

# Genetics of root-lesion nematode resistance in wheat: A review

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## Abstract

Root-lesion nematodes (RLN) are one of the most widespread and devastating plant parasitic nematodes species globally. In Australia, RLN species *Pratylenchus thornei* and *P. neglectus* are particularly important biotic constraints to wheat production. The most efficient and effective strategy for improving on-farm RLN management relies on providing wheat growers with cultivars with better levels of resistance to RLN to ensure high yields and reduce the build-up of nematode populations to invade subsequent crops. Current research efforts in Australia are focused on the genetic characterization and introgression of superior sources of resistance into commercial wheat cultivars. Studies on the inheritance of *P. thornei* resistance in wheat have revealed polygenetic and additive gene action. Superior resistance has been identified from a wide range of backgrounds, including landrace and synthetic hexaploid wheats (ABD genomes), and wild diploid (D and A genomes) and tetraploid (AB genomes) genome donors. Effective sources of dual resistance to *P. thornei* and *P. neglectus* have been identified in synthetic hexaploid wheat. A single gene conferring resistance to *P. neglectus*, *Rlnn1*, has been mapped to chromosome 7AL. QTL analysis in several bi-parental mapping populations has identified major QTL for *P. thornei* resistance on chromosomes 2BS, 6DS and 7BL, which have been verified in sources of resistance from diverse backgrounds. Genotyping-by-sequencing has provided closely linked flanking markers that are now available to Australian breeders through the Australian Wheat and Barley Program to implement marker-assisted selection.

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