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FIRST OCCURRENCE OF MELOIDOGYNE FALLAX IN NORTH AMERICA, AND MOLECULAR CHARACTERIZATION OF M. FALLAX AND M. MINOR FROM U.S. GOLF COURSE GREENS. **Skantar, Andrea M.[1], C. Nischwitz[2], Z.A. Handoo[1], M.N. Hult[1], M.E. Schmitt[3], and M.A. McClure[3].** [1] USDA-ARS Nematology Laboratory, Beltsville MD 20705; [2] Department of Biology, Utah State University, Logan UT 84322; and [3] School of Plant Sciences, University of Arizona, Tucson, AZ 85721.

Several species of root-knot nematodes (*Meloidogyne* spp.) are known to have significant presence on turfgrass in golf course greens, especially in the western United States. Nematodes isolated from a golf course in King County, WA, were identified as *Meloidogyne minor* based on analysis of the large ribosomal subunit (LSU 28S D2-D3 expansion segment), the internal transcribed spacers 1 and 2 (ITS-rDNA), the intergenic spacer region 2 (IGS2) and the nuclear protein-coding gene Hsp90. Sequence-characterized amplified region (SCAR) primers that were previously designed to be specific for *M. fallax* were found to cross-react with *M. minor*. A population from California was determined to be *M. fallax* based on juvenile tail morphology and analysis of the ribosomal markers and Hsp90. Using trees based on Hsp90 genomic alignments, the phylogenetic relationships of these populations and known root-knot nematode species were congruent with previous trees based on ribosomal genes. Resolution of *M. fallax* and *M. chitwoodi* using Hsp90 was equivalent to species separation obtained with 28S or 18S rDNA alignments. The strengths and weaknesses of ribosomal and Hsp90 markers, and the use of SCAR PCR as diagnostic tools also are discussed.