



Supplementary Fig. 3. Phylogenetic tree based on the *aroE* gene sequence comparison of all 20 isolates of *Bacillus pumilus* group using a maximum-likelihood method with MEGA 7.0. All isolates was classified into Cluster A and Cluster B. *Bacillus cereus* ATCC 14579 was used as an outgroup. Scale bar = 0.10 substitutions per nucleotide position.