

## Characterization of an isolate of *Heterorhabditis bacteriophora* (Nematoda: Heterorhabditidae) from the Northern Territory, Australia, using morphology and molecular data

JOHN HENRY SAGUN<sup>1</sup>, KERRIE ANN DAVIES<sup>2</sup> & IAN KENDRICH FONTANILLA<sup>3</sup>,  
MERAB ANTONE CHAN<sup>1</sup> & DARREN ANTON LAURENT<sup>3</sup>

<sup>1</sup>Biology Department, School of Science and Engineering, Ateneo de Manila University, Science Education Complex Building A Room 105, Katipunan Avenue, Loyola Heights, Quezon City 1108, Philippines. E-mail: johnhenry.sagun@yahoo.com

<sup>2</sup>Australian Centre for Evolutionary Biology and Biodiversity, and School of Agriculture, Food and Wine, The University of Adelaide, Waite Campus, PMB 1, Glen Osmond, South Australia 5064, Australia

<sup>3</sup>DNA Barcoding Laboratory, Institute of Biology, College of Science, University of the Philippines, Diliman, Quezon City 1101, Philippines

### Abstract

An entomopathogenic nematode, *Heterorhabditis* H39, was found in Darwin, Australia. Based on morphological and morphometric similarities, and molecular characterisation, it is an isolate of *Heterorhabditis bacteriophora*. Males, hermaphrodites, females and juveniles showed important similarities on most characters that define *H. bacteriophora*. The morphometrics of the infective juvenile of *Heterorhabditis* H39 are similar to those of *H. bacteriophora*, including average body length (562 (537–587) vs 570 (520–600) µm), maximum body width (21 (19–22) vs 24 (21–31) µm), distance from the anterior end to the EP (96 (87–104) vs 104 (94–109) µm) and tail length (101 (94–111) vs 91 (83–99) µm). The morphology of the spicules and gubernaculum of male *Heterorhabditis* H39 are indistinguishable from those of *H. bacteriophora*. The biology and life cycle of *Heterorhabditis* H39 are similar to those of other *Heterorhabditis* species. The Neighbour-Joining Tree based on 475 nucleotides of the SSU rRNA gene showed that *Heterorhabditis* H39 formed a monophyletic group with other *H. bacteriophora* isolates with a bootstrap value of 100. Thus, phylogenetic study of SSU sequence data provided strong evidence that *Heterorhabditis* H39 is an isolate of *H. bacteriophora*. This is the first record of *H. bacteriophora* in northern Australia.

**Key words:** nematodes, entomopathogenic, taxonomy, DNA sequencing, phylogeny, description

### Introduction

The entomopathogenic nematode, *Heterorhabditis bacteriophora* Poinar, 1976 was originally isolated from *Heliothis punctigera* Hall from Brecon, South Australia (Poinar 1976). Since then, it has been recorded in China (Akhurst 1987), Italy (Akhurst 1987; Tarasco *et al.* 2014), USA (Poinar & Georgis 1990), Israel (Glazer *et al.* 1993), Spain (De Doucet & Gabarra 1994), Korea (Choo *et al.* 1995), France (Emelianoff *et al.* 2008), Slovenia (Laznik *et al.* 2009) and Iran (Nikdel *et al.* 2010; Nikdel *et al.* 2012), *i.e.*, it has a wide natural distribution.

The present paper reports the finding of an isolate of *H. bacteriophora* from Darwin, Northern Territory, Australia. It was collected at Casuarina Coastal Reserve (latitude -12°22'32", longitude 130°51'40"), from the banks of Rapid Creek, in 2012. The isolate was examined using light microscopy, scanning electron microscopy (SEM), and molecular analysis.

### Materials and methods

**Nematode extraction.** Entomopathogenic nematodes (EPNs) of *Heterorhabditis* Poinar, 1976 were isolated from a