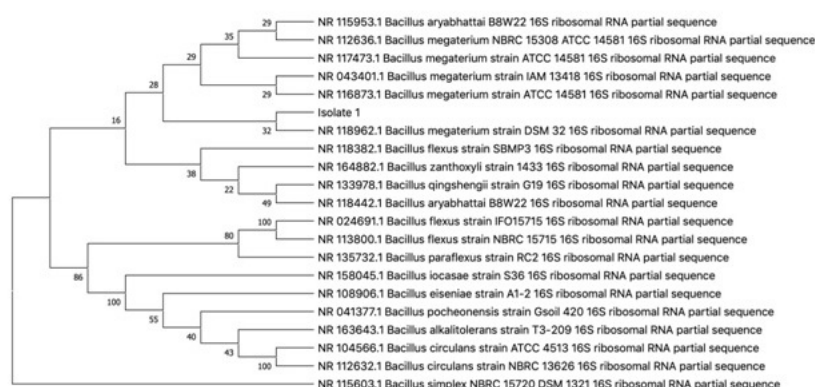


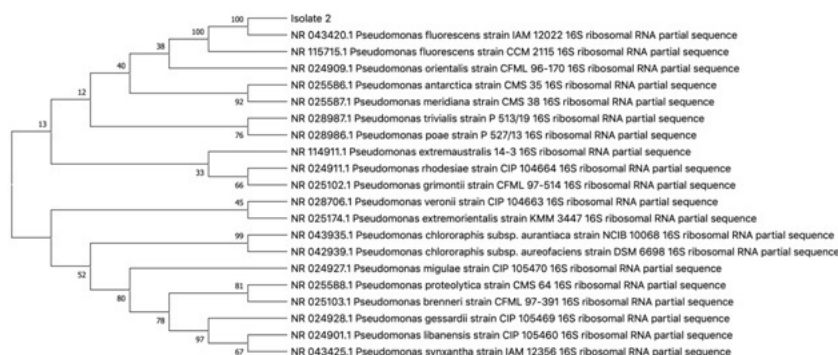
## Article

# Antimicrobial Potential of Microorganisms Isolated from the Bottom Sediments of Lake Baikal

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**Figure S1.** Phylogenetic tree showing the relative position of isolates 1 (*Bacillus megaterium*) based on 16S rDNA sequences, using the neighbor-joining method.



**Figure S2:** Phylogenetic tree showing the relative position of isolates 2 (*Pseudomonas fluorescens*) based on 16S rDNA sequences, using the neighbor-joining method.

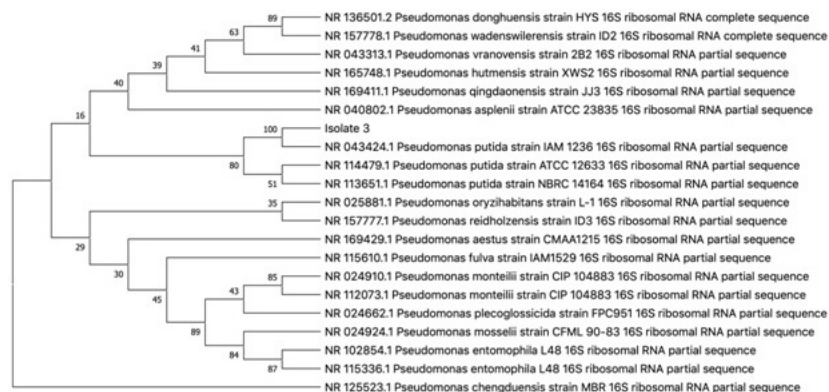


Figure S3: Phylogenetic tree showing the relative position of isolates 3 (*Pseudomonas putida*) based on 16S rDNA sequences, using the neighbor-joining method.

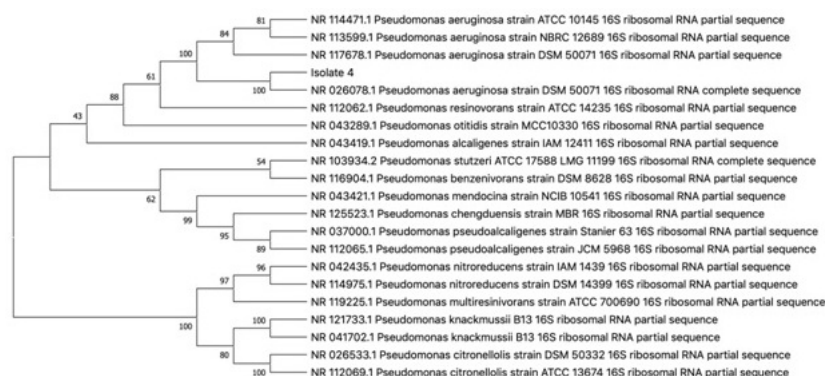


Figure S4: Phylogenetic tree showing the relative position of isolates 4 (*Pseudomonas aeruginosa*) based on 16S rDNA sequences, using the neighbor-joining method.

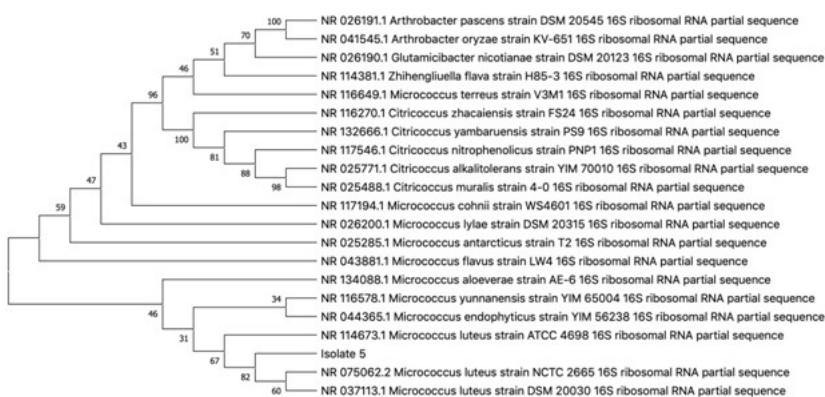


Figure S5: Phylogenetic tree showing the relative position of isolates 5 (*Micrococcus luteus*) based on 16S rDNA sequences, using the neighbor-joining method.

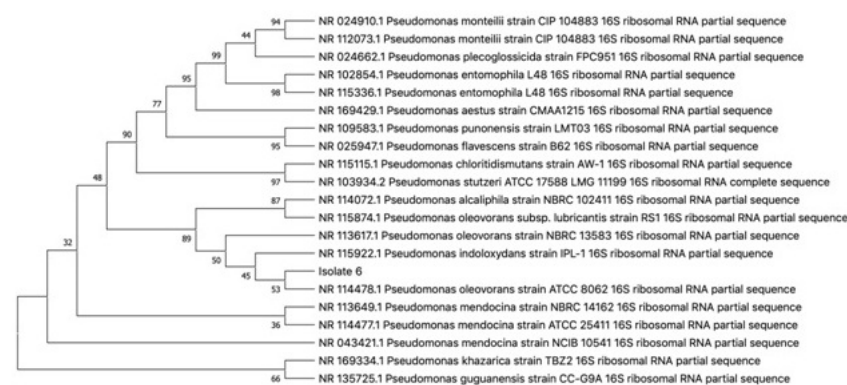


Figure S6: Phylogenetic tree showing the relative position of isolates 6 (*Pseudomonas oleovorans*) based on 16S rDNA sequences, using the neighbor-joining method.

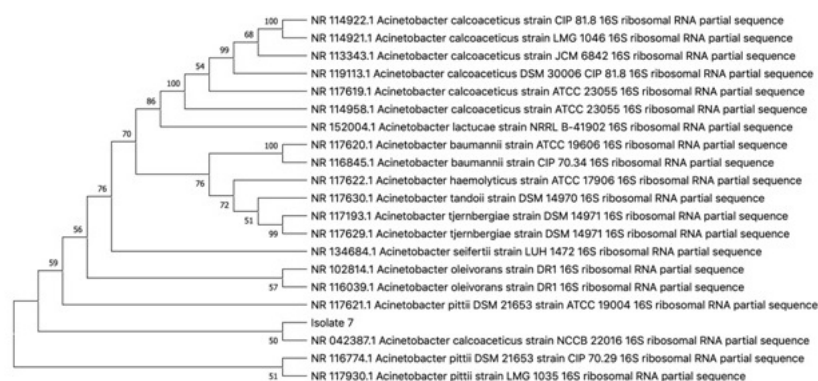


Figure S7: Phylogenetic tree showing the relative position of isolates 7 (*Acinetobacter calcoaceticus*) based on 16S rDNA sequences, using the neighbor-joining method.