

## W0115

**Structural Basis of Plant Disease Resistance in Flax against Flax Rust.** B. Kobe<sup>1</sup>, C.I. Wang<sup>1</sup>, G. Guncar<sup>1</sup>, T. Teh<sup>1</sup>, A.-M. Catanzariti<sup>2</sup>, J.G. Ellis<sup>2</sup>, P.N. Dodds<sup>2</sup>, <sup>1</sup>SMMS/IMB, Univ. of Queensland, Brisbane, Qld 4072; <sup>2</sup>Plant Industry, CSIRO, Canberra, ACT 2601, Australia.

In plants, the innate immune response involves the recognition of pathogen "avirulence" (Avr) proteins by plant resistance (R) proteins. We have focused on the flax-flax rust fungus interaction as a model system to understand the molecular basis of plant disease resistance. In flax, the L5, L6 and L7 resistance proteins recognise the pathogen AvrL567 proteins. AvrL567 proteins from different flax rust strains exhibit different recognition specificities by the corresponding resistance proteins. Yeast-two-hybrid assays suggest direct protein interactions between the R and Avr proteins. We crystallized two different Avr proteins with differing specificities. The structures were solved using SAD phasing on a home X-ray source, with the anomalous signal contributed by bound Co<sup>2+</sup> ions. The proteins have a novel  $\beta$ -barrel fold, explain the specificity of recognition of flax R proteins and suggest possible functions for the Avr proteins in the fungus. The two major topics of discussion will include: (i) implications of using Co<sup>2+</sup> ions for SAD phasing on a home X-ray source, and (ii) implications for understanding the molecular basis and evolution of plant disease resistance pathways.