

# Blackleg Disease on Canola in Australia

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## ABSTRACT

Blackleg caused by the fungus *Leptosphaeria maculans* is the major disease of canola in Australia. The major control measure is through the use of disease resistant varieties and Australian cultivars are the most blackleg-resistant spring cultivars in the world. There is a great range of pathogenic variability in isolates of the fungus and changes in sizes of chromosomes of *L. maculans* occur during crosses. This may mean that the fungus can adapt to selection pressure from newly introduced blackleg-resistant varieties.

**KEYWORDS:** *Leptosphaeria maculans*; blackleg-resistant varieties; pathogenic variability

Blackleg, caused by the fungus *Leptosphaeria maculans*, is the most serious disease of canola (rapeseed) in Australia. Rapeseed production began in Australia in the mid 1960's but by 1972, severe blackleg disease epidemics posed a major threat to the industry<sup>1</sup>. During the last decade the industry has resurged dramatically due to the success of locally bred blackleg-resistant cultivars. In the public breeding programs all early generation material is screened in field blackleg nurseries, sown on or adjacent to canola stubble from the previous season. This allows a high proportion of material to be immediately rejected on the basis of insufficient resistance. The latest varieties from breeding programs in Wagga Wagga, New South Wales (Barossa and Oscar) and Horsham, Victoria (Dunkeld and Rainbow) have higher levels of resistance than any previous Australian varieties. Indeed Australian varieties are the most blackleg-resistant spring varieties in the world. Growing resistant varieties is the best control strategy for blackleg, but other precautions that minimise infection and delay any possible breakdown in varietal resistance include growing canola on the same area only once every three years, destroying stubble and volunteer hosts.

Generally the disease has been much more severe in Australia than in Canada and Europe, possibly due to more environmentally favourable conditions in Australia for the fungus to undergo its sexual cycle. Also in Australia most of the isolates are highly virulent, whereas in Canada and Europe weakly virulent *L. maculans* isolates predominate, although in the last few

years, the incidence of highly virulent strains has increased in Canada. Recently we have evaluated 100 field isolates, collected from 12 sites representing major canola-growing regions around Australia, for their virulence on seedlings and adult plants of 12 differential *Brassica* lines. All isolates were highly virulent and could be classified into 14 seedling races. Subsequent evaluation of isolates representing each of the seedling races identified seven adult plant races. There was little relationship between seedling and adult plant reactions, indicating the two characters are distinct. Both race-specific and non-specific adult plant resistance were evident in different *Brassica* differentials to the Australian *L. maculans* isolates <sup>2</sup>.

Little is known about *L. maculans* at a genetic or molecular level, but recently research groups in Canada, France, Germany and Australia have begun to apply molecular approaches to examine the fungus. In Australia we have been studying genome organisation in highly virulent isolates of *L. maculans* using pulsed field electrophoresis, a technique that resolves chromosomal DNA molecules. Like Taylor and Seguin-Swartz's group in Canada<sup>3,4</sup>, we have shown that field isolates have highly variable karyotypes (chromosome complements), but also we have observed that novel-sized chromosomes are produced during crossing <sup>5,6</sup>. This suggests that the genome of the fungus is very 'plastic' (can readily change), and work is underway to see whether this genome 'plasticity' is involved in generating pathogenic variability of the fungus.

The canola industry is expanding rapidly in Australia, with the future looking extremely bright. Breeding for disease resistance will benefit from a better understanding of the host-pathogen interactions between *L. maculans* and *B. napus*. Knowledge of the number and nature of genes involved in resistance and the development of molecular markers, will enhance the effectiveness of selection for blackleg resistance. Likewise, a better understanding is required of the pathogenic variability within *L. maculans* and its propensity for change. Blackleg researchers and canola breeders in Australia and worldwide will benefit from the recent establishment of the International Blackleg Network, developed to foster communication and collaborative research projects among blackleg researchers to advance knowledge of the blackleg pathogen and to reduce its impact on the oilseed *Brassica* industry <sup>7</sup>.

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