

Figure S1. A + T and G + C contents and skews of 12 PCGs, rRNAs, tRNAs, and complete mt genome sequences of *Cc. elongatus*.

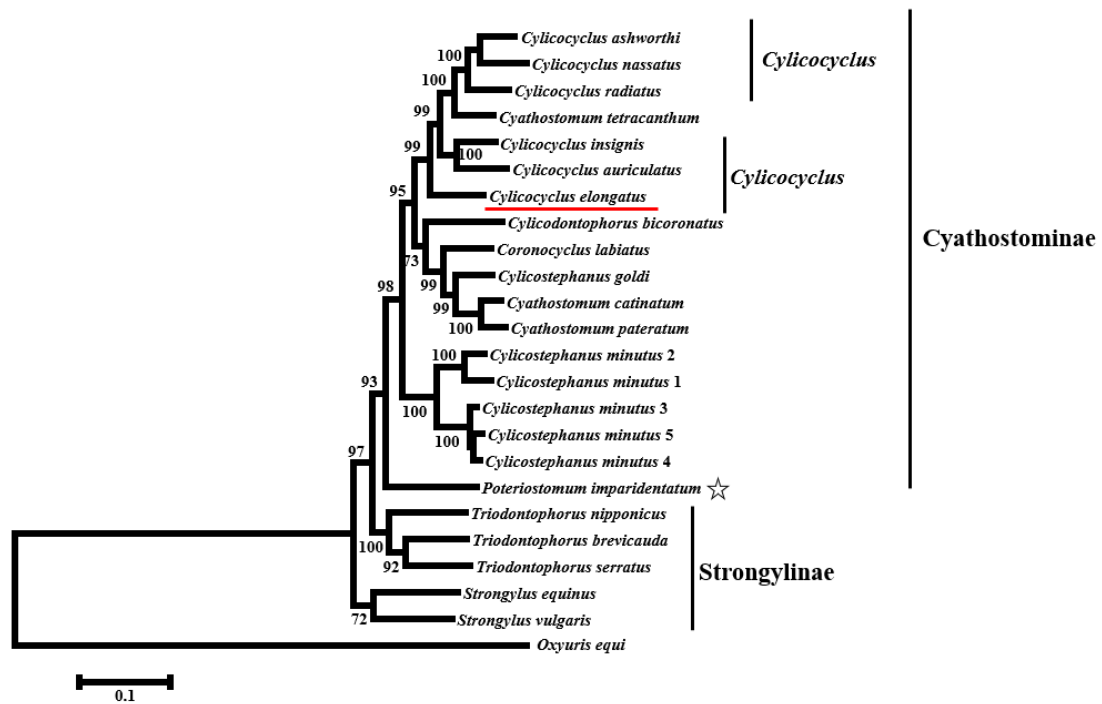


Figure S2. Phylogenetic analyses reconstructed using nucleotide sequences of complete mt genome sequences in 23 Strongylidae species. The tree was developed using ML method. *Oxyuris equi* is an outgroup. *Cc. elongatus* in current study is underlined.