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Unique localities, such as radioactive water springs, are a promising source of as-yet-undiscovered microorganisms or microorganisms with special properties. Generally, though, most such microorganisms are difficult to obtain in pure culture. The aim of this study is to perform microbial screening of radioactive water springs for a purpose of finding yet-to-be cultured organisms. In an attempt to increase cultivation yields, we investigate the use of classical cultivation approaches and diffusion methods. Four radioactive water springs were sampled in Jachymov, Czech Republic. Microorganisms for microbial screening were collected by filtering 30 L of spring water. The obtained filters were used for the isolation of DNA and for the description of microbiomes we used phylogenetic analysis based on sequencing of the 16S rRNA gene on the Illumina MiSeq platform. Plating, traditional media as well as non-traditional approaches were used for cultivation under laboratory conditions. The obtained isolates were identified by MALDI-TOF MS as members of the families Pseudomonaceae, Bacillaceae, Caulobacteraceae, etc. Many isolates remained unidentified and will be subjected to further studies. Sequencing of the 16S rRNA gene also revealed the presence of as-yet-undescribed taxa. In summary, deep spring waters contain diverse bacterial populations, including yet-to-be cultured bacterial clades of different phylogenetic origin. Furthermore, improved cultivation techniques can increase the efficiency of cultivation of these taxa.

612B - Microbiome structure of Karvachar (Nagorno-Karabakh) geothermal spring

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Geothermal springs create unique niches for formation specific biocenoses of thermophiles and serve as source for isolation of new microbes with biotechnological potentials. Numerous geothermal springs are found on the territory of Nagorno-Karabakh. Microbial communities of Nagorno-Karabakh geothermal springs are still poorly investigated and represent a potential source for new extremophlic microbes. The aim of this study was to determine the microbial diversity of water and sediment samples of a geothermal spring located in the Karvachar region of Nagorno-Karabakh. The spring is circumneutral and moderately hot, with outlet water temperature and conductivity of >70 °C and 4600 µS/cm, respectively. Metagenome analysis based on Illumina HiSeq platform yielded more than 11 million high quality sequence reads for water and sediment samples. The number of reads assigned to Bacteria were 94.2 % for water and 83.8 % for sediment samples. Archaea sequence reads were in minority, comprising 0.04% and 0.07% of total reads for water and sediment samples, respectively. The thermal water was dominated by Proteobacteria (>85% of total reads) followed by