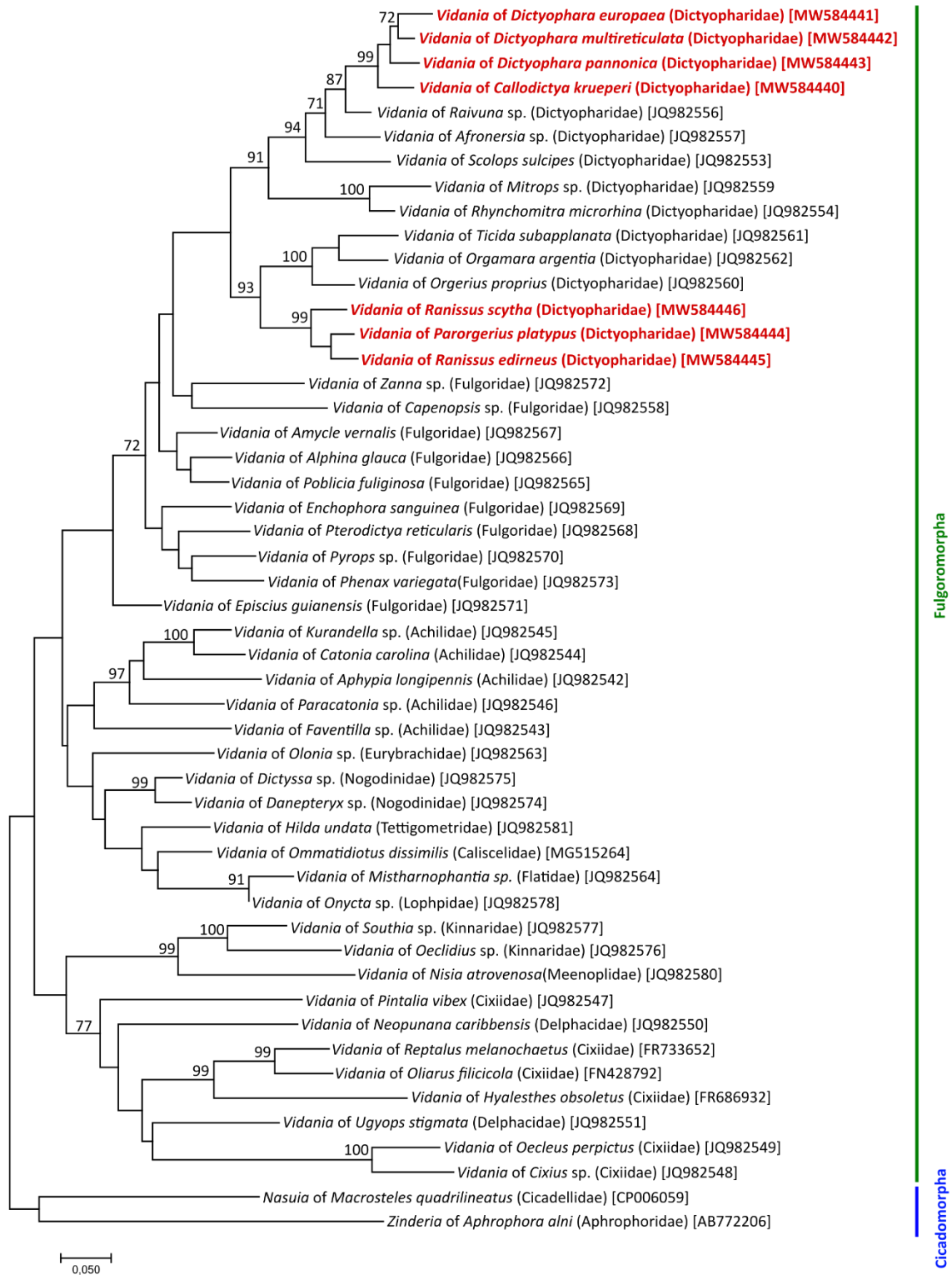
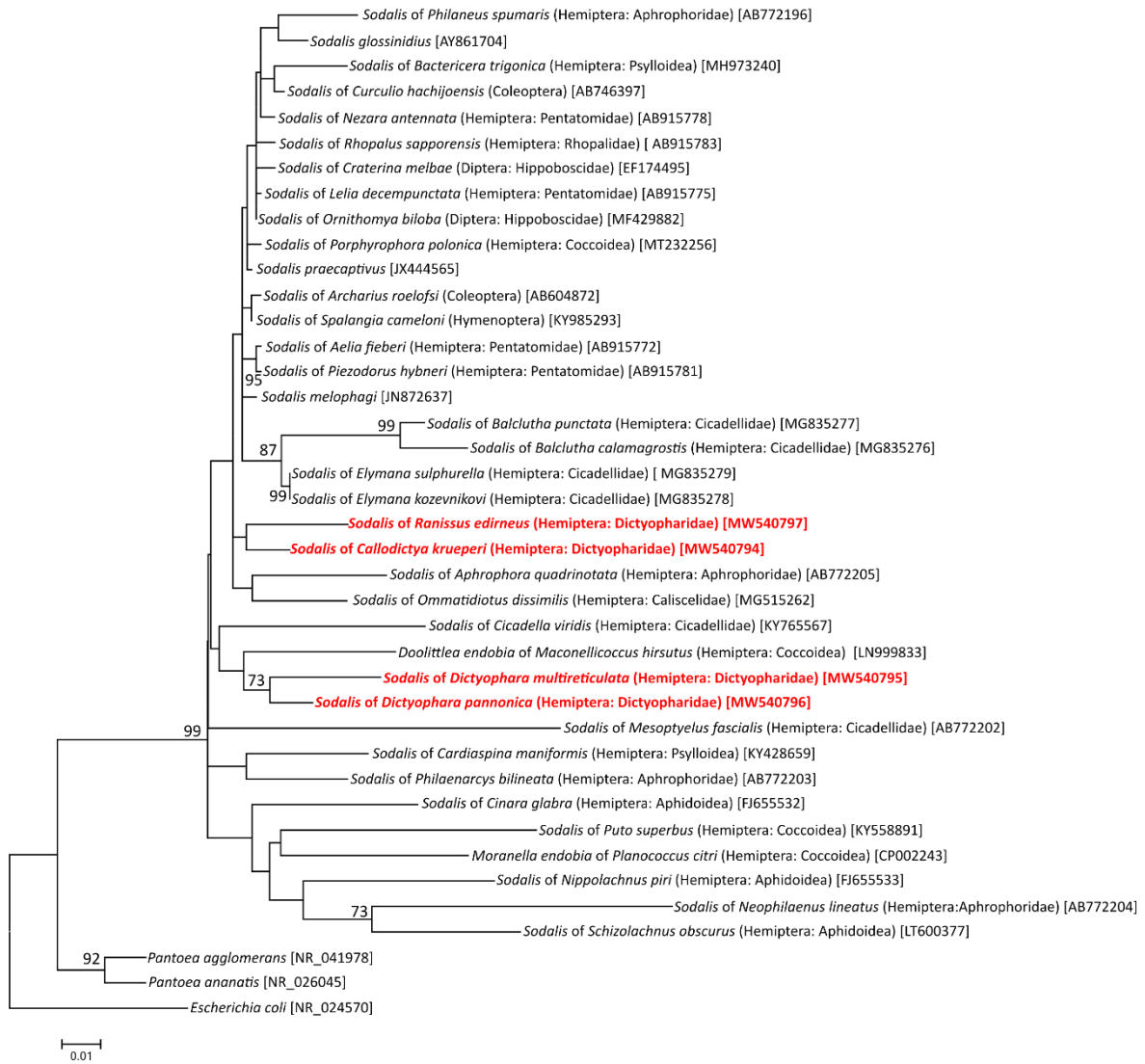


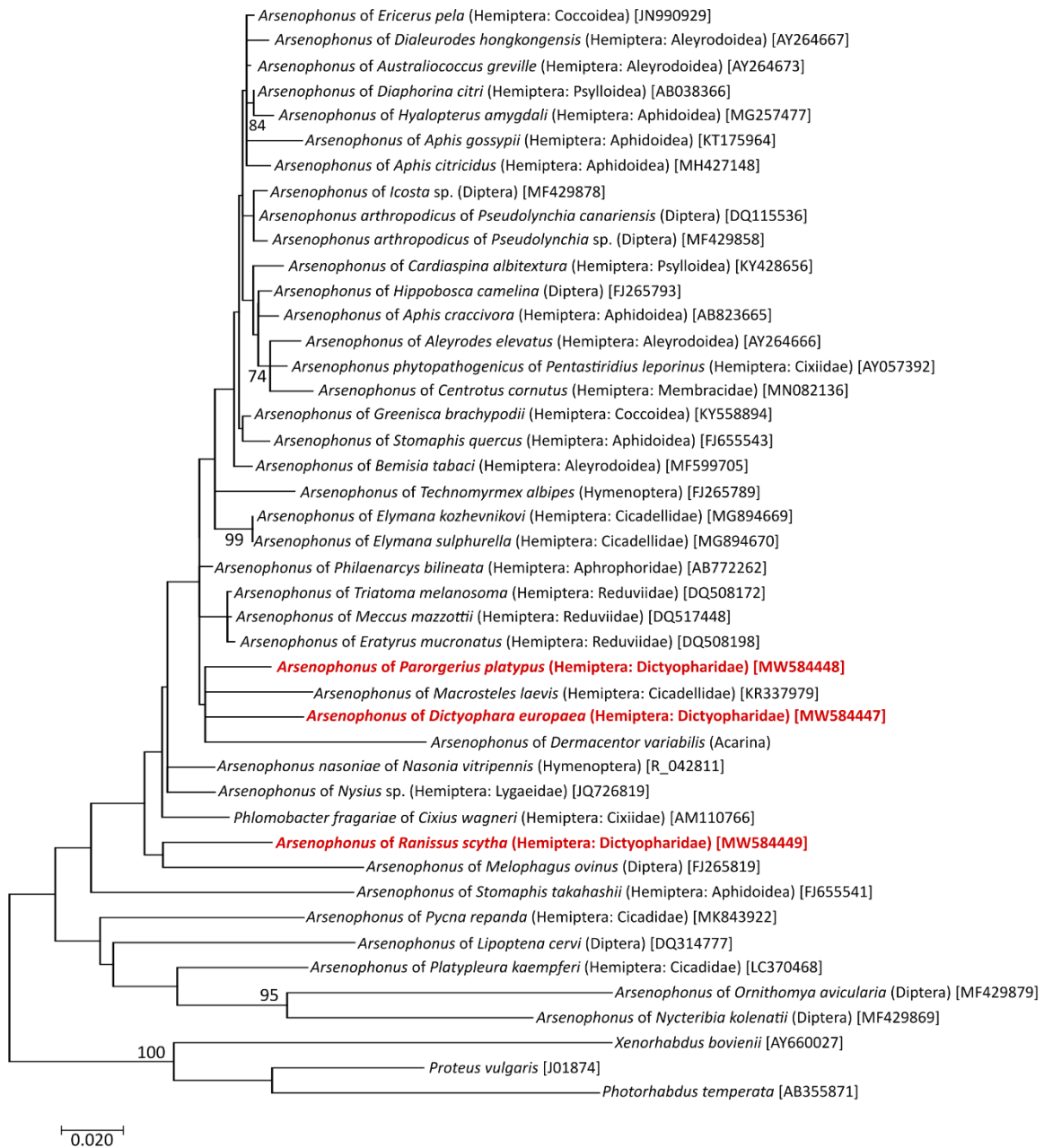
**Fig. S1A.** ML phylogeny of *Sulcia* strains from diverse planthoppers, based on full-length sequences (1373 shared nucleotide positions) of 16S rRNA gene. Only bootstrap values above 70% are shown. Sequences from the seven Dictyopharidae species studied here are highlighted using the colored font.



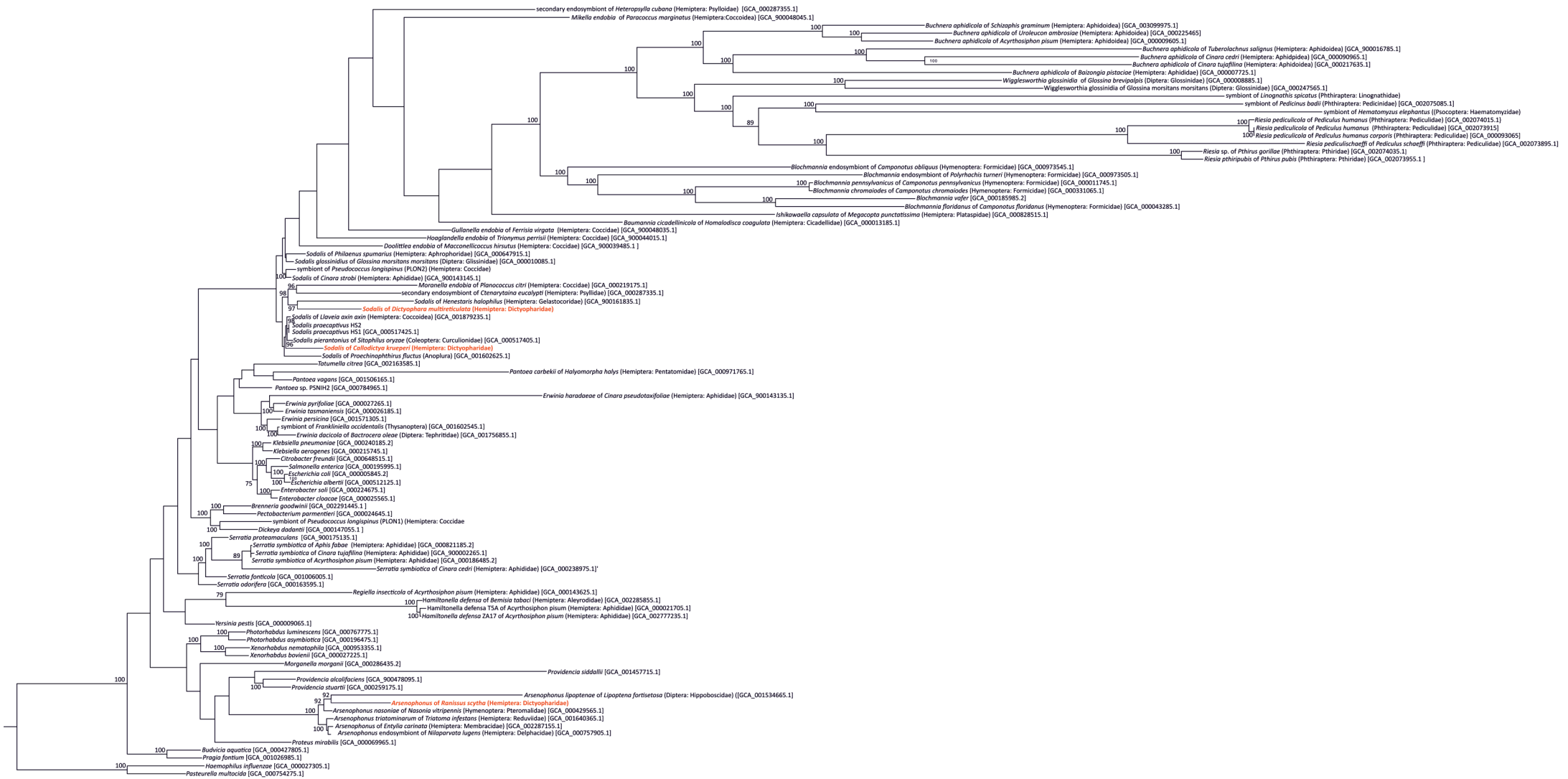
**Fig. S1B.** ML phylogeny of *Vidania* strains from diverse planthoppers based on full-length sequences (1530 shared nucleotide positions) of 16S rRNA gene. Only bootstrap values above 70% are shown. Sequences from the seven Dictyopharidae species studied here are highlighted using the colored font.



**Fig. S1C.** ML phylogeny of *Sodalis* strains from different hosts based on 16S rRNA gene sequences. Only bootstrap values above 70% are shown.



**Fig. S1D.** ML phylogeny of *Arsenophonus* strains from different hosts based on 16S rRNA gene sequences. Only bootstrap values above 70% are shown.



**Fig. S1E.** ML phylogeny based on 1<sup>th</sup> and 2<sup>th</sup> codon positions of 129 conserved single-copy protein-coding genes of symbiotic enterobacteria and relatives. Only bootstrap values above 70% are shown.