

# Molecular identification of *Mecistocirrus digitatus* and *Toxocara vitulorum* in the mithun (*Bos frontalis*) from north-east India

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**Abstract** *Mecistocirrus digitatus* and *Toxocara vitulorum* are common pathogenic nematode parasites of mithun (*Bos frontalis*). Species identification by morphological features was confirmed by molecular identification of *M. digitatus* and *T. vitulorum*. The internal transcribed spacer-2 (ITS-2) region and beta tubulin gene of *M. digitatus* were polymerase chain reaction (PCR) amplified and sequenced. ITS-2 sequence analysis showed 100% homology with other isolates of *M. digitatus* and 83% identity with *Haemonchus contortus* and *H. placei*, respectively. Likewise, ITS-1 and ITS-2 sequences of *T. vitulorum* were PCR amplified and sequenced. Sequence analysis of these internal transcribed spacers from five worms of the parasite from mithun showed no intraspecific variations with *T. vitulorum* isolates from domestic ruminants.

**Keywords** Mithun · Parasites · Internal transcribed spacers · Beta tubulin gene

## Introduction

Mithun (*Bos frontalis*) is one of the precious gifts of the rich biodiversity of north-eastern hilly region of India. Due to its congenial atmosphere and climate, north-eastern region can be considered as paradise of parasites. Parasitic

gastroenteritis is directly and indirectly associated with morbidity and mortality in mithun (Chamuah et al. 2009) but very scanty literature is available on gastrointestinal helminth parasites of mithun (Rajkhowa et al. 2005; Tandon et al. 2005; Chamuah et al. 2013, 2015). *Toxocara vitulorum* is a large roundworm commonly found in the small intestine of bovid calves in tropical and subtropical regions of the world (Murray et al. 2012) and also in temperate regions like Australia and Canada (Goossens et al. 2007). It is one of the major causes of calf-hood mortality in mithun (Rajkhowa et al. 2003, 2005). *M. digitatus* is found mainly in tropical and subtropical regions of Central and South America, Africa, Asia and sporadically in Europe. Incidence varies locally and seasonally. *M. digitatus* infection is mostly found mixed with other gastrointestinal roundworms like *Haemonchus*, *Cooperia*, *Ostertagia*, *Oesophagostomum*, etc. This parasite can be seriously harmful for livestock in endemic regions, especially for young stock. Clinical signs are similar to those of *Haemonchus* species with acute symptoms including anaemia, sometimes hemorrhagic, dark faeces and sub-mandibular oedema. Chronic infection often shows iron-deficiency anaemia, intermittent constipation, loss of appetite, weight loss and progressive wasting. Various studies have reported the presence of *M. digitatus* infection in cattle and buffaloes in different parts of India (Sreedhar et al. 2009; Bandyopadhyay 2010; Laha 2013). Morphology supported by molecular characterization of the marker sequences resolves the problem of species and genotype identification. The present work was carried out on the molecular identification of *M. digitatus* and *T. vitulorum* based on the internal transcribed spacer (ITS) sequences and beta tubulin gene.

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