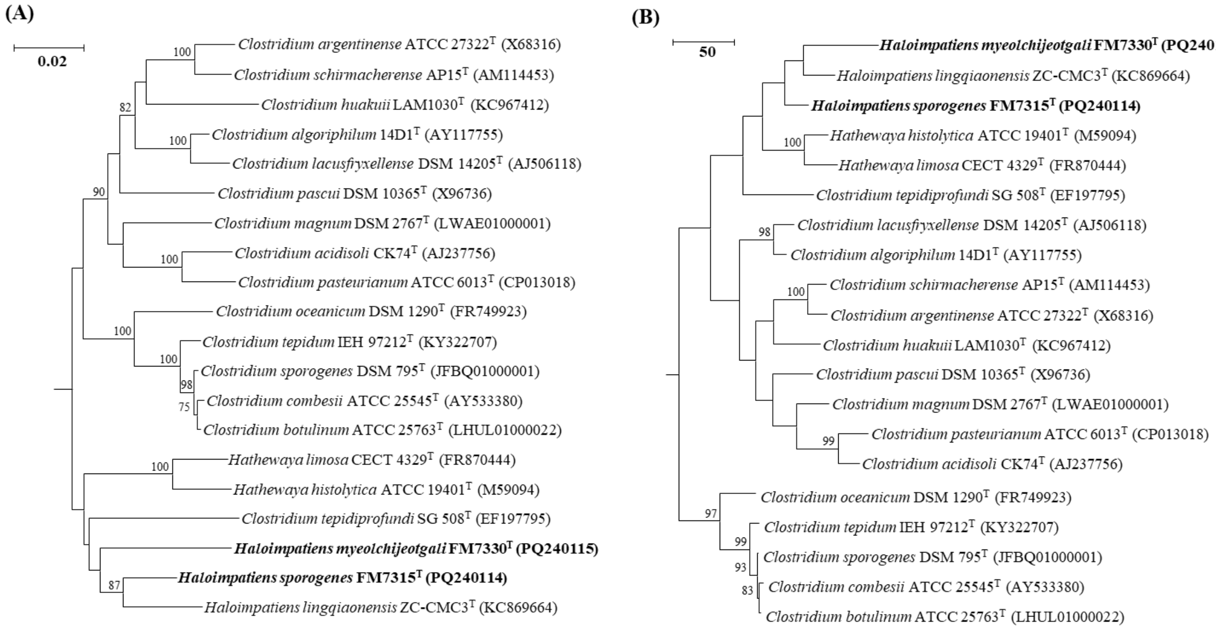

Fig. S1. Neighbor-joining (A) and maximum-parsimony (B) trees based on 16S rRNA gene sequences showing the phylogenetic relationships of strains *H. sporogenes* FM7315^T, *H. myeochijeotgali* FM7330^T, and their closely related taxa. Bootstrap values with more than 70% are shown on the nodes as percentages of 1,000 replicates. *Bacillus subtilis* NCIB 3610^T (ABQL01000001) was selected as the outgroup.