

## Effect of mineral and organic additions on the microbiocenotic composition of soil contaminated with heavy metals

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Qualitative changes in microbial populations have a significant impact on soil functional integrity, and soil microbial diversity is fundamental to sustainable environmental management. Soil microorganisms play a key role as indicators of soil quality given their participation in many biochemical processes that are essential for the environment and ecological functions of soil (Mierzwa-Hersztek *et al.* 2020). The addition of external organic matter to soil can lead to significant changes in the structural and functional diversity of microbial populations and thus alteration in the intensity of microbial degradation of organic linkages (Kopeć *et al.* 2020).

The aim of the study was to assess the effect of organic materials on changes in the microbiocenotic composition of soil. The experimental scheme included two reference treatments: C – soil without fertilisation (contaminated with  $\text{CdSO}_4 \times 8/3\text{H}_2\text{O}$ ,  $\text{C}_4\text{H}_6\text{O}_4\text{Pb} \times 3\text{H}_2\text{O}$  and  $\text{ZnSO}_4 \times 7\text{H}_2\text{O}$ ); MF – soil with NPK mineral fertilisers; CW3%, CW6% – soil with the addition of 3 or 6% of lignite and 3% of a zeolite/vermiculite composite (NaX-Ver); CL3% and CL6% – soil with the addition of 3 or 6% of leonardite and 3% of a zeolite/vermiculite composite. The pot experiment was carried out on surface soils, which are included in the agronomic category of light soils. The test plant was maize. The following were determined in the soil material: the number of bacteria, fungi, actinomycetes, *Azotobacter*, nitrifiers, denitrifiers and ammonifiers, as well as *Clostridium pasteurianum*. Microbiological analyses were performed using Koch's serial dilution method (Mierzwa-Hersztek *et al.* 2020). The species composition of the population of microorganisms colonising the soil material was also evaluated. The MALDI-TOF MS technique (Bruker Daltonik, Germany) was used to identify species of soil microorganisms of agricultural importance, whose presence in the soil increases its fertility and plant yield, and furthermore contributes to the elimination of phytopathogens (Wolny-Koładka, 2018).

The study revealed that the number of soil microorganisms depended on the type and amount of organic material applied. The soil with a 6% addition of lignite or leonardite had a significantly higher number of bacteria, fungi and actinomycetes. Bacteria constituted the most numerous group of microorganisms (Figure 1), fungi (Figure 2) and ammonifiers (Figure 3) were six times less numerous, and actinomycetes (Figure 4) were 30 times less numerous in the analysed soil. No *Azotobacter* bacteria were determined in the analysed soil samples. The titers of nitrifiers, denitrifiers and *Clostridium pasteurianum* in the soil ranged from  $10^{-2}$  to  $10^{-4}$ .



Figure 1

Figure 2

Figure 3

Figure 4

The addition of 3 or 6% of lignite and 3% of a zeolite/vermiculite composite (NaX-Ver) as well as 3% of leonardite and 3% of a zeolite/vermiculite composite significantly increased the number of bacteria, ammonifiers and fungi (Figure 5).

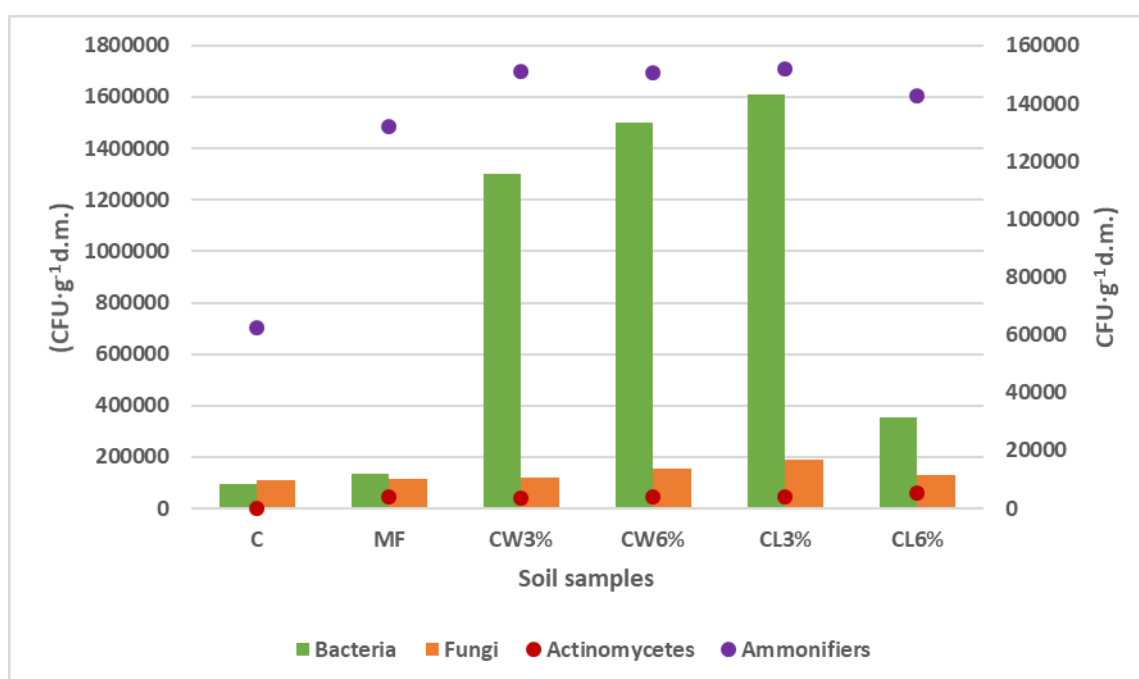


Figure 5. Average number of microorganisms in the soil samples.

The isolation of microorganisms inhabiting the soil material allowed to identify the following beneficial microorganisms: bacteria (*Pantoea agglomerans*, *Pseudomonas syringae*, *Pseudomonas fluorescense*, *Bacillus subtilis*), fungi (*Ampelomyces quisqualis*, *Coniothyrium minitans*, *Trichoderma harzianum*, *Trichoderma asperellum*, *Trichoderma atroviride*, *Trichoderma viride*), actinomycetes (*Streptomyces griseus*, *Streptomyces aureofaciens*, *Micromonospora purpurea*, *Streptomyces nodosus*, *Streptomyces antibioticus*, *Streptomyces orientalis*, *Streptomyces kanamyceticus*), yeast (*Aureobasidium pullulans*, *Candida sake*, *Candida oleophila*, *Cryptococcus albidus*, *Metschnikowia fructicola*, *Pseudozyma flocculosa*). The presence of the above microorganism species in soil is extremely desirable, because their growth and development is one of the pillars on which the proper functioning of the soil environment, as well as the growth and yielding of crops, are based.

#### References:

1. Kopeć M., Mierzwa-Hersztek M., Gondek K., Wolny-Koładka K., Zdaniewicz M., Jarosz R. 2020. Biological activity of composts obtained from hop waste generated during the brewing. *Biomass Conversion and Biorefinery*, DOI: 10.1007/s13399-020-00746-6.
2. Mierzwa-Hersztek, Wolny-Koładka K., Gondek K., Gałazka A., Gawryjolek K. 2020. Effect of coapplication of biochar and nutrients on microbiocenotic composition, dehydrogenase activity index and chemical properties of sandy soil. *Waste and Biomass Valorization*, 11:3911–3923. DOI: 10.1007/s12649-019-00757-z.
3. Wolny-Koładka K. 2018. Resistance to antibiotics and the occurrence of genes responsible for the development of methicillin resistance in *Staphylococcus* bacteria isolated from the environment of horse riding centers. *Journal of Equine Veterinary Science*, 61:65-71. DOI: 10.1016/j.jevs.2017.11.010.

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