

New strains of hydrocarbon oxidizing bacteria from Lake Beloe

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New oil-degrading bacterial strains 2012B and 2012C were isolated from Lake Beloe, one of three ice Kosinskie Lakes in Moscow region. Molecular identification of the bacterial strains was performed by using 16S rRNA gene sequence analysis (GenBank: KP779654.1, MG966152) and in case of 2012B strain, additionally *alkB* partial gene sequence (KR422620.1) was used. Phylogenetic reconstructions were performed by application of different methods (BIONJ, PhyML, DNAPars, MrBayes, and GARLI_ML). Comparison of rRNA gene sequences shows that 2012B strain belongs to genus *Rhodococcus*. Strain 2012B formed a coherent cluster with *R. erythropolis* NVI 00/50/667 (AY147876.1), *R. qingshengii* dj1-6 (NR_043535.1), *R. jialingiae* dj1-6-2 (NR_115708.1), and *R. erythropolis* DSM 43066^T(X79289). Phylogenetic analysis based on the *alkB* gene sequence placed strain 2012B in one cluster with *R. qingshengii* strain BLH-Y4 (KF696707). The morphological and chemotaxonomic properties of the isolate 2012B were typical for members of the genus *Rhodococcus*. Lipids

of the strain 2012B were comprised of C14:0-C19:0 fatty acids where the most abundant were C15:0 (54%), C16:0 (17%), and C17:0 (10%). Phylogenetic analysis by using 16S rRNA gene sequence revealed that the strain 2012C (GenBank: MG966152) has the highest identity and forms one cluster with *Pseudomonas* spp. (*P. oleovorans*, *P. oryzihabitans*, *P. psychrotolerans*, and *P. aeruginosa*). Lipids of the strain 2012C were comprised of C14:0-C19:0 fatty acids where the most abundant were C15:0 (45%), C16:0 (32%), and C17:0 (9%). These new bacterial strains could be useful in our future bioremediation experiments and in biotechnological applications.