5-induced toxicity by mutation of CDC55 and TPD3, encoding regulatory subunits of the PP2A phosphatase, indicated that AWR5 might exert its function by directly or indirectly inhibiting the TOR pathway upstream PP2A. We present evidence in planta that this T3E caused a reduction in TOR-regulated plant nitrate reductase activity and also that the bacterial growth inhibition caused by delivery of AWR5 into host cells was mediated by TOR.

Second I will describe the transcriptomic studies carried out to define the genetic programme deployed by the bacterium to infect plants. We detected expression for >90% *R. solanacearum* genes both from isolated bacteria or *in silico* selected transcripts sequenced from infected plant tissues. Global transcriptional profiling provided insight into the intercellular environment encountered by this plant pathogen and the carbon and energy sources it utilizes during plant infection. In addition, we identified several *R. solanacearum* genes that are significantly up-regulated during infection but had not been previously identified as virulence factors.

Our work will help identifying bacterial virulence genes and specific effectors that are key for successful plant infection, which can be targets for novel antibacterial drugs or can assist inbreeding for disease resistance.

主催：香川大学農学部 植物ゲノム・遺伝子源解析センター
(<http://www.ag.kagawa-u.ac.jp/phytogene/index.html>)

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