Blackleg revisited – races and resistance
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Blackleg disease of canola, caused by *Leptosphaeria maculans*, continues to be a serious
potential limitation to production in western Canada, although resistant varieties and four-year
rotations have controlled the disease very effectively over the past 15 years. Resistance in
Brassica napus may be due to quantitative factors, or to specific resistance genes that interact
with avirulence genes of the pathogen in a gene-for-gene manner. The use of race-specific
resistance to manage the disease has been beneficial; however, due to the pathogen’s ability to
change and adapt, new pathotypes have been observed to arise. Pathogen isolates have been
classified into pathogenicity groups (PGs) based on reactions of two cultivars carrying three
specific resistance genes. At present, as many as 14 specific resistance genes have been
reported. Using a differential set of varieties or lines of Brassica spp., each carrying a specific
resistance gene, the corresponding genes for avirulence in the pathogen can be identified.
Determining the frequency of avirulence genes in the pathogen population allows identification
of races, and the race structure of the pathogen. This information will facilitate the development
of management strategies to control blackleg disease of canola in western Canada.

Blackleg disease of canola (*Brassica napus*), is caused by two *Leptosphaeria* species: *L. maculans* and *L. biglobosa*; however it is *L. maculans* that is responsible for significant yield
loss of canola or oilseed rape worldwide. In western Canada, losses up to 50% have been
reported in individual fields (Gugel and Petrie 1992). Resistant varieties and four-year rotations
have controlled the disease very effectively in western Canada over the past 15 years. These
measures reduced the yield and quality losses associated with the disease but did not eliminate
the pathogen. By the late 1990s, evidence of virulence changes in the pathogen was observed
(Keri et al. 2001) and in recent years producers have reported high disease severity in
previously resistant varieties.

Resistance in *B. napus* to *L. maculans* may be quantitative or qualitative (Delourme et al. 2006).
Quantitative resistance is inherited polygenically and varieties carrying significant quantitative
resistance have reduced severity of basal stem cankers at the adult plant stage compared to
susceptible varieties. Qualitative resistance in *B. napus* is controlled by specific resistance
genes (Ansan-Melayah et al. 1998), which are effective at the site of infection on leaves as early
as the cotyledon stage. Evaluation of resistance due to specific resistance genes is conducted
using the cotyledon evaluation test method. Specific resistance genes in the host (*B. napus*)
interact with corresponding avirulence (*AvrLm*) genes of the pathogen in a gene-for-gene
manner (Flor 1942).

Early research on blackleg suggested that varietal resistance was quantitative because the
variation in response between pathogen isolates and *B. napus* lines was continuous, i.e.
differential reactions were not observed (Thurling and Venn 1977). However, further studies
found evidence of genetic variation in resistance of *B. napus* and *B. rapa* to the pathogen
(differential interactions) and indicated variation in virulence among isolates or populations of *L. maculans* from different countries (Newman 1984). Detection of differential interactions is
evidence for the presence of specific resistance genes. Differential interactions are observed
when a series of host genotypes are inoculated with a series of pathogen isolates that differ in
virulence. For example, reactions on ‘Westar’ differentiate *L. biglobosa* (resistant reaction) from
*L. maculans* (susceptible reaction) and differential interactions among isolates of *L. maculans*
have been observed when inoculated onto two varieties of *B. napus* ‘Quinta’ and ‘Glacier’
This is the basis for the differentiation of isolates into pathogenicity groups (PGs) (Mengistu et al. 1991).

**Figure 1.** Differential interactions observed among three varieties of *B. napus* canola in response to a single isolate of *L. maculans*. The susceptible reaction on the variety 'Westar' indicates the isolate is *L. maculans* and the susceptible reaction on ‘Glacier’ and resistant reaction on ‘Quinta’ indicates this isolate belongs to pathogenicity group 3 (PG3).

The PG classification system was of benefit to detect changes in virulence of the pathogen population (Chen and Fernando 2006, Kucher et al. 2007). Isolates of *L. maculans* from Manitoba and Saskatchewan collected in the late 1980’s were found to be PG2: avirulent on ‘Quinta’ and ‘Glacier’ (Kucher et al. 1993). In 1998, a new pathotype, PGT was reported from western Canada, which was virulent on ‘Quinta’ but avirulent on ‘Glacier’ (Keri et al. 2001) and in 1999 a single PG3 isolate (avirulent on ‘Quinta’, virulent on ‘Glacier’) was isolated from southern Manitoba (Kucher et al. 2007) (Figure 2). Since that time other PG3 isolates have been documented (Fernando and Chen 2003) and isolates able to elicit a susceptible reaction on both ‘Quinta’ and ‘Glacier’ (PG4) reported (Bradley et al. 2005, Chen and Fernando 2006).

It is possible to differentiate only four PGs of *L. maculans* when two varieties are used based on two reactions (resistant or susceptible). This means the PG system cannot identify variability among isolates as a result of sources of resistance not found in ‘Quinta’ and ‘Glacier’. Fourteen specific resistance genes have been reported (Rimmer 2007), which have been designated: *Rlm1* to *Rlm10* and *LepR1* to *LepR4*. By using varieties or lines of *Brassica* spp. carrying these 14 resistance genes isolates of *L. maculans* can be differentiated or characterized into races based on the reactions observed. A study of 96 western Canadian isolates of *L. maculans* using ten resistance genes indicated considerable variation in the pathogen population for many of these genes (Kucher et al. 2010) (Figure 3).
Figure 2. Percentage of 244 isolates of *Leptosphaeria maculans* in each pathogenicity group (PG). Isolates collected from infected canola stubble in western Canada in 1998 to 2000.

Figure 3. Percentage of 96 isolates of *Leptosphaeria maculans* from western Canada carrying each avirulence gene. Isolates were collected between 1997 and 2005.
Knowledge of avirulence genes in the pathogen population across the Canadian prairies and in other oilseed rape growing regions of the world benefits pathologists, breeders and farmers in choosing strategies to manage blackleg resistance. From the frequency of individual avirulence genes it is possible to deduce the presence of corresponding resistance genes in commercially grown varieties. Detection of races of *L. maculans* that can overcome the resistance of current varieties of canola might be used to make recommendations to canola growers to consider the use of different varieties, if the specific resistance genes of the varieties are known. The presence of specific resistance genes in varieties of *B. napus* can be determined by using isolates of *L. maculans* in which avirulence genes have been identified. This has been done in many European oilseed rape varieties (Rouxel et al. 2003) and some investigation of Canadian varieties has been conducted (Kutcher et al. 2008).

New resistance genes could be identified in *Brassica* spp. by using combinations of *L. maculans* isolates that overcome all currently characterized resistance genes. It might also be possible to identify levels of quantitative resistance in a *Brassica* variety even if it carries an effective major gene by using both an isolate without the corresponding avirulence allele and a pathological test able to characterize quantitative resistance. Combining effective specific resistance in a background of good quantitative resistance may provide an improved method of managing blackleg disease rather than relying only on single specific resistance genes. This strategy is used in France, where detailed information on management of resistance to blackleg, including mention of the type of resistance (qualitative, quantitative or both), identification of the specific resistance gene carried by varieties and whether that resistance has been overcome or remains effective, is available to growers and industry (CETIOM 2009).

Use of specific resistance has been observed to be very effective in controlling blackleg (Howlett 2004). However, in Europe and Australia populations of *L. maculans* were noted to rapidly adapt to selection pressure as a result of the use of the same specific resistance gene in many popular varieties that were seeded over large areas. The use of specific resistance genes to combat blackleg disease in canola or oilseed rape is relatively recent, approximately 15-20 years in western Canada. Studies of *L. maculans* isolates collected worldwide have indicated that many of the single resistance genes identified at the present time have been overcome in one or more continents (Dilmaghani et al. 2009).

To effectively employ specific resistance genes, either alone or in a background of quantitative resistance, the pathogen must be monitored at regular intervals to detect races with the ability to overcome current resistance genes before varieties fail. The durability of specific resistance genes depends on the size of the *L. maculans* pathogen population, which is directly related to the amount of diseased *B. napus* residue. A larger pathogen population will result in the multiplication of a greater number of virulent isolates. Cultural practices, particularly less intensive rotation of *B. napus* (Kutcher and Brandt 2009), should be recommended to preserve resistance durability.

The canola industry in Canada and in other countries has benefited from the successful development of varieties resistant to *L. maculans*, often due to incorporation of specific genes for resistance. Loss of resistance in France and Australia due to dependence on specific resistance genes however, has demonstrated that specific resistance genes exert strong selection pressure on pathogen populations. Monitoring of *L. maculans* populations for shifts in virulence should provide advance warning of new virulent races with the potential to overcome specific resistance genes. The use of management strategies such as variety selection or rotation of resistance genes over time, in combination with good quantitative resistance and best agronomic practices will be needed to manage blackleg for successful canola production.
References


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