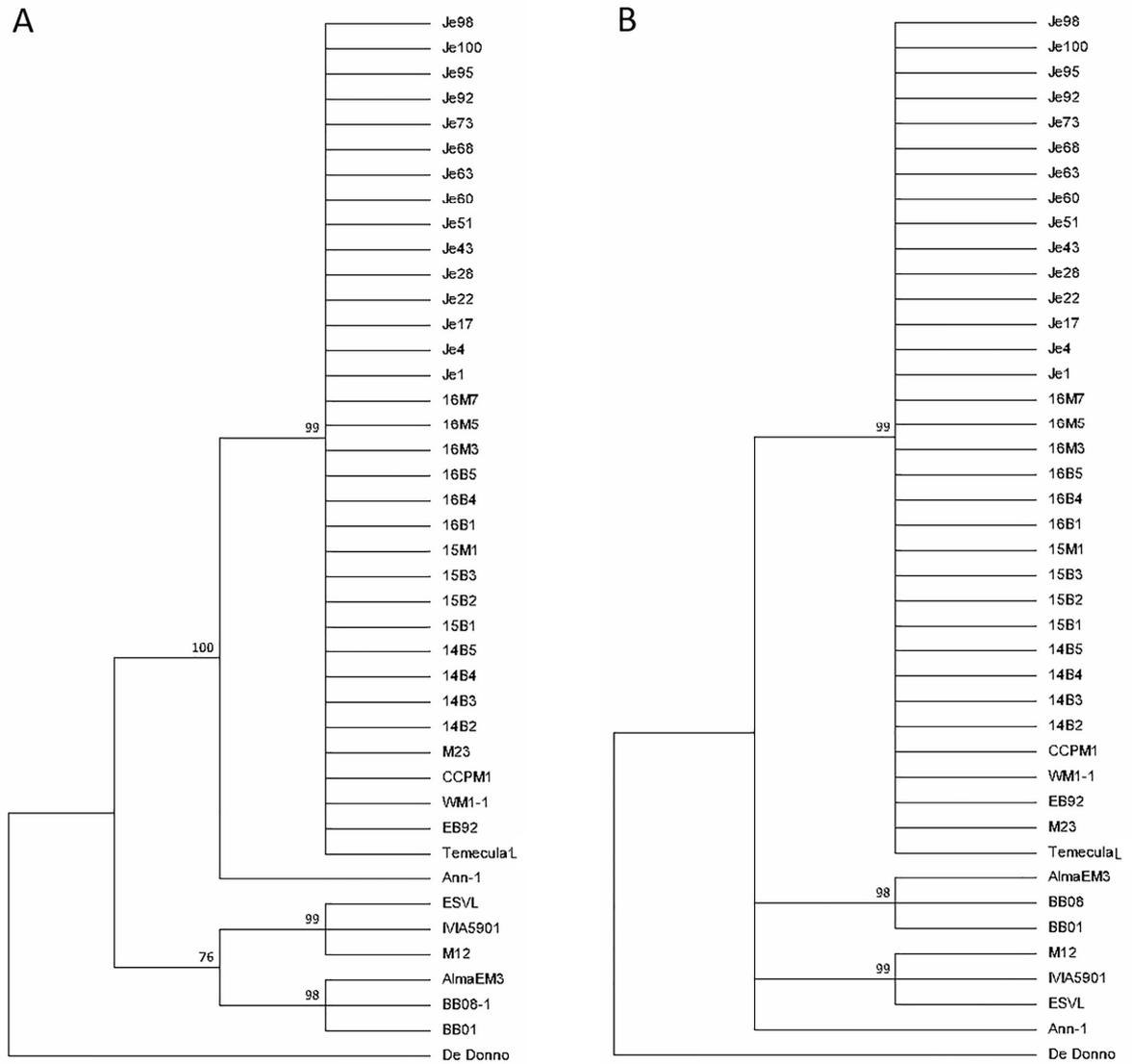
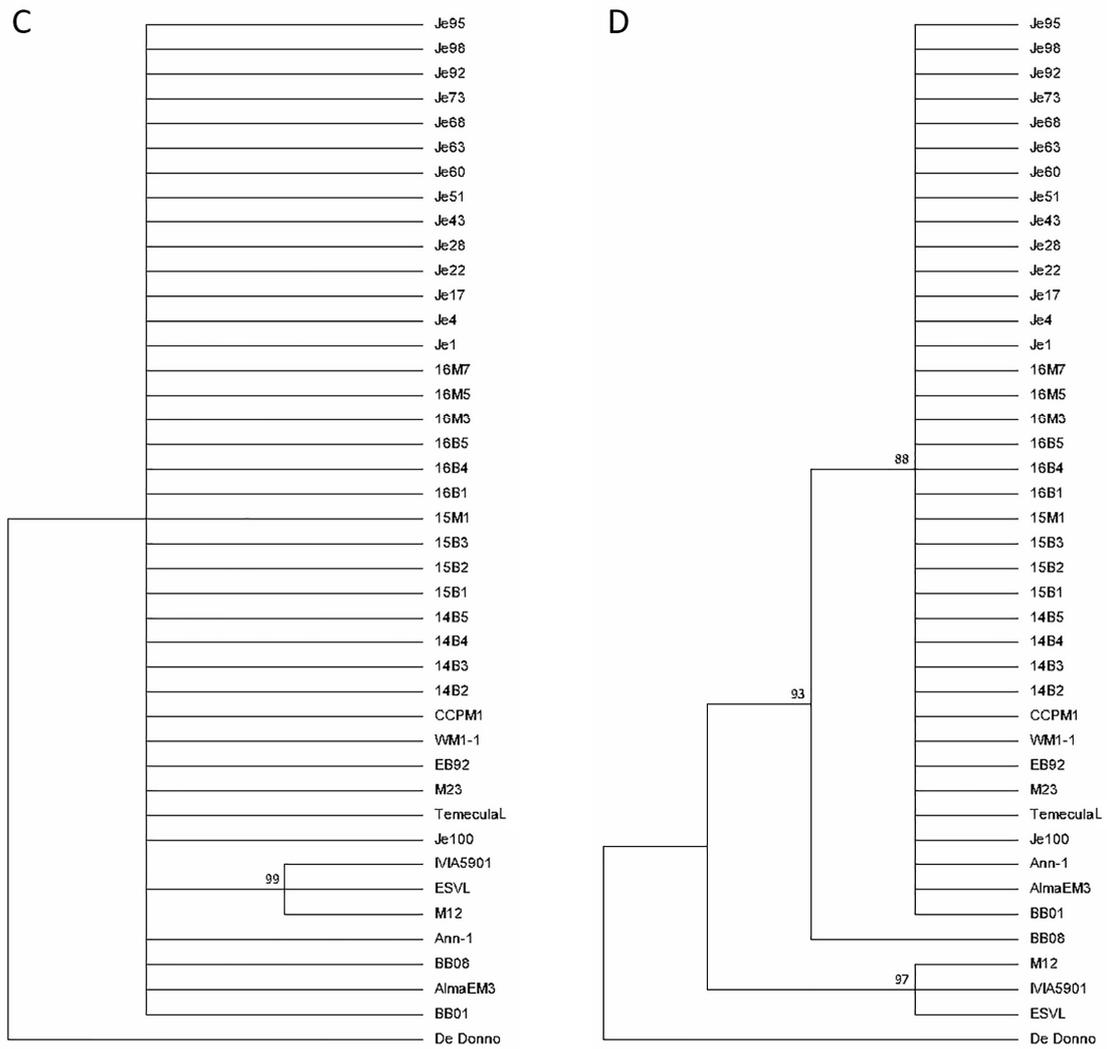


Figure S2: Phylogenetic trees of *copA*, *copB*, *copL* and *cutC* genes in the strains with Cu MIC that were tested.





Phylogenetic trees of *copA*, *copB*, *copL* and *cutC* genes in the strains with Cu MIC been assessed. Phylogenetic trees of (A) *copA*; (B) *copB*; (C) *copL* and (D) *cutC* genes in the strains that has been analyzed in Cu MIC experiment. Maximum-likelihood phylogenetic trees were built using MEGA 7.0, Branches below 70% of bootstraps value were collapsed