



**FIG. S2.** Molecular phylogenetic analysis of the symbiont of *P. japonensis* together with  $\gamma$ -proteobacterial representatives on the basis of *groE* gene sequences. Bayesian phylogenies are presented as in figure 2. Aligned 1,088 nucleotide sites at 1st and 2nd codon positions were subjected to the analyses. Although the 3rd codon positions were not used in the phylogenetic analyses because of saturated nucleotide substitutions, the AT content values were calculated from the data of all codon positions.