The effect of compost and sand addition on microbial respiration and denitrification in prepared reclamation substrates

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Introduction: Microbial soil respiration results from the mineralization of organic substances. In this process, organic substances are oxidized to the end products CO_2 and water. Respiration and denitrification are a measure of the overall activity of soil microorganisms.
Methods: One control variant (only arable soil) and fourteen variants with reclamation substrates (soil + compost or soil + compost + sand) were prepared. In each variant was monitored basal respiration – BR (CO_2 release) and microorganism's denitrification ability (N_2O release). Gas production was analyzed by gas chromatography (Agilent Technologies 7890A) in accordance with Czech Technical Standard (CSN EN ISO 16072).
Results and discussion: Cumulative CO_2 and N_2O production was determined during 24 h incubation and under laboratory conditions. In control variant was BR 0,59 μg C-$CO_2 \cdot g^{-1} \cdot h^{-1}$ and N_2O release 0,12 ng N-$N_2O \cdot g^{-1} \cdot h^{-1}$. In prepared reclamation substrates BR varies from 0,73 (10 % compost + 90 % soil) to 1,77 μg C-$CO_2 \cdot g^{-1} \cdot h^{-1}$ (40 % compost + 50 % soil + 10 % sand) and
N_2O production varies from 0,38 (10 % compost + 70 % soil + 20 % sand) to 8,09 ng N-$N_2O \cdot g^{-1} \cdot h^{-1}$ (40 % compost + 40 % soil + 20 % sand).
Conclusion: Organic carbon which is contained in compost represents the energy for microorganisms. The growth in microbial activity is reflected in rise of their respiration and denitrification of nitrates. The addition of sand gas production in most variants even increased (with the same amount of compost addition).
Key words: compost, soil, sand, respiration.
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The isolation of heavily cultivable and previously uncultivated bacteria from heavy-metal-contaminated soil by using a diffusion chamber

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Introduction: With accordance to the fact that majority of living bacteria leaving "uncultured", the aim of the present study was to isolate and identify heavily cultivable and previously uncultured bacterial isolates from toxic metal contaminated soil by using a diffusion chamber.
Materials and methods: The heavy-metal-contaminated soil was used to inoculate the diffusion chamber, and a phylogenetic analysis was performed to determine both, the structure of the chamber-derived bacteria using partial sequences of the 16S rRNA (16S rDNA) and heavy-metal resistance genes.
Results and discussion: A total of 128 chamber-derived isolates represented 65 species belonged to 5 bacterial phyla. The majority of the bacteria were classified as *Proteobacteria* or *Firmicutes*. In addition, 34 % of the isolates were found as previously uncultivated bacteria, and 45 % of isolated bacteria were considered to belong to new species or genera. The majority (59 %) of these "new" species or genera were found as previously uncultivated bacteria. Furthermore, the heavy-metal-resistance genes of 16 previously uncultured bacteria were identified by phylogenetic analysis of their protein sequences. These results suggested that the cultivation strategy used offers a new approach to enlarge the access to the diversity of environmental organisms.
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