

Figure S1

(A) *Bacillus velezensis* UQ9000N phylogenetic tree

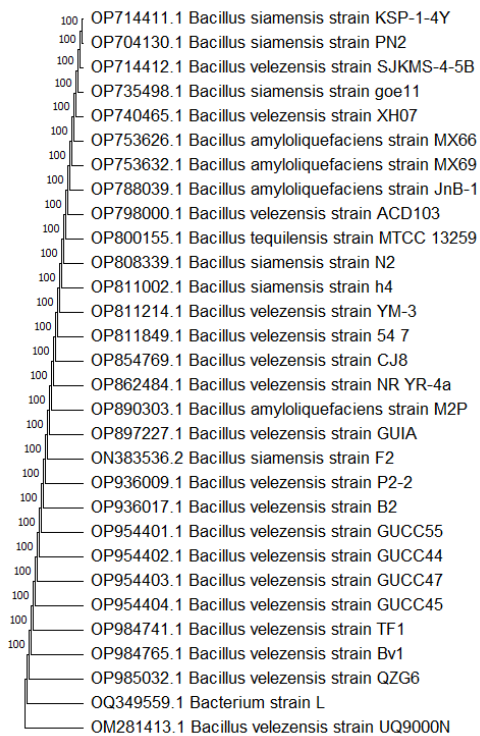
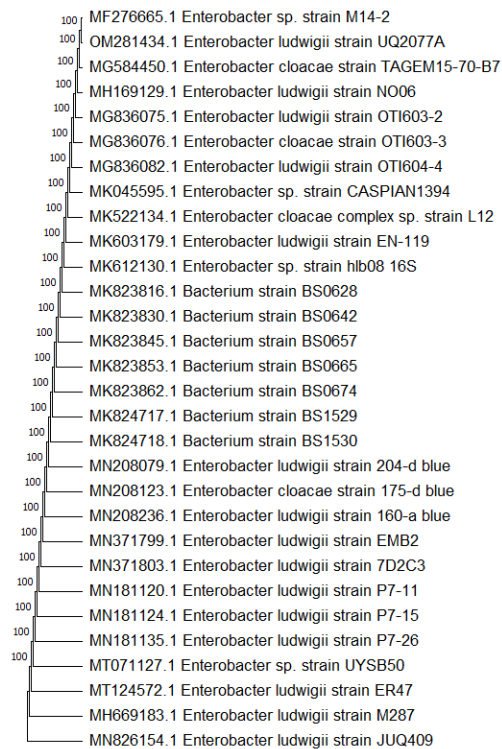


Figure S1. Phylogenetic trees based on 16S rRNA gene sequences. The relationships between each of the (A) *Bacillus velezensis* UQ9000N, (B) *Enterobacter ludwigii* UQ2077A and (C) *Pseudomonas azotoformans* UQ4510An and other known related strains/species derived from NCBI accessions. The tree was inferred using the neighbor-joining method and MEGA 11.0 software with 1000 bootstrap replicates (bootstrap values are shown next to nodes).

(B) *Enterobacter ludwigii* UQ2077A



(C) *Pseudomonas azotoformans* UQ4510An

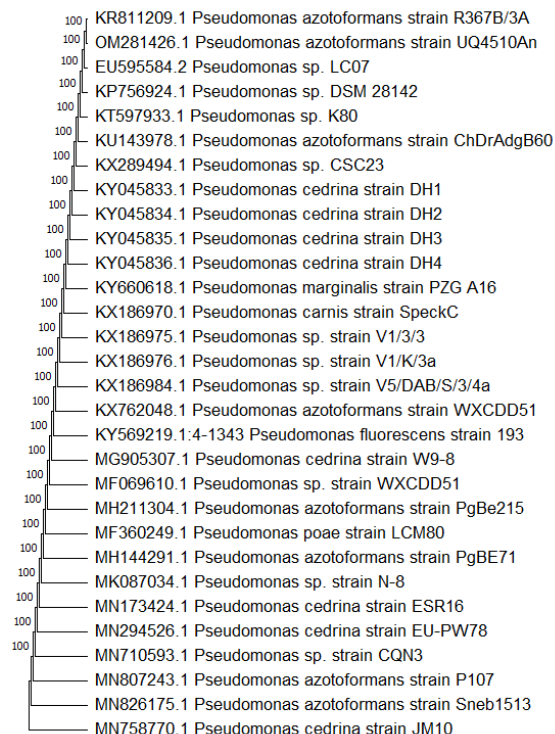


Figure S1. Continued.