

Population genetic structure of the seed pathogen *Pyrenophora semeniperda* on *Bromus tectorum* in western North America

David Boose

Department of Biology, Gonzaga University, 502 East Boone Avenue, Spokane, Washington 99258

Steven Harrison

Department of Plant and Wildlife Sciences, 275 WIDB, Brigham Young University, Provo, Utah 84602-5183

Suzette Clement

Susan Meyer

U.S. Forest Service, Rocky Mountain Research Station, Shrub Sciences Laboratory, 735 North 500 East, Provo, Utah 84606-1856

Abstract: We examined genetic variation in the ascomycete pathogen *Pyrenophora semeniperda* cultured from seeds of the invasive grass *Bromus tectorum* in the Intermountain West of North America. We sequenced the internal transcribed spacer (ITS) region of the nuclear ribosomal RNA genome in 417 monoconidial cultures collected from 20 sites in Washington, Idaho, Utah and Colorado, USA. ITS sequence diversity was surprisingly high; 12 unique haplotypes were identified, averaging 1.3% pairwise sequence divergence. All sites had at least two haplotypes present, and three sites had seven or more. One haplotype composed 60% of the isolates and occurred at all 20 locations; the remaining haplotypes generally occurred at low frequencies within sites but at multiple sites throughout the region. Sites in Washington and Idaho were more diverse than those in Utah and Colorado, averaging two more haplotypes and 67% more pairwise differences among haplotypes at a site. Analysis of molecular variance (AMOVA) indicated that more than 80% of the genetic variation was found within sampling locations, while 7–11% of the variation can be attributed to differences between northern (Washington and Idaho) and southern (Utah and Colorado) populations. The wide distribution of even uncommon haplotypes among sampling sites and weak correlations between genetic and geographic distances among populations ($r = 0.2$) suggested that these populations recently were established from a common source. We hypothesize that the strains of *P. semeniperda* infecting *B. tectorum* in western North America probably arrived with the invasive grass from its native Eurasian range.

Key words: analysis of molecular variance (AMOVA), ascomycete, *Drechslera campanulata*, genetic diversity, internal transcribed spacer (ITS), invasive species, ribosomal RNA