Genetic analysis of *Pyrenopeziza brassicae*, cause of light leaf spot of brassicas, in the European Union, Oceania, and North America.

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Light leaf spot (LLS), caused by *Pyrenopeziza brassicae,* is an important disease of *Brassica napus* (canola and oilseed rape) and *B. oleracea* (vegetable brassicas) in Europe (EU) as well as New Zealand and Australia (Oceania, OC). LLS was first reported in North America (NA) on *B. juncea, B. napus,* and *B. rapa* in six counties in western Oregon in 2014; and on *B. juncea* cover crops and wild *B. rapa* in three counties in northwestern Washington in 2016. Multi-locus sequence analysis (ITS ribosomal DNA, beta-tubulin, and elongation factor 1-α sequences) and comparison of the mating type genes (*MAT1-1* and *MAT1-2*) grouped isolates from the EU (n = 28) and OC (n = 4) with the *P. brassicae* type specimen, IMI 204290, whereas isolates from NA (n = 16) represented a novel genotype. Sexual compatibility of NA and EU strains of complementary *MAT1-1* and *MAT1-2* genotypes is being determined to assess if NA isolates represent a distinct evolutionary lineage or a cryptic sibling species. Fungicide resistance has been documented in some EU populations of *P. brassicae*, but none of the NA isolates possessed amino acid substitutions E198A and L240F in the beta-tubulin sequences that confer resistance to benzimidazole fungicides; comparison of these sequences for the NA isolates revealed 100% identity to wild type EU *P. brassicae* isolates and the closely related fungus *Rhynchosporium commune*; and 98 and 99% identities to *Sclerotinia sclerotiorum* and *Venturia inaequalis*, respectively.