

The thesis focuses on studying changes of microbial communities living in the soil contaminated by heavy metals. Two sites with different degree of contamination were selected in the Příbram area. Respiration was measured *in vitro* in the soil samples supplemented with various carbon sources and different concentration of cadmium. The respiration showed that even at cadmium concentration of 1000 mg.kg⁻¹ the community is viable and capable of utilization of substrates while increasing the respiration rate.

Environmental DNA from soil samples was isolated and 16S rRNA gene of actinobacteria was amplified. The terminal restriction fragment length polymorphism analysis showed a clear difference between the profiles of both sites. The shifts in the community profiles were observed also after the addition of substrates.

The quantification of total bacteria and actinobacteria was performed by quantitative PCR based on amplification of part of the 16S rRNA gene. The more contaminated site contained slightly more bacteria, but almost twice the actinobacteria than the less contaminated one. The sequencing of amplicons of a part of 16S rRNA gene by Illumina showed an increase in proportion of actinobacteria and changes of their community structure in the more contaminated site.

The conclusion was made that, high long-term contamination with heavy metals increases respiratory activity even more so under stress conditions induced by added cadmium and reduced stability of the bacterial community.