

Molecular Identification of Microfilariae in Native Cattle in Thepha District, Songkhla Province

Tharika Chantamaneechote^{1,*}, Juntra Wattanamethamethanont² and Muncharee Tattiyapong²

Abstract

Background: Microfilariae are blood-borne nematode larvae transmitted by mosquito vectors and are widely distributed in tropical and subtropical regions. In cattle, adult worms typically reside in the peritoneal cavity. Infections are generally asymptomatic; however, aberrant larval migration to the central nervous system can result in paralysis. Morphological diagnosis has limited capacity to differentiate species, posing a challenge for identifying the specific species circulating within a region. Therefore, molecular techniques employing highly specific primers are required for accurate species identification, which is essential for the development of effective prevention and control strategies.

Objective: To identify microfilarial species in native cattle in Thepha District, Songkhla Province, based on the mitochondrial cytochrome *c* oxidase subunit 1 (*cox1*) gene.

Methods: Blood samples were collected from three asymptomatic native cattle at a farm in Thepha District, Songkhla Province. All cattle had previously tested positive for microfilariae using Woo's method and Giemsa-stained blood smear examination. Genomic DNA was extracted from blood samples, and polymerase chain reaction (PCR) amplification targeting the *cox1* gene was performed, followed by DNA sequencing. The obtained sequences were analyzed using BLASTn and compared with reference sequences in the NCBI GenBank database to confirm species identity.

Results: An approximately 682 bp amplicon of the *cox1* gene was successfully obtained from all three microfilaria-positive samples. All sequences showed high similarity to GenBank entries assigned to *Setaria* spp. Two sequences exhibited 100% identity with *Setaria digitata* (GenBank accession no. KY284626). The third sequence showed high similarity to both *Setaria marshalli* (LC719467) and *Setaria labiatopapillosa* (NC044071), with sequence identities of 99.66% and 99.38%, respectively.

Conclusion: Molecular techniques based on the *cox1* gene effectively identified microfilarial species in asymptomatic cattle; however, closely related species, *Setaria marshalli* and *Setaria labiatopapillosa*, remain difficult to distinguish. Integrating morphological analysis of adult worms would improve diagnostic accuracy. Despite the limited sample size, this study provides preliminary molecular evidence of *Setaria* diversity in Thepha District, Songkhla Province, and provides baseline data for future studies and surveillance.

Keywords: Molecular identification, Microfilariae, Native cattle, Thepha District

¹ Veterinary Research and Development Center (Lower Southern Region), Hat Yai, Songkhla 90110 Thailand

² National Institute of Animal Health, Ladyao, Chatuchak, Bangkok 10900 Thailand

* Corresponding author; E-mail: tharikac@gmail.com