Abstract

The need for new antibiotics and other biologically active compounds is the reason for an increased interest in secondary metabolites of soil bacteria. The phylum *Actinobacteria* has the dominant position in the soil environment thanks to the potential of producing a broad spectrum of antibiotics and the presence of a number of defense mechanisms preventing the effects of antibiotics.

The aim of this thesis was to determine the number of copies of selected secondary metabolic genes in the soils of two sites using designed primers and primers from literature. The design of effective new primers for the detection of selected genes in the soil environment was not achieved in this work, and therefore only primers from literature that had been verified for their specificity were used. In samples taken from soil profiles of two sites, abundances of bacteria, actinobacteria, type II polyketide synthase genes and Erm methyltransferase genes mediating resistance to MLS_B antibiotics (macrolides, lincosamides and streptogramins B) were determined by digital PCR. The comparison of the determined copy numbers gave an information about the structure of the bacterial community and the relative abundance of bacteria carrying selected secondary metabolic genes depending on the soil condition changes due to the forest canopy and the increasing depth of the soil profile.

The amounts of bacteria and actinobacteria reached the highest levels in the litter horizons of both sites, the influence of different site was evident in the lower horizons. Distinct soil properties also affected abundance of type II polyketide synthase genes, mainly in the upper layers of the soil. In the litter horizon of the beech forest, their significantly lower absolute and relative abundances among actinobacteria were observed. Differences in abundances of Erm methyltransferase genes were also observed between soil horizons when comparing both sites. In contrast to the spruce forest, a decrease of their abundance with the depth of soil profile was observed in the beech forest. The data obtained in this work evidenced that type of vegetation cover, and consequently plant litter input, at two otherwise comparable sites determined bacterial comunity abundance and its secondary metabolic gene pool.

Key words: Actinobacteria, secondary metabolism, resistance