

# Preventing *Thelazia callipaeda* Reinfection among Humans

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## Appendix



**Appendix Figure.** Molecular phylogenetic analysis of the *Thelazia callipaeda* *cox1* gene by maximum likelihood method based on the Tamura-Nei model (1) conducted on 2,000 bootstrap replications. The tree with the highest log likelihood (-2128.91) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial trees for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the maximum composite likelihood (MCL) approach, then selecting the topology with superior log likelihood values. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories [+G, parameter = 0.2595]). The tree is drawn to scale, with branch lengths measured

in the number of substitutions per site. The analysis involved 20 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. The representative sequence from this study is in bold. *Dracunculus medinensis* sequence was used as outgroup. Evolutionary analyses were conducted using MEGA7 software.

## Reference

1. Tamura K, Nei M. Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. Mol Biol Evol. 1993;10:512–26. [PubMed](#)