





Figure S2a. Phylogenetic analysis tree of 16S rRNA genes of the strains isolated from the Mojave Desert soil, which were sequenced using 1100r primer. The tree was constructed using the Neighbor-Joining method with the use of the most closely related sequences from GenBank. The number of taxa—92. The number of significant characters—375. The number of bootstrap replicates—500. Confidence values of branching are given for cases of 50% and higher. Rhombus indicate strains isolated on the PYG media, triangles—isolated on the CM media; green and blue colors indicate strains isolated at 25 and 10°C, respectively. Red circle indicates subtree genera (Figures S2b, S2c). The scale under the tree indicates the number of phylogenetical significant changes of nucleotides.