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Utilisation of host resistance to manage blackleg of canola in South Africa

***Huibrecht Schreuder*[1]**

Gert Van Coller[2]
Diane Mostert[1]

[1] Stellenbosch University, Stellenbosch, South Africa

[2] Western Cape Department of Agriculture, Elsenburg, South Africa

Background:

Blackleg, caused by *Leptosphaeria maculans* and *L. biglobosa*, is a major constraint in South African canola production. Genetic resistance is one of the most efficient ways to manage blackleg, but due to a lack of knowledge on the pathogen population present in South Africa, it is currently not being utilised effectively.

Objective:

The aims of this study were to obtain data on the avirulence race structure of the local pathogen population and to determine the blackleg resistance of all commercially available cultivars in South Africa in the two canola production regions (Southern Cape and Swartland).

Methods:

The genomes of 34 *L. maculans* isolates representative of the two production regions were sequenced. The identity and distribution of avirulence gene alleles were determined in these isolates.

Cultivar trials that included all commercially available cultivars, were established at two locations in 2021 and four locations in 2022. Blackleg severity ratings were done before harvest and the disease severity index (DSI) calculated.

Results:

The frequencies of avirulence alleles were consistent between the different locations and strongly reflected the cultivars grown in South Africa over the last ten years. The qualitative resistance genes predominant in cultivars planted over the last ten years have been overcome by more than 90% of the isolates.

Significant differences in DSI were found between cultivars at all locations, with cultivars performing similar within regions. Even though the genome data have shown that all local isolates have the virulent phenotypic expression of AvrLm3, cultivars with the corresponding resistance gene (Rlm3) had the lowest DSI. All cultivars included in the trials were Australian cultivars and because there is also no major gene resistance in Australia against AvrLm3, these cultivars have been bred to have good quantitative resistance.

Conclusions:

The data from this study show that none of the cultivars planted in South Africa have resistance genes corresponding to the avirulent expression of avirulence genes in the pathogen population and that qualitative resistance is, therefore, not being utilised in South Africa. The resistance of cultivars as exhibited in the cultivar trials is due to quantitative resistance.