Impacts of heavy metal contamination and phytoremediation on a microbial community during a twelve-month microcosm experiment

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Abstract

The effects of heavy metals and phytoextraction practices on a soil microbial community were studied during 12 months using a hyperaccumulating plant (Thlaspi caerulescens) grown in an artificially contaminated soil. The 16S ribosomal RNA genes of the Bacteria and the β-Proteobacteria and the amoA gene (encoding the α-subunit of ammonia monooxygenase) were PCR-amplified and analysed by denaturing gradient gel electrophoresis (DGGE). Principal component analysis (PCA) of the DGGE data revealed that: (i) the heavy metals had the most drastic effects on the bacterial groups targeted, (ii) the plant induced changes which could be observed in the amoA and in the Bacteria 16S rRNA gene patterns, (iii) the changes observed during 12 months in the DGGE-patterns of the planted contaminated soil did not indicate recovery of the initial bacterial community present in the non-contaminated soil. The potential function of the microbial community was assessed recording community level physiological profiles (CLPP) and analysing them by PCA. The lower capability of the bacterial community to degrade the substrates provided in the BIOLOG plates, in particular the amino acids, amides and amines, as well as a delay in the average well colour development (AWCD) differentiated the bacterial community of the contaminated samples from that of the non-contaminated ones. However, the plant had a positive effect on substrate utilization as shown by the greater number of substrates used in all planted samples compared to unplanted ones. Finally, the measurement of the potential ammonia oxidation indicated that ammonia oxidising bacteria were completely inhibited in the contaminated soil. The stimulation of ammonia oxidation by the plant observed in the non-contaminated samples was surpassed by the inhibitory effect of the heavy metals in the contaminated soil. This study emphasises the combined use of culture-independent techniques with conventional methods to investigate the ecology of bacteria in their natural habitats.

Keywords: Heavy metal contaminated soil; DGGE; CLPP; Potential ammonia-oxidation; Thlaspi caerulescens; Rhizosphere

1. Introduction

Heavy metal contamination of soils originating from agricultural (e.g., fertilizers and sewage sludge) or industrial activities (e.g., metal mining and smelting) is one of the major environmental problems in many parts of the world. The resulting damage is difficult to cure as metals cannot be chemically degraded [1]. Heavy metals affect all groups of organisms and ecosystem processes, including microbial activities [2–4]. Remediation approaches such as excavation and land fill, thermal treatment, electroreclamation and soil capping have been proposed depending on the extension, depth and kind of contamination, but all are expensive and environmentally destructive [5]. Phytorextraction, the use of plants to extract metals from soil, has been reported to be very efficient for cleaning up superficially contaminated soils [1,6–8]. This alternative remediation technique is promising as it is cheaper and less invasive than

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The aim of this study was to determine the impact of heavy metals and phytoextraction practices on microbial community structure at different levels of resolution and, more specifically, on a representative key soil function (ammonia oxidation). We were particularly interested in ammonia oxidising bacteria as these important catalysts of an essential step in the N cycle are known to be very sensitive to heavy metal pollution. For this purpose, we combined the two complementary fingerprinting techniques denaturing gradient gel electrophoresis (DGGE) and community level physiological profiling (CLPP) with the measurement of the potential ammonia oxidation rates. The resolution of the DGGE-approach was varied by targeting either the 16S rRNA gene (encoding the ammonia monooxygenase) as an alternative functional marker.

2. Materials and methods

2.1. Soil characteristics and sample preparation

The soil was kindly provided by the Swiss Federal Institute for Forest, Snow and Landscape Research (Birmensdorf, Switzerland). It was loamy with 15.1% clay, 49.4% silt and 35.5% sand. pH values and amounts of total and soluble heavy metals are presented in Table 1. Heavy metal dust (Zn [755 mg kg⁻¹], Cu [85 mg kg⁻¹], Cd [3 mg kg⁻¹]) was obtained from the air filters of a brass-smelter in Dornach (Switzerland) and mixed (3.7 g dust kg⁻¹ soil) into one part of the sieved soil (<2 mm). The rest remained non-contaminated. Both soils were wetted to 80% of their water-holding capacity, stored at 10 °C in the dark and mixed weekly for three months.

### Table 1

<table>
<thead>
<tr>
<th>Time</th>
<th>Sampling</th>
<th>pH&lt;sub&gt;soil&lt;/sub&gt;</th>
<th>Zn&lt;sub&gt;sol&lt;/sub&gt; (mg kg⁻¹)</th>
<th>Cd&lt;sub&gt;sol&lt;/sub&gt; (mg kg⁻¹)</th>
<th>Cu&lt;sub&gt;sol&lt;/sub&gt; (mg kg⁻¹)</th>
<th>Zn&lt;sub&gt;total&lt;/sub&gt; (mg kg⁻¹)</th>
<th>Cd&lt;sub&gt;total&lt;/sub&gt; (mg kg⁻¹)</th>
<th>Cu&lt;sub&gt;total&lt;/sub&gt; (mg kg⁻¹)</th>
<th>Zn&lt;sub&gt;uptake&lt;/sub&gt; (mg kg⁻¹)</th>
<th>Cd&lt;sub&gt;uptake&lt;/sub&gt; (mg kg⁻¹)</th>
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<tbody>
<tr>
<td>3 months</td>
<td>Unplanted</td>
<td>7.2</td>
<td>500</td>
<td>20</td>
<td>35</td>
<td>670</td>
<td>50</td>
<td>280</td>
<td>3.7</td>
<td>10</td>
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<tr>
<td>6 months</td>
<td>Unplanted</td>
<td>7.8</td>
<td>500</td>
<td>20</td>
<td>35</td>
<td>670</td>
<td>50</td>
<td>280</td>
<td>3.7</td>
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<tr>
<td>9 months</td>
<td>Unplanted</td>
<td>7.5</td>
<td>500</td>
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<td>670</td>
<td>50</td>
<td>280</td>
<td>3.7</td>
<td>10</td>
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<tr>
<td>12 months</td>
<td>Unplanted</td>
<td>7.3</td>
<td>500</td>
<td>20</td>
<td>35</td>
<td>670</td>
<td>50</td>
<td>280</td>
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<tr>
<td>6 months</td>
<td>Planted</td>
<td>7.2</td>
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<td>9 months</td>
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<td>7.5</td>
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<td>12 months</td>
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*Plant dry weight was 3.2 g at 3 months, 1.3 g at 6 months, 1.1 g at 9 months, 0.5 g at 12 months. Pots contained 2 kg soil.

The rest remained non-contaminated. Both soils were wetted to 80% of their water-holding capacity, stored at 10 °C in the dark and mixed weekly for three months.
Pot experiments were carried out in plastic flower pots containing 2 kg of soil.

2.2. Plant growth conditions

*Thlaspi caerulescens* seeds were obtained from a population grown near an ancient Pb/Zn mine in Saint-Laurent-le Minier, Southern France. They were stored at 4 °C before use. The seeds were germinated on non-contaminated garden soil for 25 days. One seedling of *T. caerulescens* was subsequently transplanted into three pots containing contaminated and three containing non-contaminated soil. The plants were grown for three months in a climate chamber at 20 °C during daytime and 16 °C during night time with 16 h of light alternating with 8 h of darkness. Three unplanted pots were filled with contaminated soil and three with non-contaminated soil and also incubated in the climate chamber. The pots were watered with 100 ml deionized water every 4 days.

2.3. Heavy metal analysis

Total heavy metal content (extracted with 2 M HNO₃) and the soluble heavy metal fraction (extracted with 0.1 M NaNO₃) of the contaminated soil were measured according to the Swiss law recommendations [20]. Plant shoots were collected, oven-dried at 70 °C, weighed and ground in a tungsten Retsch mill (Haan, Germany). They were subsequently digested according to Hammer and Keller [21] to analyze heavy metal content. All soil and plant heavy metal concentrations were determined with Inductively Coupled Plasma Atomic Emission Spectrometry (ICP-AES, Perkin-Elmer Plasma 2000) and all samples were run together with certified reference materials.

2.4. Sampling

Every 3 months, for 12 months, plants and soil were removed from pots and each plant was shaken carefully to remove the bulk soil. The soil still adhering to the roots, defined as rhizosphere soil, was separated from the roots by moderate agitation in 50 ml of sterile 0.9% NaCl solution for 5 min and then centrifuged at 8000g for 10 min [22]. Samples from unplanted pots were used as controls. Subsamples (0.6 g wet weight) were filled in 2-ml cryotubes and stored at −20 °C until further use. After sampling, pots were refilled with soil and and planted with fresh seedlings.

2.5. DNA extraction

Total soil DNA was extracted from 0.6 g (wet weight) samples of each of the three rhizosphere and unplanted soil samples from contaminated or non-contaminated pots using the protocol of Griffiths et al. [23] with some modifications. Briefly, 0.5 ml of CTAB buffer, 0.5 ml of phenol-chloroform-isoamylalcohol (25:24:1) and 0.75 g 0.1-mm glass beads were added to each sample. The mixture was shaken twice for 45 s in a Fastprep beadbeater (Bio 101) at 4 m s⁻¹. Samples were stored on ice for 1 min between each run. The lysed sample was then centrifuged (16,000g) for 5 min at 4 °C. An equal volume of chloroform-isoamylalcohol (24:1) was added to the aqueous phase to remove the remaining phenol. The supernatant was subsequently incubated for 2 h at room temperature with 2 volumes of the precipitation solution (30% polyethylene glycol 6000 in 1.6 M NaCl). DNA was pelleted by centrifugation at 18,000g for 10 min at 4 °C, washed once with ice cold 70% ethanol, and resuspended in 50 μl TE (pH 7.4). One microliter of the DNA solution was used as template for PCR amplification.

2.6. PCR amplification

PCR amplification of 16S ribosomal RNA genes was performed with a PTC-200 thermal cycler (MJ Research). The 50-μl PCR mixture contained 0.2 μM of each primer, 200 μM of each deoxynucleoside triphosphate, 1× PCR buffer (Qiagen), 2.5 mM MgCl₂, 4.95 mg ml⁻¹ BSA, and 1 U Taq Polymerase (Qiagen). To minimize non-specific annealing of the primers to non-target DNA, Taq Polymerase was always added after an initial denaturing step at 94 °C for 5 min. Bacterial 16S rRNA genes were amplified with the primer combination 341f-GC and 907r according to Muyzer et al. [24] and the following program: 30 cycles at 94 °C for 1 min, 58 °C for 1 min, 72 °C for 2 min and a final extension at 72 °C for 10 min. A semi-nested PCR was used for amplification of 16S rRNA genes of β-Proteobacteria with initial amplification with (20 cycles) with primers 948f and 1492r [25] following the protocol of Gomes et al. [26] and reamplification with 1 μl of the first PCR product with the primer pair 948f-GC and 1492r according to Heuer et al. [27]. A nested PCR was applied for the amplification of amoA genes, with initial amplification with the primer set amoA-2f and amoA-5r [28] followed by a nested amplification using the primer set amoA-1f and amoA-2r [29], resulting in a 491-bp fragment. The thermal profiles used for amplification followed the protocols of Avrahi et al. [30]. Subsequently, the PCR products were quantified in a fluorimeter (Turner Designs, TD-700, Witec) using the PicoGreen nucleic acid dye (Molecular Probes, Inc.).

2.7. Denaturing gradient gel electrophoresis

DGGE analysis was performed with the D-Code system (Bio-Rad Laboratories) using the 16 cm × 16 cm × 1 mm plates for the 16S rRNA gene PCR-products of *Bacteria* and β-Proteobacteria and the 20 cm × 20
cm × 1 mm plates for amoA PCR-products. Four hundred nanograms of each PCR product was loaded onto 6% (wt/vol) polyacrylamide gels (acrylamide/bisacrylamide ratio [37.5:1]) (Bacteria and β-Proteobacteria) or onto 8% (wt/vol) polyacrylamide gels (amoA). Gels were poured at a flow rate of 14 ml min⁻¹ using a two chamber gradient mixer linked to a peristaltic pump (Ismatec). The gradient of denaturant ranged from 35% to 58% (Bacteria), 43% to 58% (β-Proteobacteria) or 49% to 63% (amoA) where a 100% denaturing solution is defined as 7 M urea and 40% formamide. A 5-ml stacking gel (0% denaturant) was added to the top of the denaturing gel. Gels were run in 1× TAE buffer (pH 7.4) at 60 °C, for the first 15 min at 30 V, and subsequently for 14 h at 70 V. The reproducibility of the results and the analysis method was checked by loading PCR amplifications of three different extractions per treatment and triplicates within one extraction. To compare the patterns of all different treatments on a single denaturing gel, only one PCR product amplified from the DNA from one pot was finally loaded on the gel. Gels were then stained for 30 min with SYBR Green I nucleic acid gel stain (Molecular Probes) as specified by the manufacturer. The stained gels were immediately photographed on a UV transillumination table with a CCD camera (Syngene, Multigenius Bioimaging System, UK) using a short wavelength filter provided by the manufacturer. Digital images of the gels were further analysed by Quantity One image analysis software version 4.0 (Bio-Rad). A band of DNA was detected if it accounted for greater than 1% of the total lane intensity. The lanes were normalized to contain the same amount of total signal after background subtraction (rolling disc) and further used for statistical comparison by principal component analysis (PCA). We also analysed the data taking into account only the presence or absence of bands according to McCaig et al. [31].

2.8. Community level physiological profiles

CLPP was performed in BIOLOG-GN2 plates (Oxoid). Five grams of soil (wt weight) of each treatment was mixed with 12.5 ml autoclaved water and 3 g of 3 mm-glass beads. The mixture was shaken at 180 rpm for 30 min at room temperature and subsequently centrifuged at 500g for 1 min to remove larger suspended soil particles. To adjust the cell density of the inoculum in each well, total cell counts were determined. Briefly, 100 μl of the soil suspension was filtered on a polycarbonate filter and subsequently dehydrated by sucking increasing ethanol concentrations through the system and finally stained 15 min in the dark with 15 μl of SYBR Green II (5 × 10⁻³ dilution of the stock) [32]. Filters were mounted with Citifluor solution AF1 (Citifluor Ltd., London, UK) and preparations were examined with an Olympus BX-60 microscope equipped for epifluorescence with a high pressure mercury bulb (100 W) and filter set HQ-EGFP (AHF Analysetechnik AG, Germany). Each of the 96 wells of the BIOLOG-GN2 plates was inoculated with 125 μl of a 1:100 dilution of the initial soil suspension (5 × 10⁶ cells ml⁻¹). BIOLOG-analysis was performed with three replicate plates inoculated with a dilution originating from the same initial soil suspension. Plates were incubated at 20 °C in the dark and absorbance was measured at 590 nm every 12 h with a plate reader (Dynex Technologies Inc. MRX II, Chantilly, USA) for 111 h. For further analysis, the optical density (OD) of the control well was subtracted from the OD of each of the substrate-containing wells in order to obtain blanked absorbance values. The rate of substrate utilization was determined by the average well colour development (AWCD) which was calculated as the mean of the blanked absorbance values for all 95 response wells per reading time [33]. The area under the resulting curve of each substrate, using the readings between 0 and 111 h for each plate, was calculated with the trapezium rule as described in Hackett and Griffiths [34] and subsequently used for statistical analysis (PCA). Substrate richness, defined as the number of substrates utilized, was determined as the number of background-corrected absorbance values higher than 0.25 after 111 h incubation [33].

2.9. Determination of the potential ammonia oxidation activity

Five grams of planted and unplanted soil (contaminated or non-contaminated) was incubated at 25 °C in a test medium for 6 h according to the international standard draft ISO/DIS 15685 [35]. Hourly samples of the soil slurries were taken and one volume of 4 M KCl was added to stop ammonia oxidation. Nitrite accumulated was subsequently determined by colorimetry. Ammonia oxidation rates were calculated by linear regression of accumulated nitrite over time.

2.10. Statistical analysis

All experiments were performed in triplicate. Student t-tests were carried out to determine significant differences (p < 0.01) between planted and unplanted pots at different sampling times. Data obtained by DGGE and CLPP were interpreted by principal component analysis (PCA) using SPSS 10.0.5 for Windows applying a covariance matrix and no rotation. With this method, the number of variables (16S rRNA gene bands and 95 substrates) was reduced to a few axes (PCs) which explain more variance than randomly regressed variables. The first two PCs were subsequently plotted to visualize the results.
3. Results

3.1 Effects of Thlaspi caerulescens on heavy metal content and soil properties

At any sampling time, the concentrations of NaNO3-extractable Cd and Zn were significantly lower \((p < 0.05)\) in soil recovered from planted pots than from unplanted pots (Table 1). In contrast, concentrations of soluble Cu were significantly increased in planted pots for 6 months \((p < 0.05)\). After 9 and 12 months soluble Cu was also increased in unplanted pots. Analysis of the plants revealed that Cu did not accumulate in the shoots. Regarding the total heavy metals, only Cd was significantly reduced after 12 months \((p < 0.05)\). The plant was able to take up between 1.55–10.3 g Zn and 0.17–0.936 g Cd kg\(^{-1}\) soil (Table 1). Accordingly, the plant removed up to 7 times more Zn and up to 67 times more Cd than the difference observed between the soluble concentrations of planted and unplanted pots. An increase in available heavy metals and a simultaneous decrease in soil pH were observed in all pots of month 6 and 12 compared to months 3 and 9. During the whole period of the experiment, the pH in the planted contaminated soil was between 0.24 and 0.30 units higher than in the unplanted contaminated soil \((p < 0.01)\). A similar trend was observed in the non-contaminated soil \((\text{pH} 6.7–6.9 \text{ in planted soil}; \text{pH} 6.5–6.8 \text{ in unplanted soil})\). Total C and N contents were 1.5% and 0.14%, and did not change during the 12 months.

3.2 Effects of heavy metals and Thlaspi caerulescens on microbial communities

3.2.1. Potential ammonia oxidation activity

The rates of nitrite production were 335 ± 51 and 190 ± 9 ng g\(^{-1}\) dry soil h\(^{-1}\) in planted and unplanted non-contaminated soil, respectively. No nitrite was produced in planted or unplanted contaminated soil.

3.2.2. Microbial genetic diversity

PCR-amplification was performed using the different primer pairs on DNA-extracts from the four pot experiments (contaminated–non-contaminated, rhizosphere–unplanted soil) sampled at 3, 6, 9 and 12 months. Amplification products were analysed by DGGE and patterns resulting from replicate DNA-extractions obtained from one pot at a given sampling time were highly reproducible, as were those from DNA-extractions from the rhizospheres of different plants. For all sampling times and both treatments (contaminated–non-contaminated), 43 different bands positions were observed for \(Bacteria\) patterns (24–31 bands per PCR-product), 32 different bands for the \(\beta\)-Proteobacteria (13–22 bands per PCR-product) and 19 different bands for the \(amoA\) pattern (10–18 bands per PCR-product).

With each of the primer pairs used, the DGGE-patterns derived from contaminated and non-contaminated soils clearly differed. Within one treatment, the rhizosphere and unplanted soil patterns from the different sampling times were very similar but could still be differentiated by the presence of weak bands and changes in band intensities. Subsequently, DGGE gels were interpreted using principal component analysis (PCA) in which data were transformed in two ways, taking into account either the relative intensity or the presence of bands. Using the intensity data, the first two principal components (PC1 and PC2) were sufficient to explain 65.7% of the variance for the \(Bacteria\), 71.7% for the \(\beta\)-Proteobacteria and 69.2% for the \(amoA\) PCR-products (Figs. 1–3). Regardless of the target groups, the first axis (PC1) separated contaminated and non-contaminated samples. DGGE-profiles of PCR-products of \(\beta\)-Proteobacteria were most stable over the experimental period as shown by tight clustering in PCA plots. In contrast, DGGE profiles of \(Bacteria\) 16S rRNA gene PCR-products and \(amoA\) gene PCR-products formed more open clusters. Clusters of the former drifted apart with incubation time in the contaminated soil samples, whereas this tendency for \(amoA\)-clusters was more pronounced in non-contaminated samples. PCA considering only the presence or the absence of bands resulted in similar plots.

3.2.3. Potential microbial functional diversity

The potential capacity for substrate utilization of the soil microbial communities was investigated using BLAST-GN2 plates providing 95 different substrates. This method clearly differentiated contaminated and non-contaminated soil samples (Fig. 4). Average well colours of plates inoculated with non-contaminated...
samples increased rapidly after 39 h and reached significantly higher values within 111 h than plates with inocula from contaminated soil samples. The AWCD for both pristine soils was sigmoidal, the absorbance measured for the rhizosphere soil being generally higher than that of the unplanted soil. Utilization of substrates in plates with inocula from contaminated soil started only after approximately 70 h. In particular utilization rates for the unplanted contaminated samples remained very low. Soil samples were also compared at a fixed incubation time (111 h) with respect to substrate richness, i.e., the number of substrates metabolized (Table 2). BIOLOG plates with the highest AWCD values, i.e., plates inoculated with the two pristine soils, also showed significantly higher utilization of substrates than plates inoculated with contaminated soil (Table 2). Independently of the soil treatment, the number of substrates degraded increased significantly during this one-year experiment in the planted samples ($p < 0.01$). As seen in Table 2, the effect of T. caerulescens was significantly more pronounced for plates with contaminated soil samples ($p < 0.001$). The areas under the curves, summarizing statistically the substrate utilization during 111 h incubation, were used for principal component analysis (PCA). Using areas instead of endpoint optical density (OD) values enabled different parameters to be taken into account, such as lag phase, the rate of increase and the maximum absorbance obtained during the incubation time [36]. PCA discriminated all four soil
types and 92% of the variance in the BIOLOG data was explained by the first two axes (PC1 and PC2) (Fig. 5). The first principal component had the greatest power of separation as it accounted for 89.3% of the variance. This can be explained by the high number of substrates used in the non-contaminated samples, mainly carbohydrates, carboxylic acids, amino acids, amides, and amines. Seventy-two per cent of these substrates was strongly correlated to the first axis (Pearson coefficient $>0.9; p < 0.05$). The planted samples were separated from the unplanted ones along the second axis.

4. Discussion

In this study, we used an approach combining various complementary methods to determine the effect of heavy metal contamination followed by phytoextraction on indigenous soil microbial populations. During a one year pot experiment, four consecutive harvests of T. caerulescens resulted in a decrease in the soluble, bioavailable Zn- and Cd-concentration by 30% and 60%, respectively. The amounts of Zn and Cd in the shoots were higher than the depletion of the soluble heavy metal pool. It appeared that uptake of Cd and Zn from the soluble pool was partly compensated by re-equilibration of the heavy metal pools in soil, or actively driven by the plant, which may have, e.g., access to non-NaNO$_3$-extractable Zn and Cd fractions [21,37–39]. Observed variations in the available pool of heavy metals in both planted and unplanted samples during the experiment were concomitant with pH changes of the soil solution. An increase of pH-values is usually considered to be the major factor for a decrease in the concentration of available heavy metals [40]. However, our data indicate that the driving force for the observed decrease in extractable Zn and Cd is mainly the heavy metal uptake by the plant.

The impact of the heavy metals could be seen in the results obtained with all three approaches, i.e., DGGE, CLPP and potential ammonia oxidation activity measurement. These approaches account for different parts of the community. DGGE analysis was performed with two different molecular markers, i.e., genes encoding for the 16S rRNA and the $\alpha$-subunit of ammonia monooxygenase ($amoA$). DGGE using the 16S rRNA gene marker was done at two levels of resolution with different primer pairs. This approach potentially reduces the complexity of DGGE-banding patterns usually observed after PCR-amplification with primers targeting the total bacterial community. In addition, primers specific for selected populations allow analysis of less abundant groups that may be outcompeted in the PCR reaction using the Bacterial primer pair. Nested PCR has been shown to be necessary for the detection of minor but ecological significant populations which make up less than 0.01% of the total bacterial soil community [41]. Primers targeting 16S rRNA genes of ammonia oxidising bacteria (AOB) have been widely used to recover sequence information from these bacteria in terrestrial environments (see [42] and references therein). In a few cases, such as for the AOB affiliated to the $\beta$-Proteobacteria, group-specific primers may allow conclusions to be drawn about processes potentially carried out by the organisms targeted. AOB are important key-players in the nitrogen cycle since they are responsible for the rate-limiting step in the nitrification process [42]. However, a 16S rRNA based DGGE approach to assess the molecular diversity of AOB in complex environmental systems may be prone to the co-amplification of non-target sequences [29,42,43]. Targeting $amoA$ as a functional marker for the analysis of ammonia oxidising bacteria is a promising alternative [28–30], as the higher degree of sequence variation within $amoA$ sequences allows a more sensitive analysis of the genetic diversity within the AOB of the $\beta$-Proteobacteria. Normalised DGGE-profiles were used to perform statistical analysis by PCA based on number of bands or on number and intensity of bands. It is widely accepted that the number and intensity of bands in a DGGE-profile should be regarded as semi-quantitative information due to different PCR-biases [44] and to the possibility of similar melting behaviour of 16S rRNA gene fragments from organisms with different ribotypes [19]. Independently of the marker gene used, multivariate analysis of the DGGE data clearly revealed consistent differences between contaminated and non-contaminated samples. This is in accordance with other studies which detected shifts in the bacterial community caused by heavy metal
contamination using DGGE and other molecular techniques [45,46]. Therefore, we conclude that the application of group-specific primers does not offer any additional resolution power if the only goal is to distinguish a heavy metal-polluted soil from a pristine soil. DGGE-analysis of 16S rRNA gene sequences also revealed gradual changes in microbial community structure in the contaminated, unplanted soil during 12 months in contrast to the community structure in the non-contaminated, unplanted soil, which remained stable. A possible explanation for the changes at the two levels of resolution (i.e., Bacteria and β-Proteobacteria) in the contaminated, unplanted soil is that the microbial community was initially disturbed by the addition of the heavy metal dust and that community shifts towards a new steady state were not finished within the adaptation period of three months and the experimental period. In contrast to the contaminated soils, PCA of the amoA DGGE-profiles indicated some separation of the amoA DGGE-patterns between the non-contaminated planted and unplanted soils. Since this tendency was not observed to that extent with DGGE-profiles of the β-Proteobacteria and the total bacterial community, one could assume that amoA might be a more sensitive indicator of the impact of the rhizosphere in pristine environments. Kowalchuk et al. [47] have shown that shifts in dominant ammonia oxidising populations in chalk grassland soils occurred in a background of general stability in the dominant bacterial populations as determined by DGGE using a Bacterial primer pair. Our observation corroborates also with the ammonia oxidation activity measurements. In the non-contaminated soil, the potential activity of the AOB was significantly higher in planted pots than in the unplanted samples. It has been shown that plant roots may stimulate growth of AOB [48,49]. Assuming that T. caerulescens took up preferentially nitrate instead of ammonium, as indicated by an increase in pH [50], the AOB would be less in competition with the plant for this substrate.

Although growth of T. caerulescens in contaminated soil resulted in changes in the DGGE-profiles of the total bacterial community, the plant did not exert any positive influence on the potential ammonia oxidation activity in the contaminated soil as generally no activity was detected in contaminated soil samples, indicating complete inhibition of the AOB. Ammonia oxidation is a microbial process very sensitive to soil pollution [51,52]. Although the plant removed in our study a significant part of the soluble Zn and Cd, no recovery of the nitrification activity in the contaminated planted samples was observed. Whether this is due to the Zn and Cd remaining in the soil solution or the unchanged soluble Cu fraction is not clear. This result, together with the DGGE-profiling, indicates that the AOB populations present in the non-contaminated samples may have been replaced in the contaminated soil by a heavy metal resistant but probably ineffective population [53]. Our results are also in accordance with the observations of Stephen et al. [54], who studied the ammonia oxidiser community structure and nitrogen turnover in metal-treated microcosms. Population structure analysis based on amoA clone libraries as well as the ammonia concentration in the microcosms were significantly affected by heavy metal exposure. Their data suggest that ammonia oxidising bacteria representing a certain group of amoA sequences (i.e., cluster C) [54] had a selective advantage over other AOB in heavy metal-contaminated soil. Since we did not aim to sequence bands from the DGGE gels, it remains open if these cluster C sequences are also present in our soil.

Community level physiological profiles (CLPP) reflect the potential activity of that fraction of the bacterial community that is able to grow on the substrates provided on BIOLOG microtitre plates. CLPP is not necessarily related to the functional potential of the most abundant bacteria in soil [55], and is prone to the biases inherent to methods measuring diversity under culture conditions [56]. Yet, it has been shown useful as a rapid technique in providing habitat-specific patterns. One can expect that substrates in the plant rhizosphere were present in lower concentrations than the substrates in the wells. Although the bacteria grown in the BIOLOG plates were not further analysed with molecular methods, it is most likely that fast growing r-selected populations which were not necessarily dominant in the inoculum accounted for the colour development in the wells. As already shown in other studies, the potential degradation capabilities of the microbial community were drastically reduced in the heavy metal-contaminated soil [57–60]. The rate of colour development was lower and delayed in the contaminated samples as compared to the non-contaminated ones. As the inoculum size was previously adjusted in the wells, the differences in the average well colour development must be due to the heavy metal contamination [58]. In contrast to the contaminated samples, we observed a positive association of non-contaminated samples with PC1. The C-sources which were also positively correlated to this axis should consequently be metabolized at a higher rate by the non-contaminated samples [61]. Interestingly, the majority of the amino acids, amines and amides were correlated positively as well to PC1. The lower utilization of these compounds in the contaminated samples indicates that bacterial adaptation to heavy metals is probably maintained at the expense of specific or rare degradative abilities [62–65]. For instance, heavy metal contamination has been shown to delay the degradation of several compounds such as starch, cellulose, glutamic acid and casamino acids [2,66]. The higher number of substrates used in the planted samples compared to the unplanted samples suggests a stimulating effect of the plant, probably due to the root exudates [67]. Most in-
teresting, however, is the observation that the phytoextraction practice involving _T. caerulescens_ had a positive impact on some potential functional abilities of rhizosphere microbial communities in the heavy metal contaminated soil. Kojdroz et al. showed that artificial root exudates supported the development of bacterial populations in heavy metal contaminated soils [68]. Campbell et al. [69] suggested use of carbon sources reported as constituents of root exudates as BIOLOG substrates. The authors argued that the carbon sources present in exudates represent a more diverse set of substrates than the carbon sources used in the BIOLOG GN plates and consequently also select for the slower growing soil organisms. Although the commercially available microtitre plates sufficiently separated the planted from the unplanted samples, we cannot exclude that the use of plates with root exudates might provide some additional information. If we take also into account the observed changes in the DGGE-profiles of the total rhizosphere bacterial community in the contaminated soil, we could speculate that in contrast to ammonia oxidation, other microbial processes may be stimulated. Since these microorganisms may be important for the recovery of the vegetation in a soil following reduction of the pollutant, we believe that more studies should focus on the effect of metal remediation on functional diversity in soils undergoing phytoremediation. Among rhizosphere organisms deserving more attention due to their important interactions with plants are arbuscular mycorrhizal (AM) fungi. Colonization of plants by AM fungi has in particular been observed when plants are exposed to diverse stress conditions such as exposure to heavy metals [70]. However, _Thlaspi_ belongs to the few plant families which are believed not to form symbiosis with AM fungi or are at best poorly colonized [71].

Although the duration of our experiment does not allow prediction of microbial genetic diversity and potential functional abilities after a longer period of phytoextraction, we can draw the following conclusions: Firstly, exposing soil to heavy metals changed the microbial community structure as measured by DGGE analysis of 16S rRNA and amoA gene sequences representing dominant but also minor populations. Secondly, bacterial functional abilities were heavily affected by the heavy metal contamination. Thirdly, growth of the hyperaccumulator _T. caerulescens_ in the contaminated soil did not allow the potential ammonia oxidising activity in the rhizosphere to recover. Fourthly, phytoextraction with _T. caerulescens_ not only resulted in some changes in the rhizosphere microbial community structure, but Fifthly clearly improved the potential functional abilities as compared to the contaminated unplanted soil. Further studies are needed to predict if, in particular, the functional abilities of soil microbial communities will be fully re-established after the endpoint of phytoremediation has been reached.

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**References**


