

Identification of genes associated with transformations of metals and metalloids in metagenome of the microbial mats

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Microbial mats found in bottom sediments of ancient gold mine located in Złoty Stok (SW Poland) are example of highly diversified community adapted to function in extreme environment. It can grow in the presence of different heavy metal minerals [like arsenic (loellingite, scorodite, arsenopyrite), iron (magnetite, pyrrhotine, pyrite) lead (galena), zinc (sphalerite) and copper (chalcopyrite)] as well as high concentration of soluble forms of heavy metal (like As, Co, Cu, Fe, Ni, Mn) compounds. Adaptation to survive under such unfavorable conditions is determined by physiological and genetical abilities of the individual bacteria, as well as the whole community.

The aim of this work was identification of genes present in metagenome of the microbial mats associated with transformation of metals and metalloids, and assigning them to the individual bacteria creating the structure of microbial mats.

To assess the genetic potential of organisms found within microbial mats to mobilize heavy metals a shotgun sequencing strategy of metagenomic DNA was used. Obtained NGS data were analysed using query sequences of proteins associated with specific autotrophic (CO₂ fixation) pathways, electron transfer involving C, Fe, S, As, N, H₂ or O₂ and heavy metal detoxification systems (for Ag⁺, AsO₂⁻, AsO₄³⁻, Cd²⁺, Co²⁺, CrO₄²⁻, Cu²⁺, Hg²⁺, Ni²⁺, Pb²⁺, and Zn²⁺).

The metagenomic analysis of microbial mats showed that the most abundant group of microorganisms able to transform mineral deposits and heavy metal compounds are chemolithoautotrophic bacteria with genes responsible for CO₂ binding as well as iron, sulfur and arsenic oxidation. Moreover, metagenomic data suggest that methanotrophs, highly represented in microbial mat, play an important role in dissolution of many metal minerals.