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Exploiting fungal genomics to minimise blackleg disease of canola

Wednesday 19 June 2013 1.00 – 2pm

Barbara Howlett Professor, University of Melbourne

Slatyer seminar room R.N. Robertson Building (Bldg. 46), Linnaeus Way, ANU



Blackleg caused by the fungus *Leptosphaeria maculans*, is the most important disease of canola worldwide. Field populations of the fungus can 'overcome' resistance within a few years of release of a canola variety. Genome sequencing has revealed the basis of the high evolutionary potential of this fungus. Key disease-related genes (effectors) are housed in unstable genomic regions and thus are easily gained, lost or inactivated during sexual reproduction, which occurs prolifically on canola stubble.

We monitor virulence of blackleg populations in field sites across Australia, and also by the use of high throughput glasshouse and molecular assays. The acquired data are used to predict the risk of breakdown of blackleg resistance and to advise grain growers on suitable canola varieties to sow in their region. In 2012 these approaches enabled farmers on the Eyre Peninsula, South Australia to avoid severe yield losses worth about \$18 million.

Presented by
ANU College of
**Medicine, Biology
& Environment**

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