First insight into microbial community composition in a phosphogypsum waste heap soil

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The aim of this study was to investigate the soil microbial communities of a phosphogypsum waste heap. The soil microbial community structures can differ over time, as they are affected by the changing environmental conditions caused by a long-term exposure to different kinds of pollutions, like is the case of soil in the post-production waste area in Wiślinka (in the northern part of Poland) currently undergoing restoration. Our analyses indicated that the most abundant phyla were Proteobacteria, Acidobacteria, and Actinobacteria, and generally such an abundance is common for most of the studied soils. The most dominant class was Alphaproteobacteria, with their participation in 33.46% of the total reads. Among this class, the most numbered order was Sphingomonadas, whereas among this order the Sphingomonadaceae family was the most abundant one. The Sphingomonadaceae family is currently in the center of interest of many researchers, due to the ability of some of its members to utilize a wide range of naturally occurring organic compounds and many types of environmental contaminants. This kind of knowledge about microbial populations can support efforts in bioremediation and can improve monitoring changes in the contaminated environments.

Key words: microbial community, 16S rRNA gene, soil sample, post-production waste, phosphogypsum, reclamation

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INTRODUCTION

Microbial communities in the natural environment are usually very complex and consist of many species. Vast majority of the species present in such communities cannot be propagated in the laboratory in the form of pure culture. Some estimations say that we lack the ability to culture almost 99% of all bacteria using traditional microbiology methods. Even improved methods of culturing soil bacteria allow for culturing only up to 14.1% of all bacterial cells present in a given sample, which leaves the vast majority of cells uncultured (Janssen et al., 2010). Among this class, the most numbered order was Sphingomonadas, whereas among this order the Sphingomonadaceae family was the most abundant one. The Sphingomonadaceae family is currently in the center of interest of many researchers, due to the ability of some of its members to utilize a wide range of naturally occurring organic compounds and many types of environmental contaminants. This kind of knowledge about microbial populations can support efforts in bioremediation and can improve monitoring changes in the contaminated environments.
The aim of this study was to investigate the soil microbial community structure of the phosphogypsum waste heap with the use of the Next Generation Sequencing (NGS) analyses of the 16S rRNA gene. We expected a complex structure of this particular microbial community, mostly due to the composite structure of the landfill, as well as the postproduction waste and sewage sludge with the cover of vegetation. We wanted to estimate and define a microbial population’s structure that would be characteristic for the polluted soil environments, as the long-term exposure to pollutions can lead to many changes and adaptations in the microbial community’s structure.

MATERIALS AND METHODS

Study area and sample collection. The soil sample was collected in the north part of Poland (Wislinka; 54° 19’ N, 18° 50’ E) at the beginning of September 2015. The company managing the landfill did not consent to soil sampling directly from the landfill area, and thus the sample was collected from the area directly adjacent to the phosphogypsum waste heap. Area surrounding the heap has similar composition as the area of the heap itself. At the time of waste gathering, the area was unprotected and wind and rain relocated phosphogypsum wastes and soil from the strict area of the heap. Even now, there are different reports and expert opinions that strongly suggest that the area of the heap is not protected properly and wastes are being distributed around, not only within the village of Wislinka and surrounding area, but also with the water of the Vistula river directly to the sea. The soil sample was collected from an area equal to one square meter, after ground vegetation was removed, with the use of the Eijkelkamp collection soil rings. Samples from eight single rings were combined and randomly put together, mixed and sieved to form a composite sample. Plant roots were removed from the soil sample. The depth of the soil layer was above 10 cm. Immediately after collection (within an hour), the soil sample was transported in a sterile container for sieved soil, into a lab facility. Then, for the DNA extraction, the sample was divided into smaller portions and processed according to the DNA extraction kit manufacturer’s instructions and for physico-chemical soil analysis.

Physicochemical analysis. The soil physicochemical features: soil dry mass, soil conductivity, pH and nitrogen (NO₃⁻ and NH₄⁺) and phosphate (PO₄³⁻) content were measured according to the procedure published by Zawolick and coworkers (2013; 2015). The organic matter content was established according to the protocol published by Myślińska (1998). The total sulphur content was established according to the standard PN-76 B06714 (determination of sulphur content, the bromine method). The concentration of metals (Cu, Ni, Zn, Cr, Cd, and Pb) in the soil sample was determined by using Atomic Absorption Spectrometry in an acetylene-air flame (spectrometer A/Analyst 400, Perkin Elmer). The wavelengths for metals were: Cu 324.8 nm; Ni 232.0 nm; Zn 213.9 nm; Cr 357.87 nm; Cd 228.80 nm, and Pb 283.31 nm. All chemicals used were of an analytical reagent grade. All laboratory were used in the analyses was previously soaked in a nitric acid 4 mol/l solution for at least 24 h and rinsed with deionised water.

DNA extraction. DNA was extracted from the soil sample with the use of 8 commercially available kits according to the manufacturers’ protocols – detailed extraction procedure is available in Zielińska and coworkers (2017). To avoid cross contamination of the samples, the process was performed with sterile equipment. The quantity and quality of the extracted DNA were evaluated by using a Nano Drop 1000 spectrophotometer (Nanodrop Technologies). After extraction, the DNA was stored at −20°C until further use.

16S rRNA gene amplification and sequencing. The V3-V4 hypervariable regions of bacterial 16S rRNA gene region were amplified using the following primer set: 341F – CCTACGGGNGGCWGCAG and 785R – GACTACHVGGGTATCTAATCC. The targeted gene region has been shown to be the most appropriate for the Illumina sequencing (Klindworth et al., 2013). Each library (3 separate libraries for each extraction method) was prepared with a two-step PCR protocol based on Illumina’s “16S metagenomic library prep guide” (15044223 Rev. B), using Q5® Hot Start High-Fidelity 2X Master Mix (NEBNext – New England BioLabs, PCR under the following conditions: 98°C for 30 sec for initial denaturation of the DNA, followed by 25 cycles of 98°C for 10 sec, 55°C for 30 sec, 72°C for 20 sec and additionally 72°C for 2 min), and the Nextera Index kit (2×250 bp). Paired-end (PE, 2×250 nt) sequencing with a 5% PhiX spike-in was performed with an Illumina MiSeq (MiSeq Reagent kit v2) at Genomed, Warsaw, Poland; following the manufacturer’s run protocols (Illumina, Inc., San Diego, CA, USA). For each extraction method, 3 sequencing replicates were performed (Zielińska et al., 2017). The automatic primary analysis and the de-multiplexing of the raw reads were performed with MiSeq, with the use of MiSeq Reporter (MSR) v2.4 (BaseSpace).

Sequencing data analysis and statistical analysis. The samples were processed and analyzed using the Quantitative Insights Into Microbial Ecology (Qime) pipeline v 1.9.1 software (Caporaso et al., 2011). Low quality PE reads (S. 2010) and adapter sequences (Martin, 2011) were removed from further analysis. Quality-filtered reads were merged based on the overlap of PE read with the use of fastq-joint (Aronesty, 2011). The remaining sequences that did not meet the quality criteria, were removed from further analysis (mean quality >20). Clustering of operational taxonomic units (OTUs) at 97% similarity was performed by using the uclust method, version 1.2.2q (Edgar, 2010). OTUs were assigned to taxa using the GreenGenes release 13.08 as the reference (DeSantis et al., 2006), with taxonomy assignment tool PyNAST (Caporaso et al., 2010). The Biological Observation Matrix (BIOM) table was used as the core data for downstream analyses (McDonald et al., 2012) and vsearch 1.7.0 (VSEARCH GitHub website: https://github.com/torognes/vsearch) as OSS replacement of usearch 6.1. Based on clusters, the diversity indices were estimated, including the Chao1, PD (a quantitative measure of phylogenetic diversity), Shannon, and Simpson indices and also the observed OTUs. Comparison of the microbial community structure was performed with the use of UniFrac (Lozupone & Knight, 2005) and Emperor (Vázquez-Baeza et al., 2015). NGS data are deposited and fully available under study accession number PRJEB12454 in ENA – the European Nucleotide Archive.

For DNA extraction, various commercial kits were used in order to reveal the real structure of the microbial community (Zielińska et al., 2017). To due such DNA extraction strategy, in further stages we obtained various numbers of the 16S rRNA reads. Those numbers of reads cannot be directly compared to each other in order to reveal the microbial structure, and they cannot
be combined as one sample, as it would generate bias in the data analysis and interpretation. It could lead to overrepresentation of some taxa and underrepresentation of others in the tested microbial population. Therefore, in order to compare and standardize the data and to enable their interpretation, we calculated the mean value for all tested commercial kits with the data presented in percentages.

RESULTS

Physicochemical analysis

Organic matter content of the tested soil sample was at 1.63% and the dry mass at 89%. Conductivity was equal to 92.05 mS/cm. The values of soil PO$_4^{3-}$, NO$_3^-$, and NO$_2^-$ ion content (mg/kg soil dry mass) were 206, 0.04 and 0.002, respectively. The content of sulphur was at 0.03%. The soil pH was 7.06. The concentration of the following metals: Cu, Ni, Zn, Cr, Cd, and Pb (mg/kg) in the soil sample was 0.111, 0.294, 0.528, 0.276, 0.045, and 0.669, respectively.

General description of the sequencing results

On average, we obtained 160,443 raw reads and 64,150 good quality 16S rRNA gene sequences (V3-V4 region) per each sequenced sample. We were able to classify all of the obtained sequences at the phylum level. When comparing all data together, the value of the Shannon index was $8.00 \pm 1.900$, the value of the Simpson index was $0.963 \pm 0.059$, while the value of the Chao1 index was $2168.726 \pm 1008.150$ and PD was $59.480 \pm 23.240$. The diversity indices represent a randomly selected subset for a sample normalized to 26,090 sequences. The number of observed OTUs was $1631.930 \pm 732.149$. Detailed taxonomic analyses at different ranks are available in the Supplementary Data, presented as a sunburst chart for average values calculated for data obtained for all of the tested kits (Supplementary Fig. 1 at www.actabp.pl) and also as a table (Supplementary Table 1 at www.actabp.pl). Detailed data for single DNA extraction with the use of different extraction kits are in Zielińska and coworkers (2017).

Microbial community composition

The analysis of microbial community found in the phosphogypsum waste soil sample demonstrated that 99.99% of the total reads were represented by Bacteria and 0.01% by Archaea (Supplementary Fig. 1 and Supplementary Table 1 at www.actabp.pl). Taxonomy-based analysis showed that the soil microbial community consisted of 33 phyla (Supplementary Fig. 1 and Supplementary Table 1 at www.actabp.pl). The most abundant
phyla were *Proteobacteria*, *Acidobacteria*, and *Actinobacteria* (Fig. 1, Supplementary Fig. 1 and Supplementary Table 1 at www.actabp.pl). Those phyla jointly accounted for more than 78% of the total microbial sequences, followed by *Firmicutes* (4.86%), *Chloroflexi* (4.68%) and *Gemmatismonadetes* (3.8%). Jointly, 12 phyla were responsible for more than 99% of the total microbial population.

In our taxonomy analysis of the soil microbial community, we were able to identify 96 classes, 138 orders, 183 families and 264 genera. 9 classes among bacteria remained unclassified. *Alphaproteobacteria* were the most dominant class, with their participation in 33.46% of the total reads. The second most abundant class were *Actinobacteria*, with their share of 16.04% in the total reads in the microbial population. Additional 7 classes: *Gamma proteobacteria*, *Thermoleophilia*, *Acidobacteria*, *Bacilli*, *Betaproteobacteria*, *Acidimicrobia*, and *Ellin6529* separately contributed to more than 2.5% of the total share, and together those 9 classes accounted for more than 78% of the total reads (Supplementary Fig. 2 at www.actabp.pl). Among the most dominant class of *Alphaproteobacteria*, the most numerous order was *Sphingomonadales*, with contribution of 19.45% in the total microbial population. The second largest order was *Rhizobiales*, which constituted 8.82%. Among the *Sphingomonadales* order, the *Sphingomonadaeaceae* family was the most abundant, with the contribution of 18.89%. On the other hand, among the *Sphingomonadaeaceae* family, *Kaisitobacter* was the most abundant genus with the share of 16.51%, followed by *Sphingomonas* with the total share of 1.65%.

**DISCUSSION**

Due to changing environmental conditions, the soil microbial communities are expected to contain various levels of microbial species, and in consequence constitute a valuable source of information about the functioning of a given ecosystem. Specifically, it is believed that understanding of the soil microbial communities' structures can be crucial in predicting the response of the soil environment to the climate changes and ecological disasters related to the changes in the pollution levels, or even in the reclamation processes. Therefore, many metagenomics studies focus on determining the microbial community structures and their relationship to the changing soil properties (Azarbad et al., 2015; Campbell et al., 2010; Ramirez et al., 2010; Kim et al., 2014). Chu and coworkers (2010) had demonstrated, with an example of the Arctic soil bacterial communities, that those bacterial communities are characterized with similar levels of variability, richness and phylogenetic diversity as soil samples from a wide range of lower latitudes. This suggests a common diversity structure within the soil bacterial communities around the globe. It also suggested that the Arctic soil bacterial communities are strongly influenced by local environmental factors, especially by the soil acidity. This can lead to a conclusion that the established biome definitions are not useful for predicting variability in the soil bacterial communities across the globe, as it is in the case of well-established latitudinal gradients in animal and plant diversity. Azarbad and coworkers (2015) had shown, based on the 16S rRNA gene sequencing and GeoChip data, that the soil microbial communities adapted to the elevated metal concentrations in the polluted soils. They presented data that the relative abundance of particular groups of microorganism was changed, although the whole composition of the microbial communities, at the high taxonomic ranks, is common for most of the studied soil samples.

In this study, we have observed a high number of good quality reads, and generally, 15,000–100,000 reads per sample are sufficient for classification, as described by Illumina 16S Metagenomic Sequencing Protocol. Moreover, in this analysis we were able to classify all of the obtained sequences at a phylum level. A relatively high number of OTUs, as well as high values of microbial diversity indexes (Shannon’s and Simpson’s indexes), suggest a high number of species in the tested soil sample. Moreover, the number of OTUs observed in the sample indicates that the microbial population is highly complex, and together with rarefaction trends analysis, indicates that sampling of this microbial community is close to being complete. Still, Azarbad and coworkers (2015) had implied, based on their studies where they sequenced about 20,000 amplicons from a metal polluted soil and with over 5,000 different OTUs observed, that this may not be enough for a quantitative representation of a highly diverse microbial community. However, based on the high values of microbial diversity indexes and the high number of OTUs, we suggest that the specific nature of the postproduction waste heap did not reduce the microbial diversity. Additionally, it did not considerably affect the microbial structure at the high taxonomic ranks, when compared to the soil samples of different origin.

The most abundant phyla in the tested sample are: *Proteobacteria*, *Actinobacteria*, *Acidobacteria* and *Chloroflexi*. Generally, such an abundance and composition of share in a microbial community is common for most of the studied soil samples of different origin (Neufeld & Mohn, 2005; Janssen, 2006; Xu et al., 2014). Most, minor groups of the microbial community structure were similar to those previously described (Ramirez et al., 2010; Kim et al., 2014; Chu et al., 2010). Furthermore, high abundance of *Alphaproteobacteria* is often associated with an elevated concentration of mobile metals (Reith et al., 2012), especially the presence of *Sphingomonas*, which have a broad physiological tolerance to metals, resulting in a specialized community structure. Additionally, high abundance of the *Alphaproteobacteria* class is linked to a low level of the organic matter present. Low content of C and N in the soil favours genera that are phototrophic and/or are capable of nitrogen fixation which make them ideal inhabitants for a soil sample with a low organic matter content (Reith et al., 2012), as in this case. For this particular soil sample, the microbial population structure is characteristic for polluted soil environments, although the concentration of mobile metals in this soil sample is relatively low, whereas the concentration of phosphate ions is quite high. Nonetheless, the ratio of mobile metals is quite high when compared to the content of organic matter, in the tested sample.

Organisms related to the *Kaisitobacter* genus are mainly represented by the *Sphingomonadaeaceae* group, and no information is available on their possible function in the soil ecosystems (Ceja-Navarro et al., 2010). However, members of the *Kaisitobacter* genus have been detected in methane enriched (Kravchenko et al., 2010), diesel contaminated arctic soils (Ferrera-Rodriguez et al., 2013) and soils containing isoprene (Gray et al., 2015). Moreover, the entire *Sphingomonadaeaceae* family, due to the ability of some of their species to utilize a wide range of naturally occurring organic compounds, as well as many types of refractory environmental contaminants, is in the center of interest of many scientists, in the context of biore-
mediation of environmental contaminants (Balkwill et al., 2006).

Likewise, an increased abundance of the Chloroflexi and Gemmatimonadetes phyla (4.68% and 3.84% in the tested soil sample, respectively), is often found at the metal-polluted sites (Azarbad et al., 2015). Unfortunately, little is known about those phyla, especially about Gemmatimonadetes, as to their ecology and metabolism. However, the presence and increased abundance of those groups can suggest that they play an important role in the contaminated soils. As those bacteria can be highly adapted to extreme environments, their presence may also provide a stabilizing element in the microbial population (Azarbad et al., 2015). Elevated abundance of the Firmicutes phyla, also observed in this study, is frequently found in the contaminated soils, especially in the case of the Bacilli class (Ellis et al., 2015; Dell’Amico et al., 2008; Berg et al., 2012).

As microorganisms can play an extremely important role in the decomposition of dead organic matter, any adverse effects in soil parameters, such as pollution, can potentially lead to distortions of the nutrient cycle. This may have an impact on the functioning of the whole ecosystem (Stefanowicz et al., 2009). Therefore, monitoring of the changes in the microbial populations may be an indicator of fluctuations in the natural environment, caused for e.g. by pollutants or environmental disasters. This can be very useful especially when one considers monitoring or even dealing with ecological changes after natural disasters, or at the post-production areas and undergoing restoration. This report gives the first insight into microbial community structure of a phospshogypsum waste heap soil and can be exploit to better understanding which group of microorganisms can be involved in dealing with various contaminations and how the microbial communities deal with those contaminations (Handelsman and et al., Committee on Metagenomics: Challenges and Functional Applications (2007), and can support our efforts in bioremediation of environmental contaminations.

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