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Genetic Mapping and Characterisation of the Novel Blackleg Resistance Genes LepR5 and LepR6

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Control of blackleg disease in canola/rapeseed crops worldwide relies primarily on genetic resistance, which despite the large number of race-specific R genes available to breeding programs, has become eroded over time due to the adaption of pathogen populations. Work carried out at Agriculture & Agri-Food Canada's Saskatoon Research Centre, in conjunction with a consortium of industry partners, has identified two novel blackleg R genes through the detailed phenotypic evaluation of a collection of domesticated and exotic *B. napus* germplasm. A set of highly-characterised *L. maculans* isolates were used to tease the novel R genes away from other known R genes present in the material. LepR5 and LepR6 have been genetically mapped to chromosomes A01 and C03, respectively, in locations independent of other known blackleg R genes or QTL. Characterisation of these genes using a worldwide collection of historic and modern *L. maculans* isolates, along with a set of transgenic isolates representing most known avirulence genes, has proven LepR5 and LepR6 to be both novel and highly-effective resistance sources for incorporation into modern *B. napus* cultivars.

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