

Illegal Dumping of Oil and Gas Wastewaters Alters Semi-Arid Soil Microbial Communities

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Abstract

The Permian Basin, underlying New Mexico and Texas, is one of the most productive oil and gas (OG) provinces in the United States. Oil and gas production yields large volumes of wastewater with complex chemistries. The environmental health risks posed by these OG wastewaters are not well understood, particularly in the case of accidental or intentional releases. Starting in November 2017, 39 illegal dumps of OG wastewater were identified in southeastern New Mexico that released approximately 6.4×10^5 liters of fluid onto desert soils. To evaluate the impacts of these releases on soils, we analyzed changes in soil geochemistry and microbial community composition by comparing soils from within OG wastewater dump-affected zones to corresponding unaffected zones with no known releases. We observed significant ($p < 0.01$) changes in soil geochemistry for all dump-affected samples compared to controls, reflecting the residual salts and hydrocarbons left behind by the OG-wastewater release (e.g., enriched in sodium (Na), chloride (Cl), and bromide (Br)). Illumina 16S iTag sequencing revealed significant ($p < 0.01$) differences in microbial community structure between dump and control zones. Furthermore, soils from dump areas had significantly ($p < 0.01$) lower alpha diversity and exhibited differences in phylogenetic composition. Dump-affected soil samples showed an increase in halophilic and halotolerant taxa, such as members of the Marinobacteraceae, Halomonadaceae, and Halobacteroidaceae, suggesting that the high salinity of the dumped OG wastewater exerted a selective pressure on microbial communities. Taxa related to known hydrocarbon-degrading organisms, e.g., *Marinobacter*, *Salegentibacter*, *Chromohalobacter*, and *Alcanivorax*, were also detected in the dump-affected soil-sample communities. The microbial communities in control soils were dominated by taxa ubiquitous in, and well adapted to, arid and nutrient-deprived soil environments including photosynthetic Cyanobacteria, hydrogen-oxidizing Actinobacteria and Acidobacteria, and nitrogen-fixing Alphaproteobacteria. This study demonstrated that OG-wastewater dumps can lead to shifts in microbial community

composition and function towards salt- and hydrocarbon-tolerant taxa that are not typically found in desert soils, thus altering the impacted dryland soil ecosystem. Loss of key microbial taxa, such as those that increase arid soil fertility, or promote plant health, could result in cascading affects to myriad ecosystem services such as loss of flora. Further studies are needed to explore the potential for using halophilic and hydrocarbon-degrading taxa to bioremediate OG-wastewater affected lands.

Keywords

microbial ecology, contaminants, environmental health, desert, ecosystems, energy development

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Conflicts of interest

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