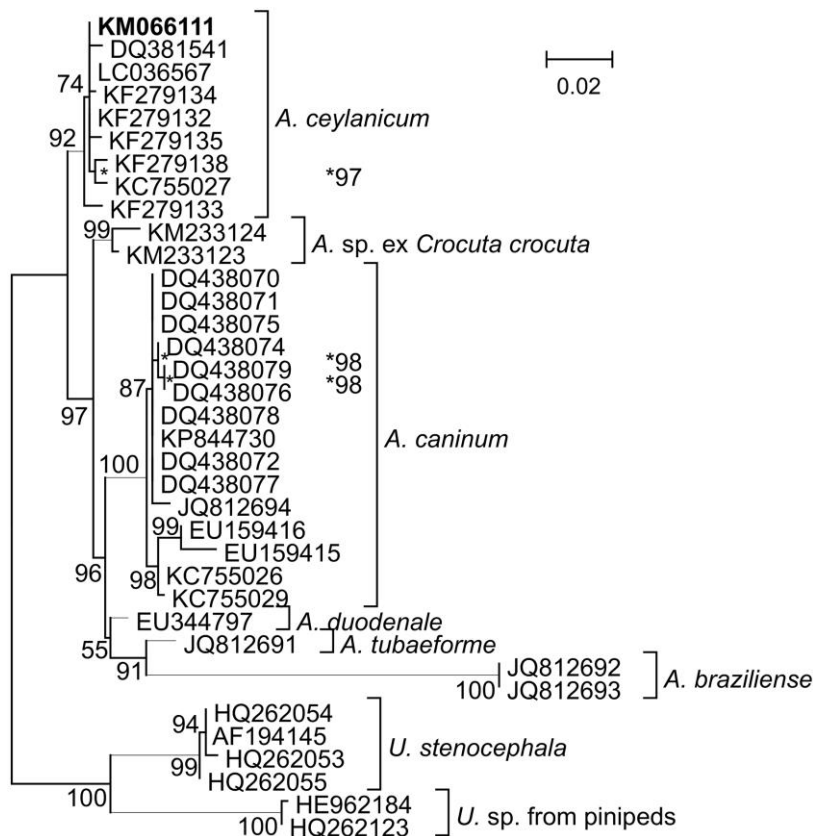


# Diffuse Unilateral Subacute Neuroretinitis Caused by *Ancylostoma* Hookworm

## Technical Appendix



**Technical Appendix Figure.** All intergenic transcribed spacer 1 and 2 sequences (GenBank accession no. KM066110.1) from *Ancylostoma* spp. and a few *Uncinaria* spp. as outgroup were aligned separately by using MAFFT (<http://mafft.cbrc.jp/alignment/software>) with the Q-INS-I to consider RNA secondary structure. The phylogram was calculated by using PhyML3.1 (1) and applying a GTR+I+F+G model with 25 substitution rate categories based on the concatenated alignments. Branch support was obtained by using a Bayesian transformation of the approximate-likelihood-ratio test. Sequences are represented by GenBank accession numbers, and the specimen found in the present study is shown in bold type.

## Reference

1. Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O. New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. *Syst Biol.* 2010;59:307–21. [PubMed <http://dx.doi.org/10.1093/sysbio/syq010>](http://dx.doi.org/10.1093/sysbio/syq010)