Surface Coal Mineland Reclamation Using a Dry Flue Gas Desulfurization Product and Soil: Long-Term Microbial Responses

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ABSTRACT

Abandoned surface coal-mined lands are an environmental concern worldwide because of their potential strong negative impact on water and soil quality. A field study was conducted to investigate the use of a dry flue gas desulfurization (FGD) product and of soil for reclamation of an abandoned surface coal-mined land in Ohio, USA. Treatments were (1) FGD product applied alone at a rate of 280 Mg ha^{-1} (2) FGD product at the same rate applied together with 112 Mg ha^{-1} yard waste compost (3) 20 cm of resoil material plus 157 Mg ha^{-1} of agricultural limestone and (4) an untreated control. A grass-legume sward was planted, and microbial abundance and diversity in the soil were analyzed in the 20th year after treatments using pyrosequencing of bacterial 16S rRNA and eukaryotic 18S rRNA genes. The results revealed approximately 7,000 and 2,000 operational taxonomic units (OTU) for bacteria and eukaryotes, respectively, in the treated soil, and 2,500 and 1,000 in the untreated soil. The five most abundant bacterial phyla were *Proteobacteria, Acidobacteria, Actinobacteria, Bacteroidetes*, and *Chloroflexi.* There were more *Acidobacteria* in the untreated than treated soil. Fungi represented approximately 70% of the total eukaryotes in treated soils and more than 90% in the untreated soil. Microbial diversity in the reclaimed coal mine plots was significantly increased compared to untreated areas and were generally similar among reclamation treatments. Over the long-term, FGD product, used alone or in combination with compost for reclamation of acidic surface coal-mined lands, can create a more diverse microbial community that is less dominated by acid-loving fungi and *Acidobacteria*.

INTRODUCTION

Coal mining and coal preparation practices in the years prior to the enactment of strict reclamation laws frequently resulted in environmental degradation. Abandoned coal-mined lands are a worldwide environmental concern because they impact surface water and groundwater quality. In Ohio, USA more than 14,000 hectares of highly degraded abandoned coal-mine lands have not yet been reclaimed. The Clean Air Act of 1990 confirmed the need to develop and implement processes to remove SO_2 from flue gases produced when fossil fuels are burned for energy. Some flue gas desulfurization (FGD) products have significant potential for reclamation of abandoned and acid coal-mine lands. Previously, the long-term effects of FGD product and soil on plant (Chen et al., 2013a), soil (Chen et al., 2013b), and water (Chen et al., 2015) have been reported. The objective of this study was to assess the long-term effects of the reclamation treatments on the soil microbial community

METHODS

The study site (**Fig. 1**), the Fleming abandoned surface coal mine, is located in Ohio, USA. Acid mine drainage was a significant problem with surface water pH ranging from 2.4 to 3.9. In 1994, six 0.4-ha plots were constructed by regrading underclay and mine spoil. The three treatments applied to the six plots (shown in **Fig. 1)** are described in **Table 1**. The FGD was a fluidized bed combustion product. The plots were seeded with a mixture of grasses and legumes. Soil samples (0-10 cm depth) from each plot, untreated area and an adjacent forest were collected in the 20th year after reclamation. Microbial diversity was determined by analyzing the bacterial 16s rRNA and eukaryotic 18s rRNA genes using PCR and pyrosequencing analysis (Sengupta and Dick, 2015; Tian and Gao, 2014).

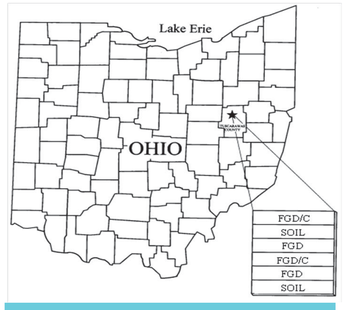
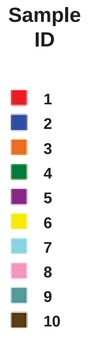


Fig. 1. Location of the Fleming abandoned surface coal mined land site in Ohio.

Table 1.Treatments applied to the plots at the Fleming abandoned surface coal mine land.

Treatment codes	Sample ID	Treatments
SOIL	1, 5	112 Mg ha^{-1} of agricultural limestone was incorporated into graded spoil with a chisel plow to a depth of 20 cm and then covered with 20 cm of borrowed soil treated with additional 45 Mg ha^{-1} of agricultural limestone.
FGD	2, 4	280 Mg ha^{-1} of FGD product was incorporated into graded spoil with a chisel plow to a depth of 20 cm.
FGD/C	3, 6	280 Mg ha^{-1} of FGD product and 112 Mg ha^{-1} of yard-waste compost were incorporated into graded spoil with a chisel plow to a depth of 20 cm.
Control	7, 8	Untreated abandoned surface coal mine soil
Forest	9, 10	Adjacent forest



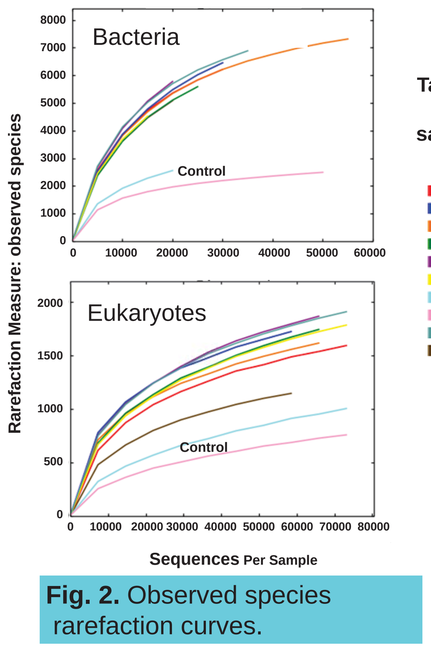


Fig. 2. Observed species rarefaction curves.

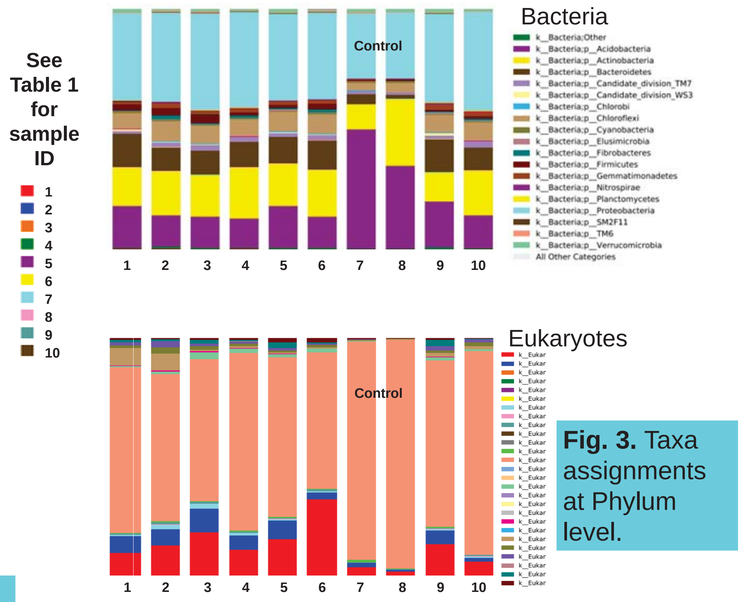


Fig. 3. Taxa assignments at Phylum level.

RESULTS

Rarefaction curves, depicting the effect of dissimilarity on the number of OTUs, showed reclamation with FGD or soil treatment increased the number of species of bacteria and eukaryote (**Fig. 2**). *Proteobacteria*, *Acidobacteria*, *Actinobacteria*, *Bacteroidetes*, and *Chloroflexi* were the five most abundant bacterial phyla in all treatments (**Fig. 3**). In the untreated soil there were more *Acidobacteria* and less other bacteria. Approximately 70% of eukaryotes in treated soils and more than 90% in adjacent untreated areas were fungi due to almost no plant growth on the control plots. The Shannon diversity rarefaction curves, a graphical representation of valid reads and OTUs obtained, is increased by the treatments only up to a value of 10,000 sequences or less per sample (**Fig. 4**). The species richness indices (i.e. the Chao1 rarefaction curves) showed values that were higher in the treated than untreated soils (**Fig. 5**).

The 16S rRNA gene-based cluster analysis using an unweighted pair group method with arithmetic mean (UPGMA) tree showed that bacterial communities of the treatments and forest had a much lower Euclidean distance and were much more closely linked together than the bacterial community of the untreated abandoned coal mine soil (**Fig. 6**).

CONCLUSIONS

Use of FGD product for reclamation of acidic surface coal-mined lands can create a more diverse microbial community that is less dominated by fungi and *Acidobacteria*, and a more diverse eukaryotic community.

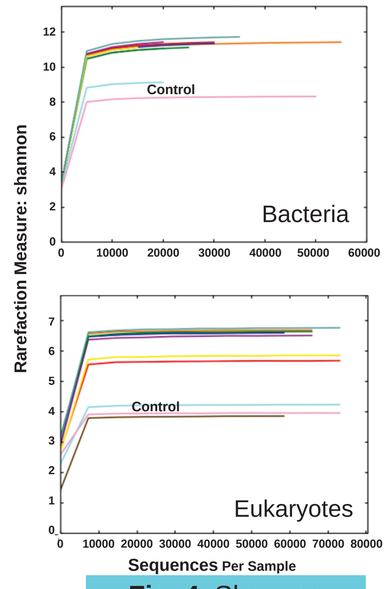


Fig. 4. Shannon rarefaction curves.

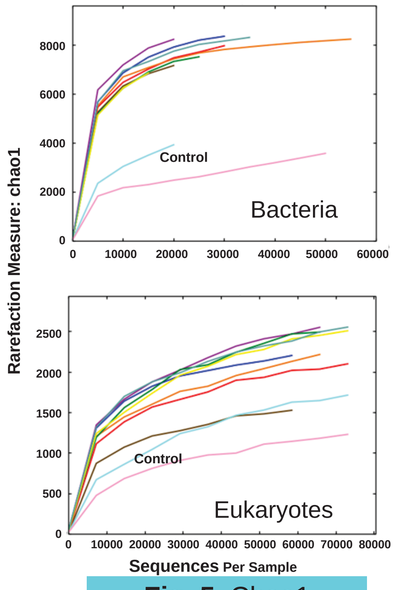


Fig. 5. Chao1 rarefaction curves.

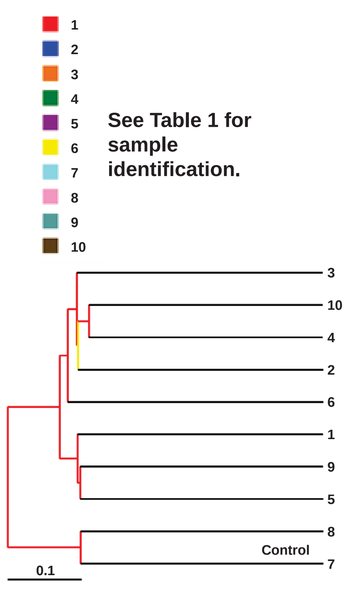


Fig. 6. UPGMA tree.

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