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# Molecular Confirmation of Autochthonous *Taenia saginata* Infection, Timor-Leste, 2019

## Appendix

### Evolutionary relationships of taxa

The evolutionary history was inferred using the Neighbor-Joining method (1). The optimal tree is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown below the branches (2). The evolutionary distances were computed using the Kimura 2-parameter method (3) and are in the units of the number of base substitutions per site. This analysis involved 14 nt sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 458 positions in the final dataset. Evolutionary analyses were conducted in MEGA11 (4,5)

### References

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