**Supplementary fig. S1.** Phylogenetic tree inferred from the maximum-likelihood (ML) analysis based on 16S rRNA and 16S-23S ITS sequences. Asterisks at the nodes indicate maximum likelihood bootstrap support (≥ 0.99). Based on the monophyletic criterion, strains were associated with thirteen lineages (1-13). The outgroup is indicated as O. Strains forming singleton nodes are indicated as #. Scale bar indicates substitutions per site.