

Methods of molecular biology enable studies on microbial diversity based on analysis of genes encoding processes and biochemical pathways of individual microorganisms and also complete microbial consortia. For this a crucial step was elaboration of new technologies of high-throughput DNA sequencing. These methods made it possible to advance studies of diversity from analysis of genomes of model microorganisms easily cultivated in laboratories to simple communities living in extreme environments and further to complex microbial consortia. This experimental approach is based on metagenomic analyses.

Important are studies on ecosystems negatively affected by human activity where microorganisms not only survive but they can convert their metabolism to degrade compounds toxic for higher organisms. An example is bacterium *Achromobacter xylosoxidans* A8 isolated from soils contaminated by toxic chlorobenzoates. Sequencing and analysis of *Achromobacter xylosoxidans* A8 genome made it possible to study genes coding for enzymes that are involved in chlorobenzoates degradation in the context of the complete genetic background.

An interesting microbial biofilm – gelatinous stalactites – was discovered in an extremely acidic environment of the abandoned mine in Zlaté Hory (the Czech Republic). It is formed by a simple consortium with predominantly present bacterial genus *Ferroplasma* and genus *Acidithiobacillus*. DNA sequencing of the biofilm sample and bioinformatic analysis of the obtained data enabled us to reconstruct two nearly complete genomes without growing individual bacterial strains that are difficult to cultivate. By RNA analysis expressed genes of the consortium were identified. Thus, metabolic processes of the present bacterial strains can be described. Comparative analysis shows unique properties of individual members of the analyzed consortium that are important in the particular natural conditions.

Much more complex systems are found in soil. We sequenced „soil DNA“, amplified 16S rRNA genes and constructed metagenomic profiles of the samples. Using this approach we discovered effect of different plant species on taxonomic composition and functional potential of microbial communities that can degrade pollutants.