

This work is focused on microbial communities living in the soil affected by long-term exposure to heavy metals. The soil was sampled at two sites with different levels of contamination near Příbram. In the samples, respiration rate was measured in vitro after addition of carbon sources and at different levels of cadmium, one of the contaminating metals found in the soil. After the incubation with carbon sources, soil samples were collected for environmental DNA isolation. Gene coding for 16S rRNA in Actinobacteria was amplified from the environmental DNA samples and the amplicon composition was assessed by terminal restriction fragment length polymorphism analysis. The resulting profiles were used to compare actinobacterial communities in both groups of soil samples and in individual treatments. The analysis showed a clear distinction between the two sites differing in the contamination level and shifts in the community composition of various intensity depending on the added substrate.