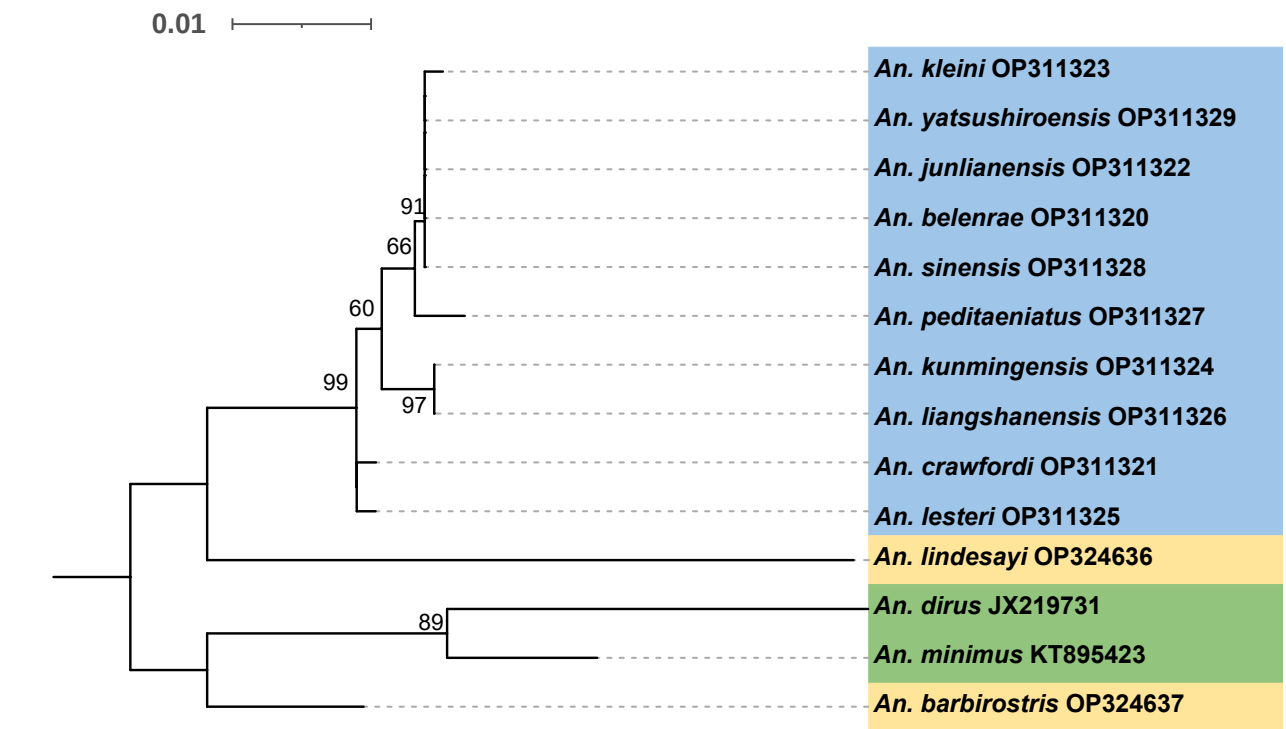
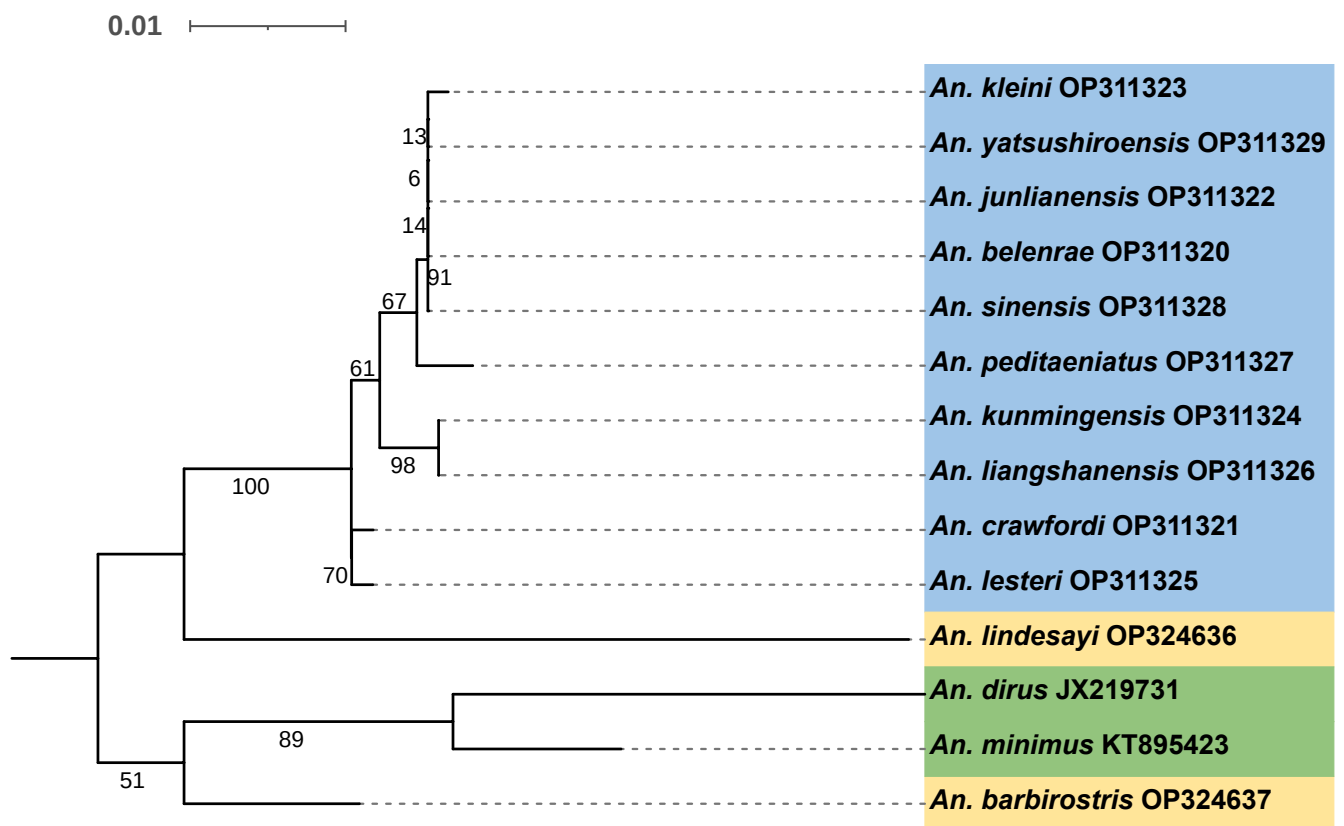


a



b



c

Fig. S6 Phylogenetic reconstruction by maximum likelihood based on tRNA and rRNA coding region concatenated of the species sequenced in this study and two other taxa with data available from GenBank. a tRNAs. b 12S rRNA c 16S rRNA. The values of bootstrapping support are shown to the left of the branch point.