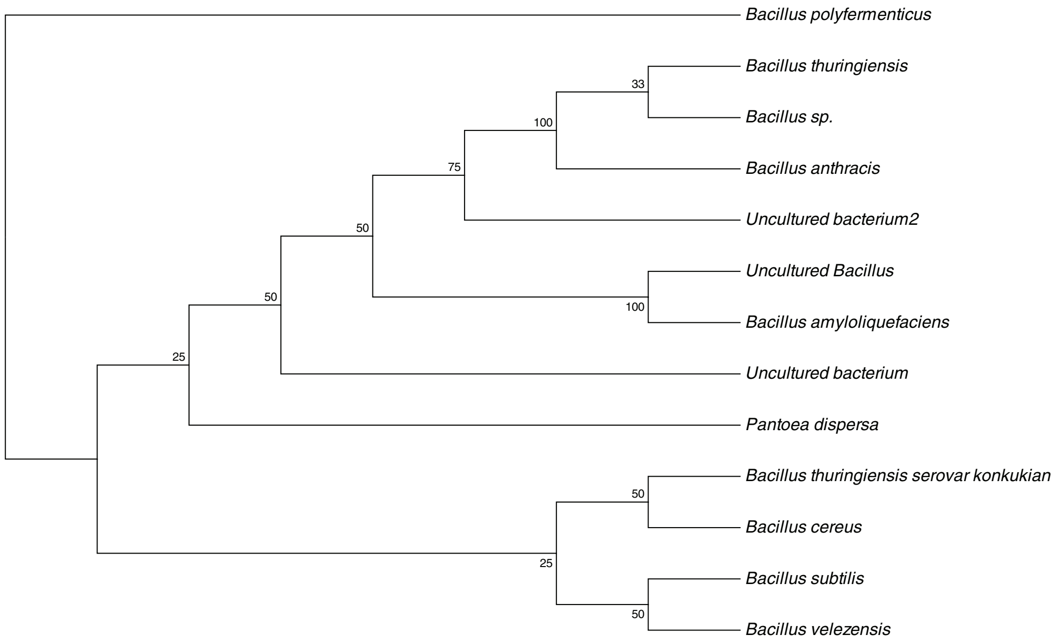
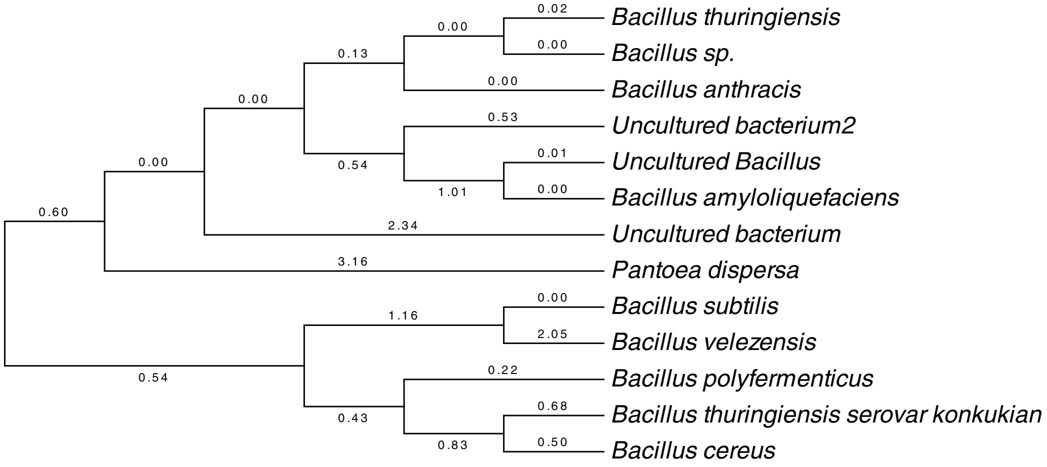


(a)



(b)

Figure S2 – Phylogenetic analysis showing the relationship of the 16S rRNA gene sequences of isolates. The trees were generated using (a) Molecular Phylogenetic anaylsis by Maximum Parsimony (MP) analysis of taxa and (b) Maximum Likelihood (ML) method.