



## An integrative taxonomic approach to the identification of three new New Zealand endemic earthworm species (Acanthodrilidae, Octochaetidae: Oligochaeta)

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### Abstract

This work adds three new species to the ca. 200 currently known from New Zealand. In Acanthodrilidae is *Maoridrilus felix* and in Octochaetidae are *Deinodrilus gorgon* and *Octochaetus kenleei*. All three are endemics that often have restricted ranges; however, little is yet known of their distribution, ecology nor conservation status. DNA barcoding was conducted, which is the first time that New Zealand endemic holotypes have been so characterized. The barcoding region COI (cytochrome c oxidase subunit 1) as well as the 16S rDNA region were sequenced using tissue from the holotype specimen to provide indisputable uniqueness of the species. These DNA sequences are publically available on GenBank to allow accurate cross checking to verify the identification of other specimens or even to identify specimens on the basis of their DNA sequences alone. Based on their 16S rDNA sequences, the position of the three newly described species in the phylogeny of New Zealand earthworms was discussed.

The description of new species using this approach is encouraged, to provide a user-friendly identification tool for ecologists studying diverse endemic faunas of poorly known earthworm species.

**Key words:** Morphological description, DNA barcoding, phylogeny, COI, 16S rDNA

### Introduction

The definitive study of New Zealand earthworms by Ken Lee (1959) was updated and checklisted by Blakemore (2004, 2006) as modified by Blakemore in Lee *et al.*, (2000). While the enduring work by Lee (1959) listed approximately 193 species, the current list has about 200 taxa with natives now given separate family status in either Acanthodrilidae, Octochaetidae or Megascolecidae *sensu* Blakemore (2000).

Because of this high diversity, ecological studies focusing on New Zealand earthworms require the expertise of a taxonomist for accurate identification of the species. Indeed, earthworm taxonomy is based on complex and variable morphological diagnostic characters, which require a high level of expertise (Pop *et al.*, 2007).

Modern molecular-based species identification is a promising way for researchers with basic molecular knowledge to identify earthworm species using barcoding regions of the genome (Pop *et al.*, 2007). However, this requires a comprehensive database of earthworm DNA sequences. More than 6,000 species of earthworm have been named to date and this figure is continuously growing as illustrated in the current study. At the same time, the Genbank database (<http://www.ncbi.nlm.nih.gov/genbank/>) contains barcoding sequences (COI) for only earthworm 600 taxa (i.e., 10% of the species), and for most of these (~400) the DNA description is not associated with any morphological taxonomic description and no valid species name is provided.

Although thousands of described species are still requiring DNA barcoding, molecular ecologists are releasing many barcoding sequences for new undescribed species, with little or no taxonomic support. Because of this imbalance between the taxonomically described species and the 'DNA barcoded' species, earthworm DNA barcoding can rarely be used for its original purpose: identifying species (Hebert *et al.*, 2003). In ecological studies it is often