



S2 Fig. Phylogeny demonstrating variation of *cphA* gene in *Aeromonas* isolates found in this study. Nucleotide sequences of *cphA* were aligned using Muscle version 3.8.31 (Edgar, RC. 2004. Nucleic Acids Research, 32(5), 1792–1797) and a parsimony based phylogeny was inferred using PAUP*version 4.0b10 (Wilgenbusch, J. C., & Swofford, D. (2003). Current Protocols in Bioinformatics / Editorial Board, Andreas D Baxevanis [Et Al], Chapter 6, Unit 6.4. <http://doi.org/10.1002/0471250953.bi0604s00>), using the heuristic search option. Values on the branches are the inferred number of steps (single nucleotide substitutions). The search resulted in 1 tree (317 steps, C.I.=0.647). Values below the branches indicate bootstrap values based on 500 replicates, bootstrap values below < 50 are not shown.