Mn(II) oxidation and remediation in polluted environments

C. M. SANTELLI[1]*, D. L. CHAPUT[1], C. M. HANSEL[2],
W. D. BURGOS[3], O. W. DUCKWORTH[4] AND
T. G. GARDNER[4]

[1]Smithsonian Institution, NMNH, Washington, DC 20013, USA (*correspondence: santellic@si.edu; chaputdl@si.edu)
[2]Woods Hole Oceanographic Institution, Woods Hole, MA 02543, USA (chansel@whoi.edu)
[3]The Pennsylvania State University, University Park, PA 16802, USA (wdb3@psu.edu)
[4]North Carolina State University, Raleigh, NC 27695, USA (owen_duckworth@ncsu.edu; terrence_gardner@ncsu.edu)

The distribution and speciation of manganese (Mn) in terrestrial and aquatic environments is heavily influenced by microbiological processes. A diversity of microorganisms (bacteria, fungi, and algae) are known to catalyze Mn(II) oxidation in aerobic environments, which results in the formation of sparingly soluble Mn(III/IV)(hydr)oxide minerals. The formation of these Mn oxides is important for remediating environments with hazardous levels of soluble Mn. Furthermore, biogenic Mn oxide minerals have high sorptive capacities and redox potentials, thus contributing to the subsequent remediation of a variety of toxic organic and inorganic compounds.

We have examined the microbial communities existing in several Mn-rich and heavily polluted environments to identify the key organisms promoting Mn(II) oxidation and bioremediation. We used both culture-based and high-throughput sequencing approaches to examine organisms in a Superfund Site treating scientific and agricultural wastewater, a freshwater pond undergoing remediation, and several passive treatment systems cleaning up metalliferous wastewater from abandoned coal mines. We have isolated a number of Mn(II)-oxidizing bacteria, fungi, and algae from these environments. Thus far, a greater diversity and number of fungal cultures (relative to bacteria and algae) promoting Mn(II) oxidation were obtained from each of these environments. Culture-independent techniques further show that the sequences of these cultured fungi can make up a large fraction (up to ~15%) of the total fungal sequences in each of the samples. Since we rely on culturing to determine Mn oxidation capabilities, these estimates are likely an underestimation of the total community contributing to the remediation of Mn in these environments. Results from this study emphasize the role of eukaryotes, particularly fungi, in contributing to Mn remediation in impacted environments.