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# Molecular Confirmation of *Taenia solium* Taeniasis in Child, Timor-Leste

## **Appendix**

#### **Additional Methods and Data**

#### **PCR**

For molecular confirmation, we amplified a 491 bp fragment of the *Taenia solium cox-1* gene (1). The PCR primers used were T1F (5'-ATA TTT ACT TTA GAT CAT AAG CGG-3') and T1R (5'-ACG AGA AAA TAT ATT AGT CAT AAA-3') (2).

We used AccuPower Hotstart PCR PreMix tubes (Bioneer Co., Ltd, https://www.bioneer.co.kr) for PCR. The reaction mixture contained 1 μL of template DNA (100 ng/μL) and 10 μmol/L of each primer, and diethyl pyrocarbonate—treated water was added to reach a total volume of 20 μL. PCR entailed an initial denaturation phase at 94°C for 3 minutes, succeeded by 40 cycles of denaturation (94°C for 1 minute), annealing (52°C for 1 minute), and extension (72°C for 1 minute), culminating in a final extension at 72°C for 10 minutes.

### Phylogenetic analysis

The evolutionary history was inferred by using the neighbor-joining method (3). The percentages of replicate trees in which the associated taxa clustered together in the bootstrap test (1,000 replicates) were calculated (4). The tree was drawn to scale; branch lengths were in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed by using the Kimura 2–parameter method (5) and are designated as the number of base substitutions per site. The analysis involved 20-nt sequences. Codon positions were first + second + third + noncoding. All ambiguous positions were removed for each sequence pair (pairwise deletion option). A total of 480 positions were in the final dataset. Evolutionary analyses were conducted by using MEGA11 (6).

Sequence Amplified by Using *Taenia* spp. *cox-1* Restriction Fragment Length Polymorphism–PCR Primers

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