

Comparative genomic and transcriptomic investigation of an acidic pit lake in the Iberian Pyrite Belt

DIANA AYALA¹, JAVIER SÁNCHEZ-ESPAÑA², SEAN CROWE³, JENNIFER MACALADY⁴ AND WILLIAM BURGOS^{1,*}

¹ Dept. Civil Environ. Eng., Penn State Univ., University Park, PA 16802, USA (dka9@psu.edu, *correspondence wdb3@psu.edu)

² Instituto Geológico y Minero de España, Tres Cantos, Madrid, Spain (j.sanchez@igme.es)

³ Dept. Microbiol. Immunol., University of British Columbia, Vancouver, BC, Canada. (sean.crowe@ubc.ca)

⁴ Dept. of Geosciences, Penn State Univ., University Park, PA 16802, USA (jlm80@psu.edu)

The Iberian Pyrite Belt (IPB) hosts the world's largest massive sulfide deposit and has been mined from pre-Roman times to the present day for precious (Au, Ag) and base (Cu, Pb, Zn) metals and sulfur. Most of the mines were abandoned during the twentieth century leaving an extensive legacy of waste rock dumps, tailings impoundments, and flooded open-pit pits. Most of the acidic pit lakes are meromictic and display a permanent stratification pattern, the water column being composed of an upper oxic layer (the mixolimnion), a bottom anaerobic layer (the monimolimnion), and a transitional chemocline separating the two zones. Cueva de la Mora (CM) is a well-characterized acidic pit lake in SW Spain whose biogeochemistry and limnology has been extensively studied. Of particular interest is the anoxic bottom layer of these lakes, in which the absence of Fe(III) (omnipresent in oxidizing environments) allows detailed study of the geochemical behavior of other important dissolved substances such as Al or SiO₂(aq). Through the use of scanning transmission electron microscopy combined with other complementary techniques (SEM, cryo-TEM, and EELS), we discovered different biomineralization patterns around and within morphologically-distinct microbial cells. We also identified cells coated with thin (<100 nm) mineral coatings despite the fact that surrounding waters were thermodynamically undersaturated with respect to these minerals. Based on these findings, we have initiated a project using metagenomics and metatranscriptomics sequence analyses to better understand the biogeochemistry of these two lakes. The goal is to discover how environmental conditions affect taxonomic and functional diversity, community interactions, and gene expression levels in the deep anoxic waters of acidic pit lakes.