

Phylogenetic diversity and community structure of sponge-associated bacteria from mangroves of the Caribbean Sea

Jiangke Yang¹, Jin Sun², On On Lee¹, Yim Him Wong¹, Pei Yuan Qian^{1,*}

¹KAUST Global Collaborative Research Program, Department of Biology, Hong Kong University of Science and Technology, Clear Water Bay, Kowloon, Hong Kong SAR

²Department of Biology, Hong Kong Baptist University, Hong Kong SAR

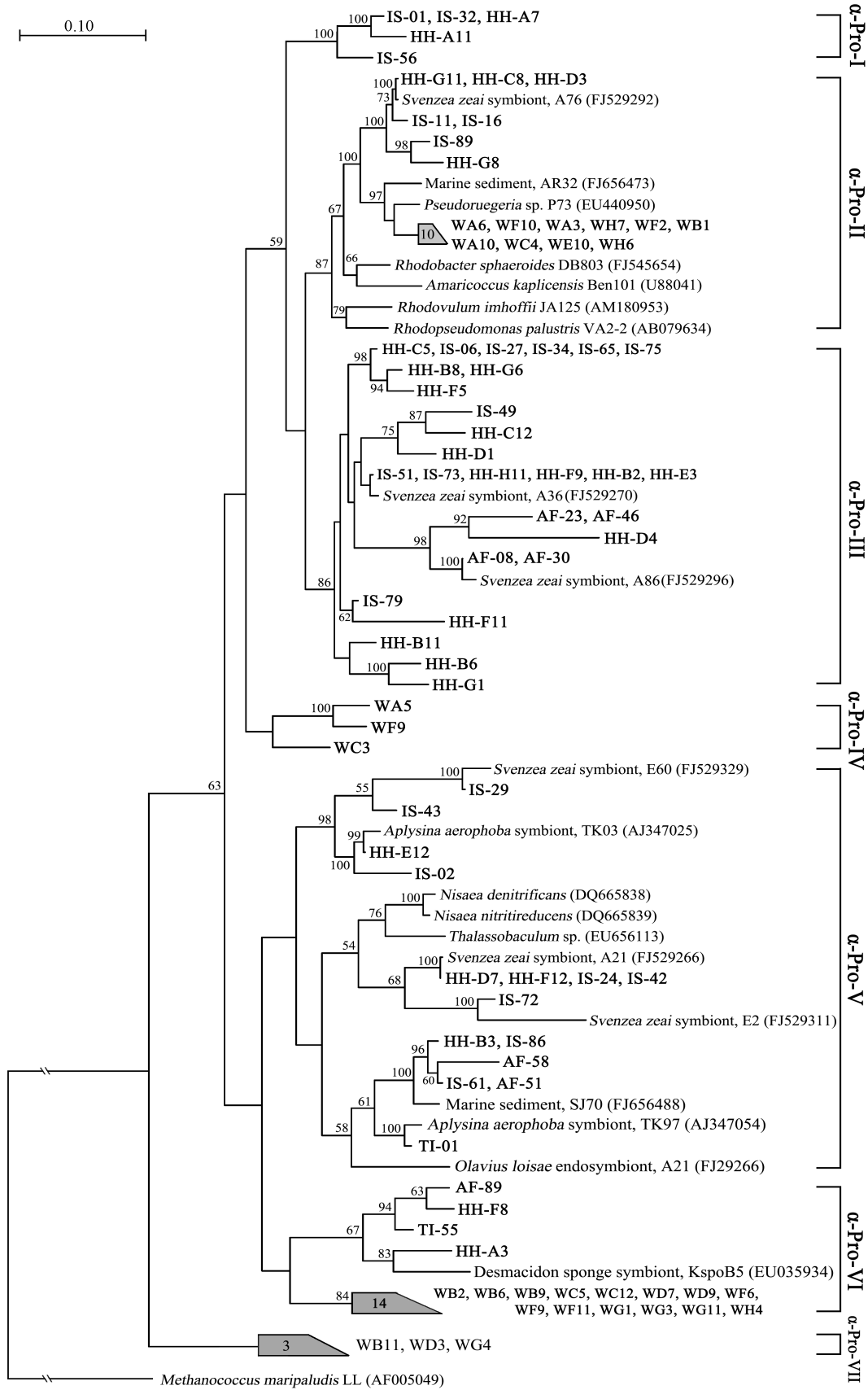
*Corresponding author. Email: boqianpy@ust.hk

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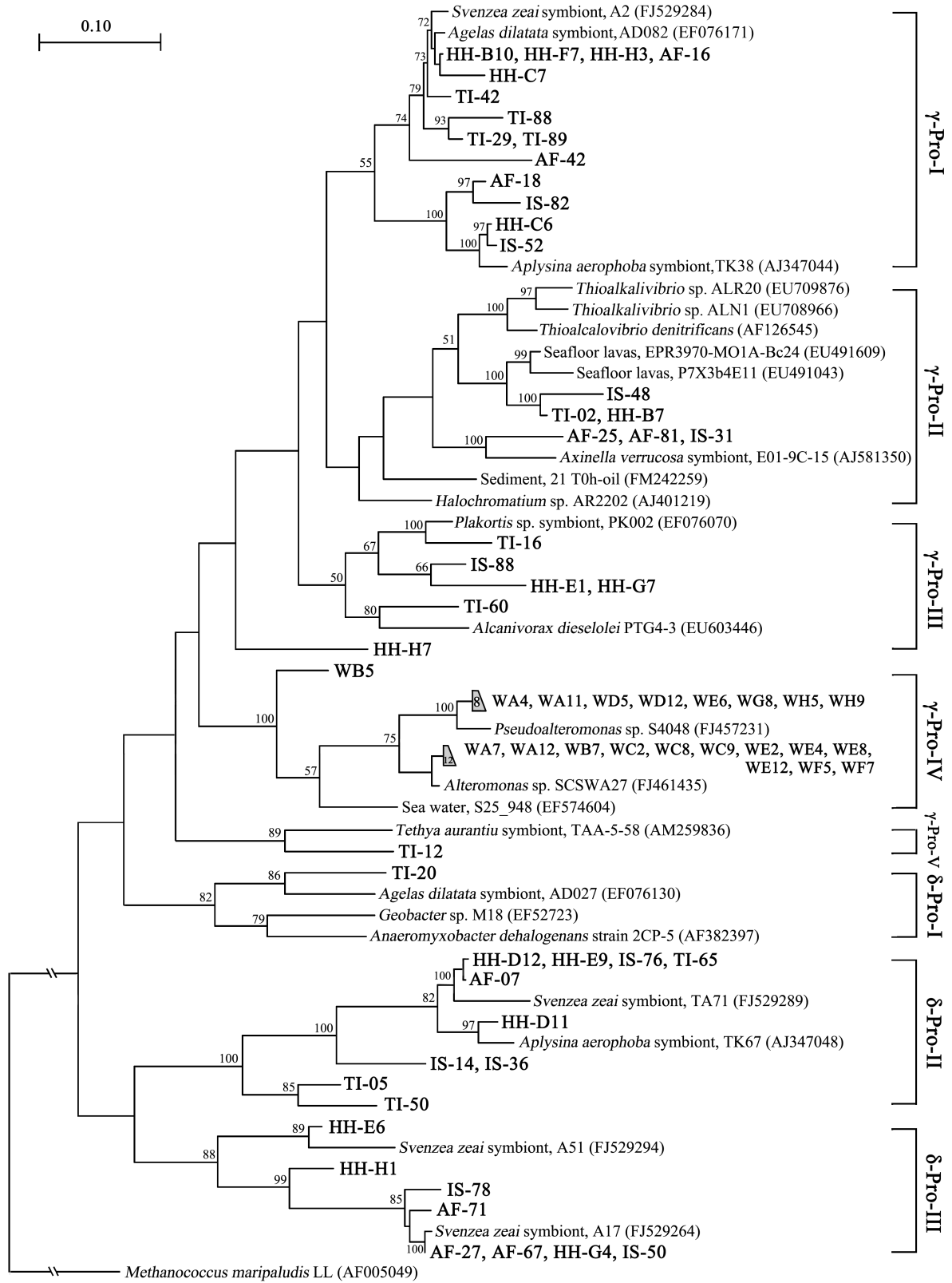
Supplement 1. Additional data.

Fig. S1. Rooted neighbor-joining phylogenetic trees showing the relatedness of the clones from the present study with other deposited sequences of (A) *Alphaproteobacteria*; (B) Beta- and *Gammaproteobacteria*; (C) *Chloroflexi*; and (D) *Acidobacteria*, *Actinobacteria*, *Bacteroidetes*, *Cyanobacteria*, *Deinococcus-Thermus*, *Nitrospirae*, *Poribacteria*, *Proteobacteria*, *Spirochaetes*, *Verrucomicrobia* and an unclassified phylum. Clones from the present study are prefixed with W, HH, AF, IS and TI, representing clones retrieved from seawater and the sponges *Haliclona hogarhi*, *Aplysina fulva*, *Ircinia strobilina* and *Tedania ignis*, respectively; sequences from other studies were also included in the trees with corresponding accession number in parentheses. Bootstrap confidence values >50% are shown at the nodes. The polygons represent clones that are >98% similar. *Methanococcus maripaludis* was used as an outgroup. Scale bar = 0.10 substitutions per nucleotide position

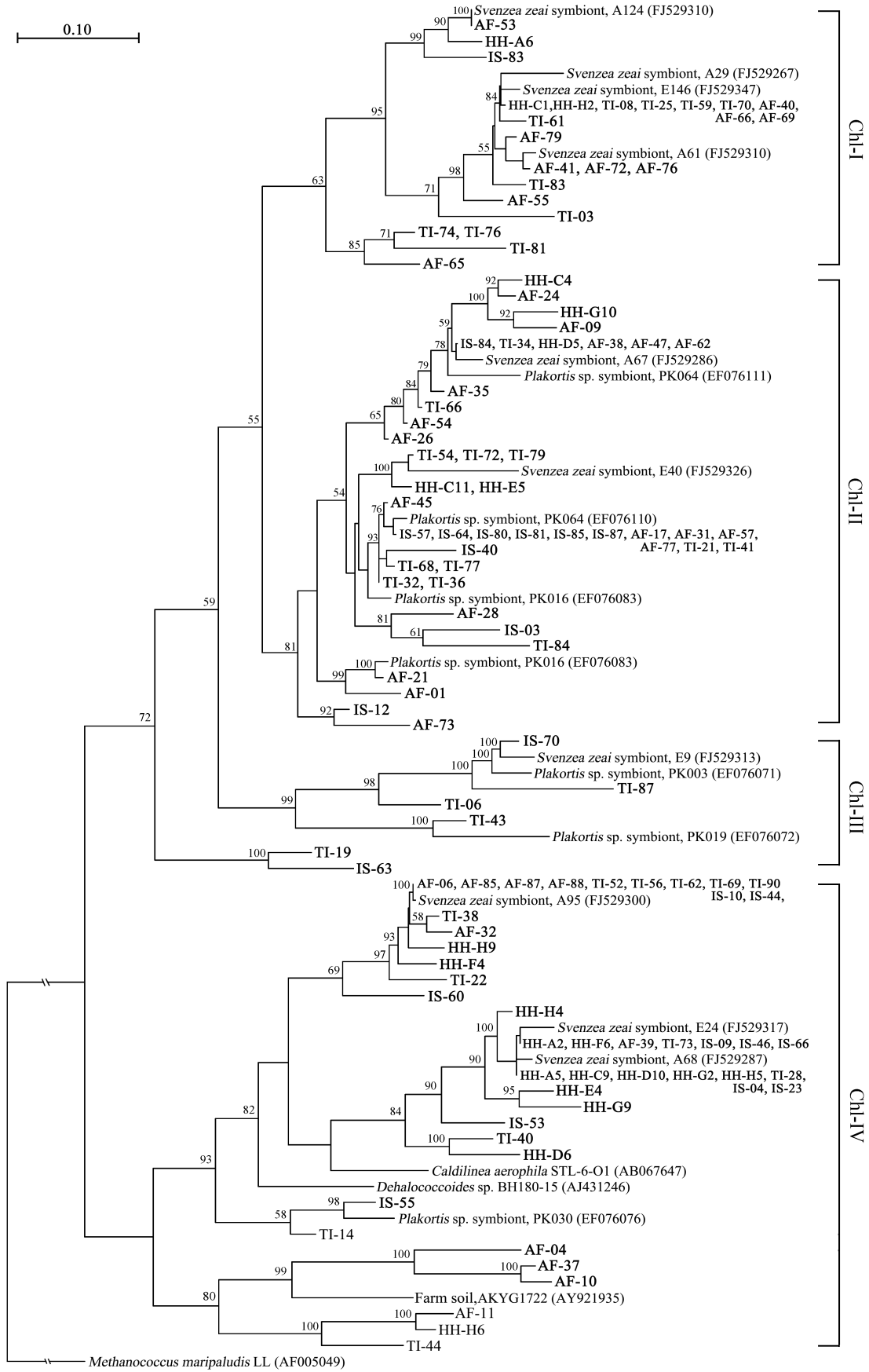
A.



B.



C.



D.

