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## COI haplotype groups in *Mesocriconema* (Nematoda: Criconematidae) and their morphospecies associations

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### Abstract

Without applying an *a priori* bias for species boundaries, specimen identities in the plant-parasitic nematode genus *Mesocriconema* were evaluated by examining mitochondrial COI nucleotide sequences, morphology, and biogeography. A total of 242 specimens that morphologically conformed to the genus were individually photographed, measured, and amplified by a PCR primer set to preserve the linkage between specimen morphology and a specific DNA barcode sequence. Specimens were extracted from soil samples representing 45 locations across 23 ecoregions in North America. Dendrograms constructed by neighbor-joining, maximum likelihood, and Bayesian Inference using a 721-bp COI barcode were used to group COI haplotypes. Each tree-building approach resulted in 24 major haplotype groups within the dataset. The distinctiveness of these groups was evaluated by node support, genetic distance, absence of intermediates, and several measures of distinctiveness included in software used for the exploration of species boundaries. Five of the 24 COI haplotype groups corresponded to morphologically characterized, Linnaean species. Morphospecies conforming to *M. discus*, *Discocriconemella inarata*, *M. rusticum*, *M. onoense*, and *M. kirjanovae* were represented by groups composed of multiple closely related or identical COI haplotypes. In other cases, morphospecies names could be equally applied to multiple haplotype groups that were genetically distant from each other. Identification based on morphology alone resulted in *M. curvatum* and *M. ornatum* species designations applied to seven and three groups, respectively. Morphological characters typically used for species level identification were demonstrably variable within haplotype groups, suggesting caution in assigning species names based on published compendia that solely consider morphological characters. Morphospecies classified as *M. xenoplax* formed a monophyletic group composed of seven genetically distinct COI subgroups. The spe-

cies *Discoicriconemella inarata* is transferred to *Mesocriconema inaratum* based on its phylogenetic position on the COI tree as well as previous phylogenetic analyses using 18S, ITS1, and cytochrome b nucleotide sequences. This study indicates that some of the species considered cosmopolitan in their distribution are actually multispecies polyphyletic groupings and an accurate assessment of *Mesocriconema* species distributions will benefit from molecular determination of haplotype relationships. The groups revealed by COI analysis should provide a useful framework for the evaluation of additional *Mesocriconema* species and will improve the reliability of designating taxonomic units in studies of nematode biodiversity.

**Key words:** DNA barcode, identification, North America, plant-parasitic nematode, taxonomy

## Introduction

Nematodes are frequently cited as a major source of undiscovered biodiversity on earth (Creer *et al.* 2010; Wilson 2007). The vivid imagery evoked by N.A. Cobb (1915) of a world covered by a film of nematodes has permeated popular science literature and reinforces the impression of remarkable nematode abundance and diversity (White 1998). Yet in spite of the popular perception, there are surprisingly few described species when compared to other groups of invertebrates (Bik *et al.* 2012). A recent accounting of described species in the phylum Nematoda at 24,783 is conservatively believed to represent 5–10% of extant species (Hodda 2011). One contributing factor to this relatively low number of described species may be the actual process of species delimitation typically used in the description of a new nematode species. A large percentage of nematode species have been characterized solely on the basis of a comparatively small set of morphological characters and measurements. Species delimited in this fashion have been called morphospecies. The delimitation process in nematology is seldom articulated, although it generally involves the search for discriminating morphological characters. Discriminating or diagnostic characters often are identified by the authors as those that exceed the known range of a morphometric variable, or combine measurements in a novel form to satisfy implicit criteria of diagnosability. If no morphologically diagnosable characters are identified, the species is assumed to be conspecific with an existing nominal species. Given the limited set of available morphological characters easily resolved by light microscopy, this approach has resulted in the recognition of a large number of cosmopolitan species (Artois *et al.* 2011).

The addition of DNA characters to the discovery process has revealed that many of these cosmopolitan species may actually consist of multiple genetically distinct subgroups (Kiontke *et al.* 2011; Nadler, S.A. & Pérez-Ponce De León, G. 2012). In this study we examined North American species in the plant-parasitic nematode genus *Mesocriconema* Andrassy, 1965. Worldwide this genus has 90 valid species (Geraert 2010). Approximately 24 species are reported from North America. Among the North American species are five morphospecies that could be considered worldwide in distribution. These species, *M. curvatum* (Raski, 1952) Loof & DeGrisse, 1989, *M. ornatum* (Raski, 1958) Loof & DeGrisse, 1989, *M. rusticum* (Micoletzky, 1915) Loof & DeGrisse, 1989, *M. sphaerocephalum* (Taylor, 1936) Loof & DeGrisse, 1989, and *M. xenoplax* (Raski, 1952) Loof & DeGrisse, 1989 are predominantly associated with agricultural plant hosts, and it is this association that is assumed responsible for their present-day cosmopolitan distribution (Wouts 2006). These species, however, are not confined to agricultural hosts, and surveys of native plant communities also record their presence. Another potential factor contributing to their perceived cosmopolitan distribution is the relatively early dates of their descriptions. All five species were described prior to 1952, a time when only 21 species were listed as belonging to the genus *Criconemoides* Taylor, 1936. Early records of occurrence leading to present-day perception of global distributions may actually reflect the limited options available in early keys, “fuzzy” species boundaries, or assumptions of identity biased by plant host association. For example, a criconematid species associated with peach in the southeastern U.S. might automatically be assumed to be *M. xenoplax*, based on that species’ role in the disease complex called peach tree short-life (Nyczepir *et al.* 1985).

Our study encompasses collections from within 23 of the 118 North American World Wildlife Federation (WWF) ecoregions (Olson *et al.* 2004) including both native plant communities and cultivated soils (Table 1). From these soils we have extracted and analyzed specimens morphologically conforming to the genus *Mesocriconema*. Each specimen is measured, photographed, and then processed for PCR by primers that permit nucleotide sequencing of a 721-bp portion of the mitochondrial COI gene. This approach preserves the link between specimen morphology and COI haplotype, and allows us to link morphologically distinct juvenile and

difficulties in identification and the recognition of species boundaries. Obvious examples include the variation in labial plates in SEM face views, the degree of crenation on annule margins of juveniles, the size of the projections in the anterior lip of the vulva, and the interpretation of the shape of the vagina. These diagnostic morphological characters need to be systematically re-evaluated within the context of molecularly derived groupings in order to fully realize the information content of the taxonomic units. That realization will, in turn, allow nematode taxonomy to better integrate with and contribute to larger questions of global biodiversity.

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