

## Novel Metal Resistance Mechanisms from the Metagenome of Acid Rock Drainage Adapted Plants

Salvador Mirete Castañeda

Carolina G. de Figueras

José E. González-Pastor

*Laboratory of Molecular Ecology*

*Centro de Astrobiología, Madrid*

SPAIN

[gonzalezpje@inta.es](mailto:gonzalezpje@inta.es)

Microbes have been exposed to toxic heavy metals since the beginning of life on the Earth. As a result, they have developed a variety of mechanisms to survive in metal enriched environments. In this work we have investigated the metal resistance mechanisms from bacterial communities living in Rio Tinto (Spain), a naturally metal enriched and extreme acidic environment, which is considered a Mars analog. To search for genes involved in metal resistance, we analyzed the bacterial community of the rhizosphere of *Erica aldevalensis*, an endemic heather which grows at the banks of this river. The 16S rRNA gene sequence analysis of rhizosphere DNA revealed the existence of members of five phylogenetic groups of *Bacteria* and the two main groups of *Archaea*, mostly associated to uncultivated strains, and some of them associated to acid mine drainage impacted sites. Then, we constructed metagenomic libraries, containing DNA fragments from the whole microbial community (metagenome), for searching novel metal resistance determinants. A total of fourteen nickel- and eight copper-resistant clones were isolated. Insights about their possible mechanisms of nickel resistance were obtained from cellular metal content and sequence similarities. Two clones encoded putative ABC transporter components, and a novel mechanism of nickel efflux is suggested. In addition, a nickel hyperaccumulation mechanism is proposed for a clone encoding a serine O-acetyltransferase. The copper-resistance clones are still being analyzed. In summary, this approach has been useful to explore the metal resistance strategies from bacterial communities living in extreme acidic environments.