



## Analysis of primary structure loops from Hairpins 35 and 48 of the Nematoda SSU rRNA gene provides further evidence that the genera *Tripylina* Brzeski, 1963, *Trischistoma* Cobb, 1913 and *Rhabdolaimus* de Man, 1880 are members of Enoplida

ZENGQI ZHAO<sup>1\*</sup>, DONGMEI LI<sup>2</sup> & THOMAS R. BUCKLEY<sup>1</sup>

<sup>1</sup> Landcare Research, Private Bag 92170, Auckland, New Zealand.

zhaoz@landcareresearch.co.nz

buckley@landcareresearch.co.nz

<sup>2</sup> CSIRO Food and Nutritional Sciences, P.O. Box 52, North Ryde, NSW 1670, Australia. dongmei.li@csiro.au

\*Corresponding author: zhaoz@landcareresearch.co.nz

### Abstract

A comparison of small subunit (SSU) rDNA sequences has revealed that a rare nucleotide transition A → G and a transversion G → Y occurred simultaneously in the evolutionarily conserved loops of Hairpins 35 and 48 of the SSU rRNA gene of *Tripylina* Brzeski 1963, *Trischistoma* Cobb 1913 and *Rhabdolaimus* de Man 1880. The same pair of substitutions occurred in all Enoplida analysed but not in other nematodes. This evidence from the primary structure of Hairpins 35 and 48 indicates that *Tripylina*, *Trischistoma* and *Rhabdolaimus* are members of Enoplida, supporting previous phylogenetic analyses.

**Key words:** 18S rRNA, Molecular alignment, Triplonchida, Tripylidae, Trischistomatidae, Rhabdolaimidae

### Introduction

Since 2007, we have been extensively studying nematodes from the family Tripylidae de Man, 1876, in New Zealand. The family includes 63 nominal species/subspecies, 39 may be regarded as valid species in 5 genera (Andrássy 2007): *Tripyla* Bastian, 1876 (24 valid species), *Tripylella* Brzeski & Winiszewska-Ślipińska, 1993 (3 valid species), *Tripylina* (6 valid species), *Trischistoma* (4 valid species), *Tobriolia* Andrásy, 1967 (2 valid species). Recent descriptions from New Zealand have included two species in *Tripyla* (Zhao 2009b), one in *Tripylella* (Z. Zhao, unpubl. data), five in *Tripylina* (Yeates 1972; Zhao 2009a) and four in *Trischistoma* (Zhao 2011). These studies included the first morphological and molecular analysis of the affinities of *Tripylina* and *Trischistoma* (Zhao 2009a; 2011). The phylogenetic analysis of small subunit (SSU) rRNA sequences demonstrated that *Trischistoma* and *Tripylina* are not closely related to *Tripyla*, the type genus of the Family Tripylidae, and are related to the Enoplida rather than to the Triplonchida, which has included Tripylidae. This finding is consistent with the results of Meldal *et al.* (2007) and the latest phylogenetic study of van Megen *et al.* (2009).

Other phylogenetic analyses of overall similarities of SSU rRNA sequences suggested that Enoplida and Triplonchida were closely related but separate orders (De Ley & Blaxter 2004; Zhao & Buckley 2009; van Megen *et al.* 2009; Bik *et al.* 2010), with *Tripylina* and *Trischistoma* members of Enoplida rather than Triplonchida. Rhabdolaimidae was also shown to group with the Enoplida (van Megen *et al.* 2009; Bik *et al.* 2010). Other analyses suggested no close relationship (Holterman *et al.* 2006; Hodda 2007; Meldal *et al.* 2007).