

0.01

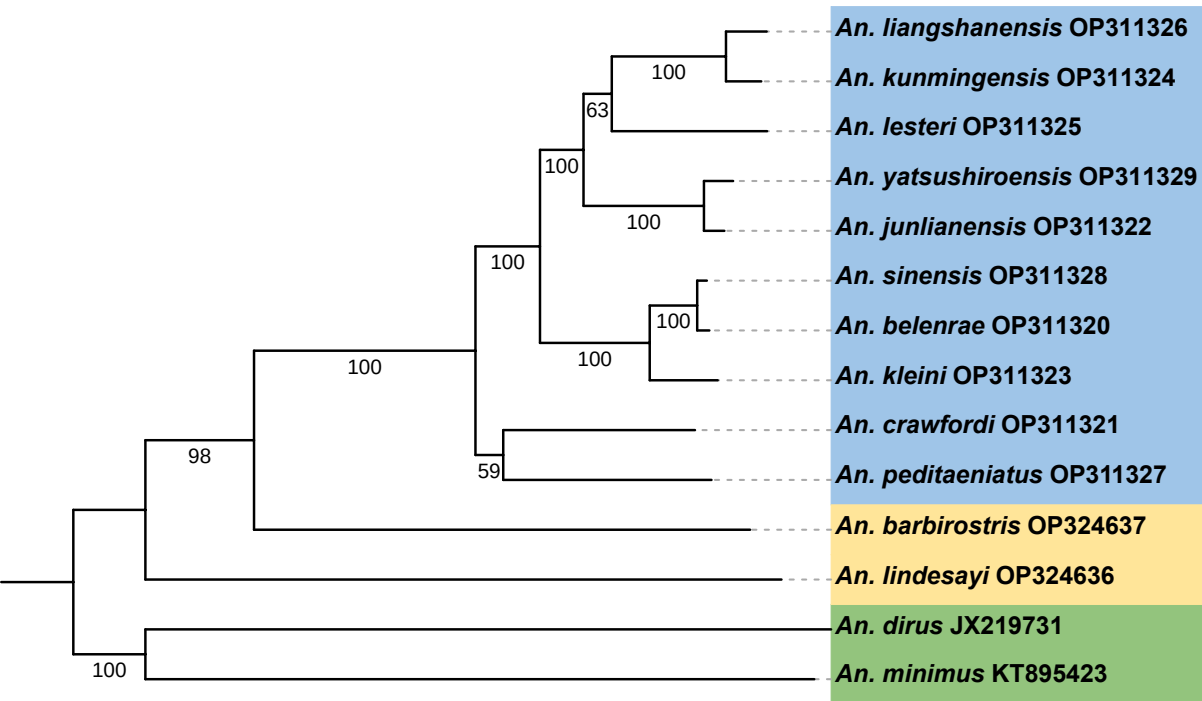


Fig. S7 Phylogenetic reconstruction by maximum likelihood based on the complete mitochondrial genome sequence concatenated of the species sequenced in this study and two other taxa with data available from GenBank. The values of bootstrapping support are shown to the left of the branch point.