A 'genome to paddock' approach to control plant disease

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Abstract

Pathogenic fungi evolve in concert with their plant hosts to invade and overcome defence responses. A detailed knowledge of these processes is essential for successful disease management strategies. Blackleg caused by the fungus, *Leptosphaeria maculans*, is the major disease of canola worldwide. In this lecture I describe how field data, such as disease incidence and severity, coupled with information about the biology, molecular genetics and genomics of the blackleg fungus has been exploited to control this important disease.

Field populations of *Leptosphaeria maculans* can evolve and overcome disease resistance bred into canola within three years of commercial release of a cultivar. The risk of breakdown of resistance can be determined by monitoring disease severity of canola cultivars and changes in virulence of fungal populations using high throughput molecular assays that are based on sequences of avirulence genes. Farmers can avoid a predicted epidemic by sowing canola cultivars with different resistance genes in subsequent years. This strategy has been exploited in Australia and has averted substantial yield losses due to disease.