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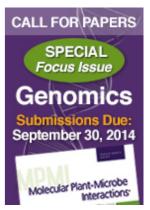
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During 2010 and 2011, Dothistroma needle blight (DNB), also known as red band needle blight, was observed for the first time in Cass and Pembina counties in North Dakota (ND). In Pembina Co., DNB was observed in two sites in the Jay V. Wessels Wildlife Management Area (JWWMA). In September 2009, yellow spots on green needles were observed on some trees along the western edge of one planting. By June 2010, DNB was found on third- and fourth-year needles in both JWWMA plantings. Symptoms had developed into dark brown bands or spots on necrotic needles that contained erumpent black acervuli. In June 2011, similar DNB symptoms were observed on Pinus nigra, P. flexilis, P. ponderosa, P. cembra, and P. albicaulis in the Dale E. Herman Research Arboretum, Cass Co., ND. DNB was collected in July 2011 in Brookings Co., South Dakota (SD), from a seed source provenance planting of P. ponderosa. To identify the species causing the infections, symptomatic needles were collected in 2010 from both sites in JWWMA and then again from all four locations in 2011 on all pine species infected. Needles of P. nigra from a private residence near Fairland in Shelby County, Indiana (IN), were also included in the sample set. The rDNA-ITS was PCRamplified either directly from conidia obtained from acervuli on the needles or from cultures obtained from isolations. Amplicons were sequenced and a BLAST search was performed in GenBank. The sequences of samples obtained from P. nigra, P. flexilis, P. cembra, and P. albicaulis in ND, P. ponderosa in SD, and P. nigra from IN showed 100% sequence homology with Dothistroma pini (Accession No. AY808302). These isolates were identical to all previously assayed isolates of D. pini from Nebraska, Minnesota, and Michigan in the United States. The P. ponderosa isolates from all three sites in ND differed from the other isolates and contained a 1-bp point mutation from a C to a T at site 72 (sequence deposited in GenBank, accession KJ933441). Mating type was determined using species-specific mating type primers for D.



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pini (3). All 26 samples from ND and SD were of the MAT-1 idiomorph, while the sample from IN contained the MAT-2 idiomorph. All cultures are maintained at FABI, University of Pretoria, South Africa. The two species that cause DNB, D. septosporum (G. Dorog.) M. Morelet and D. pini Hulbary, are morphologically indistinguishable and molecular characterization remains essential for correct species identification (1). Host and geographical distribution range determinations of Dothistroma spp. made without molecular methods are not valid. To date, species confirmed using DNA sequences in the United States include D. septosporum in the Pacific Northwest states of Oregon and Idaho on P. ponderosa, in Montana on P. contorta v. latifolia, and D. pini in the North Central states of Nebraska, Minnesota, and Michigan on P. nigra (1). This study documents the presence of D. pini in three additional states, including a first report of DNB in ND and SD. It also includes new records of D. pini infecting P. flexilis, P. cembra, P. albicaulis, and P. ponderosa. Results of this study have expanded the documented host range of D. pini in the United States from one (P. nigra) to five species. Globally, D. pini is now known to infect a total of 10 pine hosts (2,4,5).

References: (1) I. Barnes et al. Stud. Mycol. 50:551, 2004. (2) I. Barnes et al. For. Pathol. 41:361, 2011. (3) M. Groenewald et al. Phytopathology 97:825, 2007. (4) D. Piou et al. Plant Dis. 98:841, 2014. (5) B. Piskur et al. For. Pathol. 43:518, 2013.





