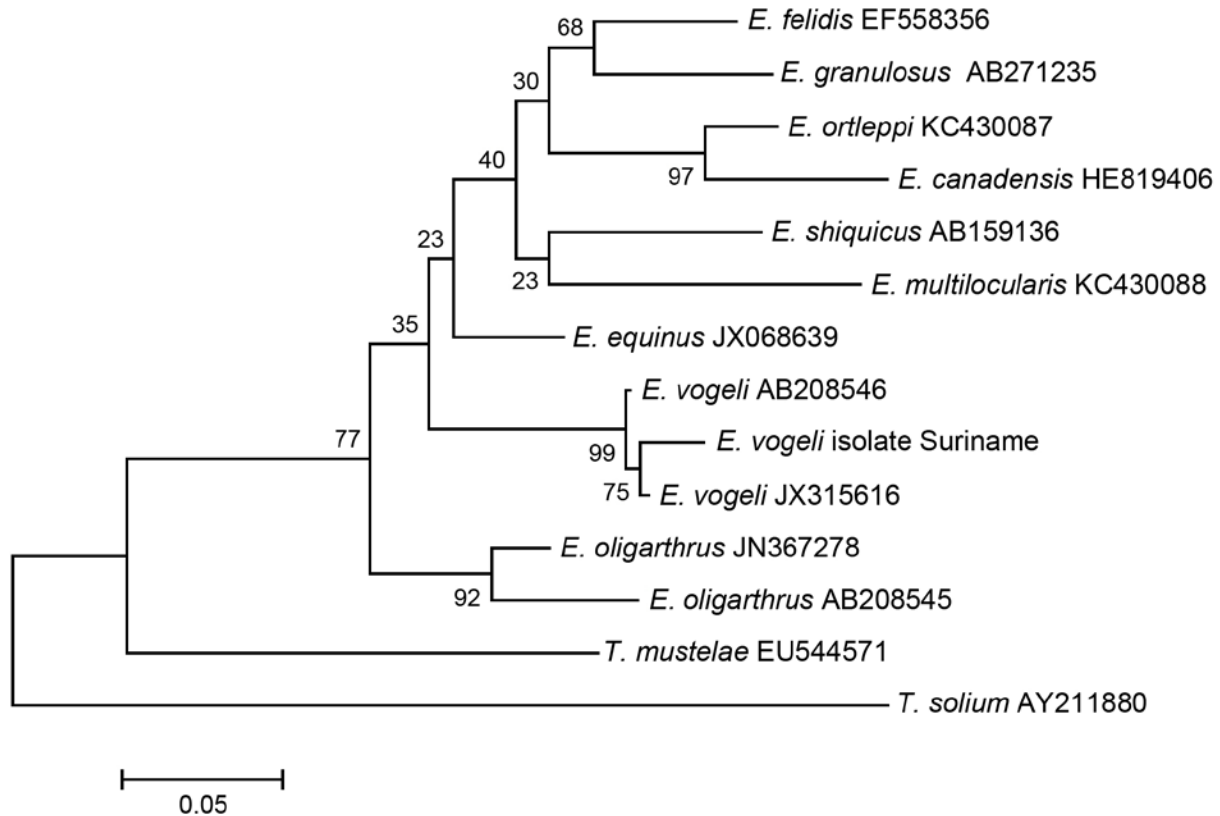


# *Echinococcus vogeli* in Immigrant from Suriname to the Netherlands

## Technical Appendix



Technical Appendix Figure. Molecular phylogenetic analysis of *Echinococcus* sequences by the maximum-likelihood method. Numbers after the tapeworm species are GenBank accession numbers. The tree using cytochrome oxidase subunit 1 gene data depicts the isolate from immigrant from Suriname close to other *E. vogeli* specimens from Brazil (GenBank accession no. JX315616) and Colombia (AB208546). The evolutionary history was inferred by using the maximum-likelihood method based on the Tamura-Nei model. The tree with the highest log likelihood ( $-5295.5104$ ) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying neighbor-join and BioNJ algorithms to a matrix of pairwise distances estimated by using the maximum composite likelihood approach and then selecting the topology with superior log likelihood value. A discrete gamma distribution was used to model

evolutionary rate differences among sites (5 categories [+G, parameter = 0.2348]). The tree is drawn to scale; branch lengths are measured in the number of substitutions per site. The analysis involved 14-nt sequences. Codon positions included were 1st+2nd+3rd+noncoding. The final dataset contained a total of 1,752 positions. Evolutionary analyses were conducted by using MEGA6 (<http://www.megasoftware.net>).