

# PARASITOLOGY & PATHOGENESIS

July 12-13, 2017 Chicago, USA

## Morphological and molecular characterization of *Gordius*, a horsehair worm recovered from Cricket

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To investigate and identify the nematode found in the body cavity of Cricket in the Mizoram state of North East of India. DNA sequence and Scanning Electron Microscopy (SEM of 18S rRNA of internal transcribe (ITS2) were used for validation of species and fine structure. Based on the morphological and molecular analysis, the nematode infesting Cricket was confirmed to be *Gordius* species. The length of the amplified ITS2 sequence of *Gordius* was found to be approximately 1048 bp. This is the first report of the nucleotide sequence of ITS2 of *Gordius* from India. Phylogenetic analysis revealed that the *Gordius* species is a close relative (100%) of Malaysian species. Present study also describes the Light Microscopy (LM) and SEM application for detailed morphological study of the isolated species. This is the first report of the occurrence of *Gordius* in India to the best of the authors' knowledge.

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## Report on the phylogenetic studies of diplostomatids parasites

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**Introduction & Aim:** *Diplostomid metacercariae* inhabit freshwater fish species as the second intermediate hosts. These parasites have been found in the eye lens, the retina, vitreous humor and the nervous system of freshwater fish. The classification of these parasitic stages to the species level using only morphology is often difficult and ambiguous. The use of molecular techniques has allowed links to be elucidated using various developmental stages of these parasites. The aim of this study was to provide a summative report on the phylogenetic tree by applying molecular biology techniques to the investigation of larval diplostomid parasites.

**Materials & Methods:** *Diplostomid metacercariae* were preserved in 70% ethanol prior to DNA extractions using Qiagen kit. Standard techniques for amplification of rRNA region were followed. The DNA amplicons were sent to inqaba biotech™ laboratory for sequencing and phylogenetic trees generated using software programs.

**Results:** The amplicons of these diplostomids had band sizes of 500 base pairs. The amplicons contained only partial regions (ITS-2). The parasitic species 28S rDNA genomic region was successfully amplified.

**Conclusion:** The application of molecular techniques on digenetic trematodes seems very promising and may yield great potential in future descriptions of morphologically similar parasitic species.

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