

Effect of *Silene vulgaris* and Heavy Metal Pollution on Soil Microbial Diversity in Long-Term Contaminated Soil

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Abstract In this study, we analysed the impact of heavy metals and plant rhizodeposition on the structure of indigenous microbial communities in rhizosphere and bulk soil that had been exposed to heavy metals for more than 150 years. Samples of the rhizosphere of *Silene vulgaris* and non-rhizosphere soils 250 and 450 m from the source of emission that had different metal concentrations were collected for analyses. The results showed that soils were collected 250 m from the smelter had a higher number of Cd-resistant CFU compared with the samples that were collected from 450 m, but no significant differences were observed in the number of total and oligotrophic CFU or the equivalent cell numbers between rhizosphere and non-

rhizosphere soils that were taken 250 and 450 m from the emitter. Unweighted pair group method with arithmetic mean (UPGMA) cluster analysis of the denaturing gradient gel electrophoresis (DGGE) profiles, as well as a cluster analysis that was generated on the phospholipid fatty acid (PLFA) profiles, showed that the bacterial community structure of rhizosphere soils depended more on the plant than on the distance and metal concentrations. The sequencing of the 16S rDNA fragments that were excised from the DGGE gel revealed representatives of the phyla *Bacteroidetes*, *Acidobacteria*, *Gemmatimonadetes*, *Actinobacteria* and *Betaproteobacteria* in the analysed soil with a predominance of the first three groups. The obtained results demonstrated that the presence of *S. vulgaris* did not affect the number of CFUs, except for those of Cd-resistant bacteria. However, the presence of *S. vulgaris* altered the soil bacterial community structure, regardless of the sampling site, which supported the thesis that plants have a higher impact on soil microbial community than metal contamination.

Highlights · Long-term exposure to heavy metals significantly decreases the bacterial number.
· Microbial communities respond to heavy metals by changing their PLFA profiles.
· Heavy metals change the genetic diversity of soil microorganisms.
· *Bacteroidetes*, *Acidobacteria* and *Gemmatimonadetes* were dominant in the polluted soils.

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1 Introduction

Industrial development and mining activities have led to a significant environmental heavy metal contamination in many locations around Europe. One such polluted area is Upper Silesia in Southern Poland where several ferrous and non-ferrous metal processing plants have emitted