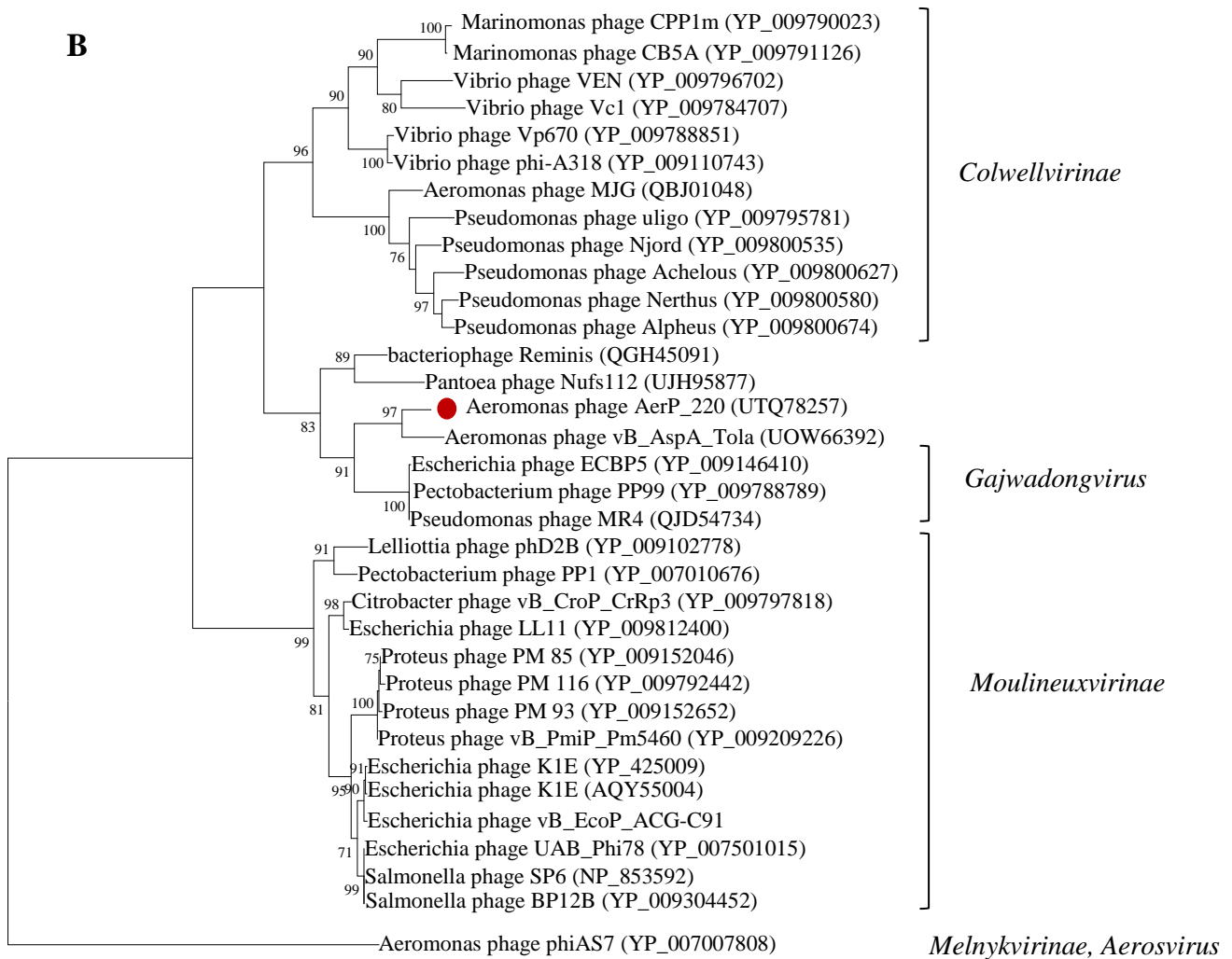


B



0,20

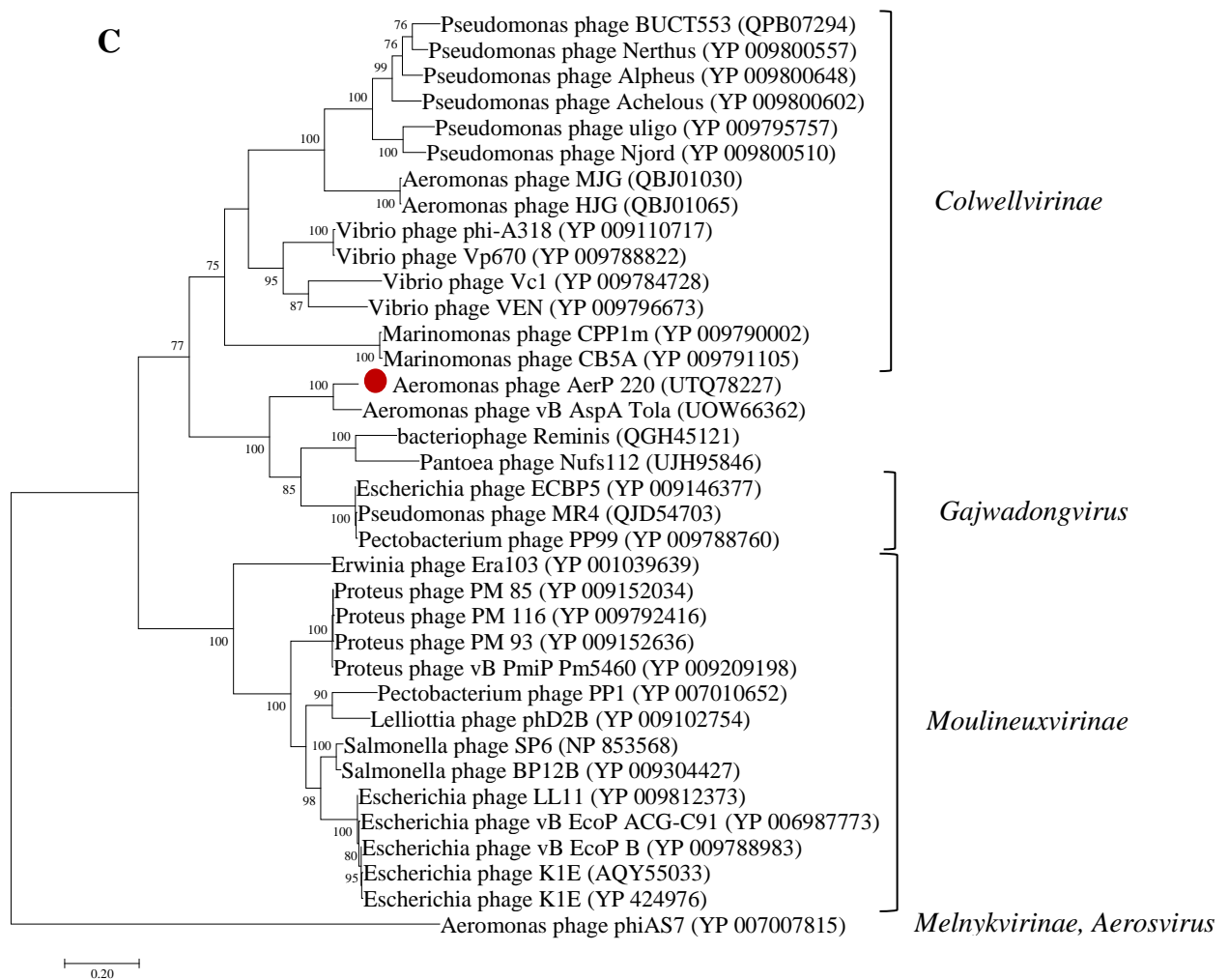


Figure S2. Phylogenetic analysis of three essential proteins of the investigated *Aeromonas* phage AerP_220 along with the most similar proteins: A, terminase large subunit; B, capsid protein; C, DNA-dependent RNA polymerase. GenBank identifiers for the protein sequences are shown in parentheses. The Maximum Likelihood method was used to construct the trees, 1000 bootstrap replications were applied. Statistical support above 70% is shown at the nodes. The sequence IDs of proteins of the investigated *Aeromonas* phage AerP_220 are marked with red circles. The appropriate proteins of *Aeromonas* phage phiAS7 were used as outgroup.