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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 were *Alphaproteobacteria*, **with their participation in 33.46% of the total reads. Among this class, the most numbered order was *Sphingomonadales*, 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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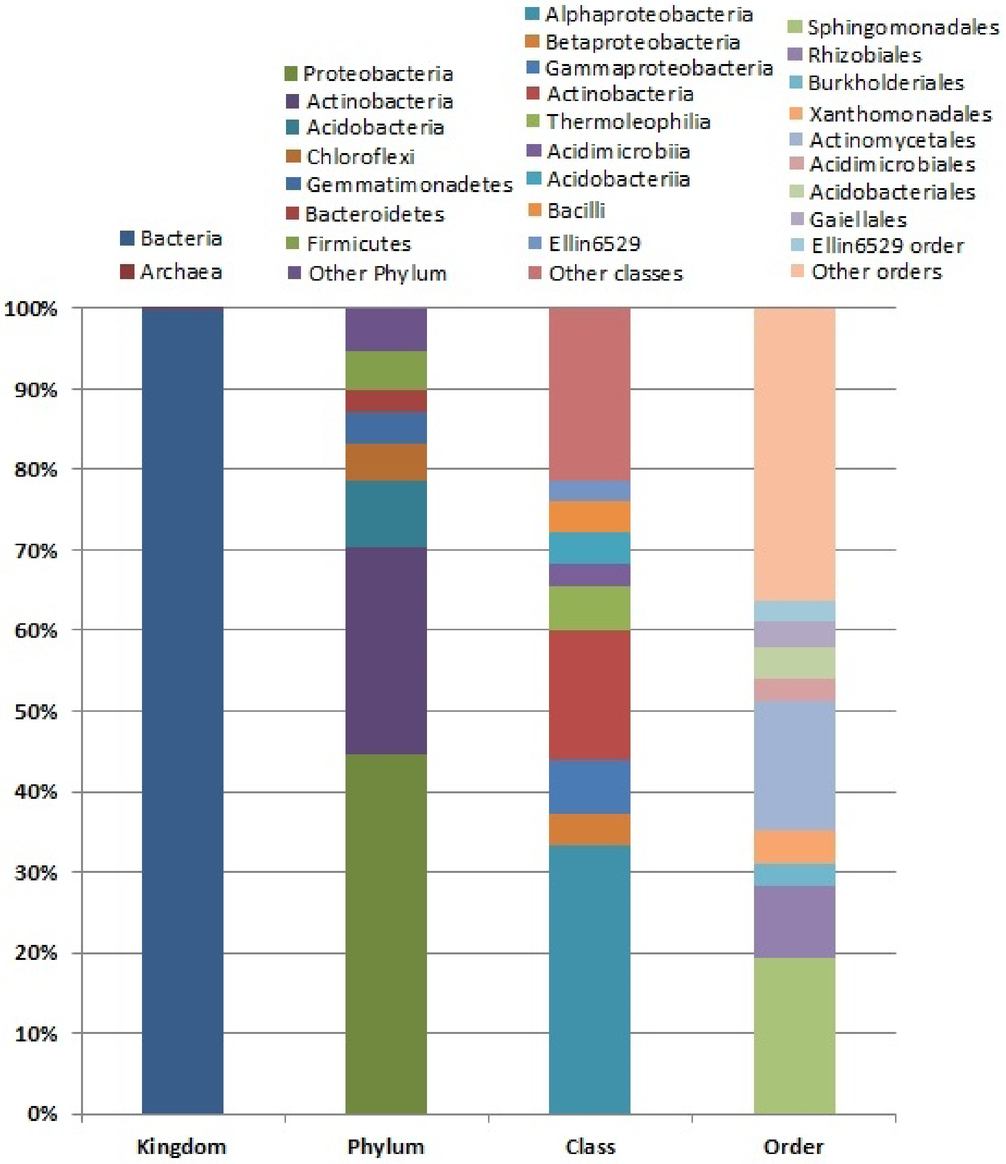
Abbreviations: NGS, Next Generation Sequencing

Supplementary Figure 1. Detailed taxonomic analysis at different taxonomic ranks. (Supplementary Figure 1.html)
Sunburst chart show the relative abundance of microbial 16S rRNA sequences at different taxonomic levels for the average value calculated based on DNA samples extracted with the tested kits. The first level represents the kingdom, the second level represents all phyla present in the sample, and the next levels represent the class, order, family and genus, respectively. The most suitable browser for viewing these sunburst charts is Firefox. The html data are available under the following link: https://www.dropbox.com/sh/pnnqix8nhjik9m3/AABKDXLZvoM_kbToO2mKdFAUa?dl=0
Representative results for all the extraction kits used are presented and are available under the following link (Zielińska ***et al.*** 2017) https://www.dropbox.com/sh/s9mylexjnjxo5lr/AADjnNydHvWm3JGAIvkTlkgKa?dl=0



Supplementary Figure 2. Abundance of microbial 16S rRNA sequences in the total population.
Column chart shows the relative abundance of the top classification results at different taxonomic levels. The first column represents the total reads for bacteria and archaea. Next columns represent the total reads at different taxonomic levels. “Other” corresponds to microorganisms with only a small share in the total population and to those unidentified at a particular taxonomic rank. Detailed taxonomic analyses at different ranks are also available in Supplementary Fig. 1 and Supplementary Table 1.