Australian National University

PhD exit seminar: Identification of strategies for wheat stripe rust pathogenicity by deep transcriptome sequencing

Wednesday 5 June 2013, 1pm

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Slatyer Seminar Room R.N. Robertson Building (Bldg. 46), Linnaeus Way, ANU

Stripe rust is a major constraint to wheat production worldwide. The causal agent is the fungus *Puccinia striiformis f*.sp. *tritici* (*Pst*), a close relative of the pathogens which cause the devastating wheat stem and leaf rust diseases. The fungus makes spores prolifically, which are distributed by wind and rain, and form the basis of the inoculum that causes epidemics. The molecular events that underlie host colonisation are largely unknown. One of the key ways pathogenic strategies of biotrophic fungi is secretion of small proteinaceous virulence molecules called 'effectors', which are suspected to manipulate the physiological and immune responses of host cells during infection. In certain cases the host has evolved to recognize effectors, in which case the recognized effector is called an avirulence protein (Avr) and serves as a signal for the plant to induce defences to block pathogen growth. In my PhD, I extensively investigated *Pst* using genomics, transcriptomics and proteomics techniques to obtain a better understanding of how the pathogen establishes a compatible interaction with its host, and to identify the effector proteins that are synthesised and secreted during infection. Digital gene expression of two contrasting transcriptomes (*in vitro* germinated spores and haustoria from the infectious stage) of *Pst* revealed many differentially expressed genes which highlight key metabolic differences between these cell types, and provide insight into their different roles during infection. Spores rely mainly on stored energy reserves for growth and development, while haustoria extract host nutrients for energy production and biosynthetic pathways to support fungal growth and spore production. Moreover, I have identified the first comprehensive set of potential effector candidate genes of *Pst*, comprised of 437 genes, with two thirds of these up-regulated in haustoria compared to germinated spores. Finally, I have developed a method to isolate highly purified haustoria, which I used for proteomics analysis. This technique will be a useful aid to further effector discovery and *Pst* genome annotation. Together, these studies have substantially increased our knowledge of *Pst* effectors and have provided insights into the pathogenic strategies of this important organism, opening new pathways of research with immense potential in the design of novel disease control strategies.

Presented by

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