

# Uncovering the genome secrets of the Blackleg fungus

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The genome of the Blackleg fungus, which causes the most damaging disease to canola crops worldwide, has been sequenced for the first time by a team of French and Australian scientists.

Professor Barbara Howlett from the School of Botany at the University of Melbourne, who led the Australian research team, said the discovery was a significant step towards controlling the rampant Blackleg disease.

"The 12,500 genes that constitute the genetic blue print for the fungus *Leptosphaeria maculans* have been identified and now can be mined to discover how this fungus causes the deadly disease," she said.

Blackleg disease can devastate crops and in 2003 caused 90% yield losses in some regions of Australia. The fungus reproduces so prolifically that it develops into genetically diverse populations that can quickly overcome the efficacy of [resistance genes](#) in canola crops.

"We have known for a long time that this fungus can evolve to become virulent and cause disease very quickly. Now we are much better placed to tell farmers which canola varieties they should sow to maximise their yield," she said.

The study published today in the prestigious on-line journal *Nature Communications* also involved researchers from the French National Institute for Agricultural Research (INRA), led by Dr Thierry Rouxel and the Australian Centre for Necrotrophic [Fungal Pathogens](#) in Perth,

Western Australia, led by Professor Richard Oliver.

Using information from the genome sequence, researchers have developed molecular markers that can predict whether [disease outbreaks](#) will occur.

"If an epidemic is predicted then farmers can plant a different canola variety, which will not readily succumb to disease," Professor Howlett said.

The study revealed a unique compartmentalisation of the genome into discrete alternating blocks that are either gene-rich or gene-poor. "Such a feature has not been seen previously in a fungal genome," Professor Howlett said.

"These gene-poor regions have few active genes but those that are present play important roles in the disease."

She said other regions of the [genome](#) are gene-rich and contained the 'housekeeping' genes, the pedestrian but essential genes necessary for an organism to survive.

"What our study revealed is that it is the location of the disease-related genes within the junk DNA which allows the genes to be readily mutated, lost or gained. This enables the blackleg fungus to cause disease outbreaks on canola varieties with particular resistant genes."

"The development of markers using information from the [genome sequence](#) enable us to better target the disease making genes and provide us with better information for crop protection strategies," she said.

These findings feed into a national project led by Professor Howlett and funded by the Grains Research and Development Corporation which is

aimed at developing disease management strategies for canola farmers in a 'genome to paddock' approach.

Provided by University of Melbourne

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