

NEW REPORTS AND MOLECULAR DIAGNOSTICS OF ROOT-KNOT NEMATODES FROM GOLF COURSE GREENS IN THE WESTERN UNITED STATES. **Skantar¹, A.M., C. Nischwitz², Z.A. Handoo¹, S. Subbotin³, M.N. Hult¹, M.E. Schmitt⁴ and M.A. McClure⁴.** ¹ USDA-ARS Nematology Laboratory, Beltsville, Maryland, 20705; ² Dept. of Biology, Utah State University, Logan, Utah, 84322; ³ California Department of Food and Agriculture, Sacramento, California 95832; ⁴ School of Plant Sciences, University of Arizona, Tucson, Arizona 85721.

Several species of root-knot nematodes (*Meloidogyne* spp.) are known to occur on turfgrass. A survey of 238 golf courses in the Western United States found root-knot nematodes in 60% of putting greens sampled. Morphology and phylogenetic trees inferred from multiple DNA markers were used to identify specimens from 110 golf courses. *Meloidogyne naasi* was the most common species, distributed from coastal Southern California to Washington; *Meloidogyne graminis* and *Meloidogyne marylandi* were found mostly in the warmer regions of the Southwest. PCR-RFLP of a mitochondrial DNA region distinguished these two species, providing a simple method for future diagnosis of these nematodes from turf. Specimens from two golf courses in Washington were identified as *Meloidogyne minor* based on analysis of the 28S, ITS1&2, and IGS2 ribosomal markers and the nuclear protein-coding gene Hsp90 sequences. Sequence-characterized amplified region (SCAR) primers previously reported as specific for *Meloidogyne fallax* were found to cross-react with *M. minor*. A population from California was determined to be *M. fallax* based on juvenile morphology and analysis of the ribosomal markers and Hsp90. The phylogenetic relationships of these populations and known root-knot nematode species reconstructed using Hsp90 gene sequences were congruent with those obtained from ribosomal RNA genes. Resolution of *M. fallax* and *Meloidogyne chitwoodi* using Hsp90 was equivalent to species separation obtained with 28S rDNA alignments. The strengths and weaknesses of ribosomal and Hsp90 markers, and the use of SCAR PCR as diagnostic tools will also be discussed.