

# Investigation of promising biotechnological strains from the FRC ICG SB RAS collection using omix technologies and bioinformatics methods

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*Motivation and Aim:* Bacteria are the most common living organisms. The number of studied cultivated bacteria is limited and, particularly, among extremophilic bacteria. These bacteria may utilise various multi-component chemical compounds, but genetic mechanisms of extremophile's metabolism are poorly understood [1]. A unique extremophilic microorganisms collection has been created in the Laboratory of Molecular Biotechnologies of the ICG SB RAS. The aim of the research is an analysis of metabolic activity genetic mechanisms of the extremophilic bacteria from the collection.

*Methods and Results:* Whole genome sequence of 1860 extremophilic bacterial strains from the collection was performed (Illumina MiSeq, USA) and annotated. After, bioinformatic analysis using KEGG PATHWAY was carried out for groups of genes involved in oil sludge metabolism. Next, 263 of all studied strains were selected and grown on the oil sludge. Ten species with the most abundant growth were selected for nanopore sequences and bacterial oxidations chemical oil sludge markers chromatography-mass spectrometry identification. It was shown that bacteria have more than 50 % genes in the following maps: Benzoate degradation [PATH:ko00362]; Aminobenzoate degradation [PATH:ko00627]; Toluene degradation [PATH:ko00623]; Polycyclic aromatic hydrocarbon degradation [PATH:ko00624]; Bisphenol degradation [PATH:ko00363]; Chlorocyclohexane and chlorobenzene degradation [PATH:ko00361]; Naphthalene degradation [PATH:ko00626]; Xylene degradation [PATH:ko00622]; Ethylbenzene degradation [PATH:ko00642]; Caprolactam degradation [PATH:ko00930]; Nitrotoluene degradation [PATH:ko00633]; Fluorobenzoate degradation [PATH:ko00364]; Chloroalkane and chloroalkene degradation [PATH:ko00625].

To reconstruct obtained gene chains, these ten strains were grown on various substrates and analysed using chromatographic analysis. Compounds, related to discreet oil fractions, were selected – vaseline oil, a model mixture of linear n-alkanes, oil sludge, and bitumen. Marker compounds of all found gene chains were found on the chromatograms, with the amount of these compounds varying contingent on the strain. For more complete description of heavy oil fractions degradation genetic mechanisms interactions, it is planned to conduct a transcriptomic analysis for the selected strains.

*Conclusion:* Among 1860 extremophiles from the collection of the ICG SB RAS, strains with the ability of rapid and efficient growth on heavy oil fractions were found. Complete genomes analysis was carried out, showing that studied strains have developed genetic

mechanisms for the various heavy oil fractions utilisation. Chemical markers of the studied genetic chains were identified using chromatographic methods.

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### *References*

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