

Exploring the Geomicrobiology of the Río Tinto subsurface Mars analog by using a life detector biochip

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Introduction:

The Iberian Pyritic Belt (IPB) is one of the largest massive pyrite deposits in the world, and is considered as a Martian analog. Several studies [1][2] of the acidic, heavy metal rich-Tinto river in the IPB have revealed a surprisingly rich extreme ecosystem, yet little is known about the geomicrobiology of its subsurface. In a previous work [3] we described an antibody microarray which contains more than 200 antibodies against bacterial strains, different fractions of natural extracts, proteins, etc. and reported its usefulness for immunoprofiling of environmental samples and for the detection of biomarkers with different range of universality.

Results and conclusions:

Here we show the results obtained by using LDChip200 (Life Detector Chip) for immunoprofiling the whole depth of a drill in the IPB at the Tinto river origin. From 0,5 to 1 g of samples from cores up to 160 m depth were processed for a quick analysis with the LDChip200. The results showed the presence of Gram-positive bacteria and peptides or proteins from the ferritin superfamily which might be involved in tolerance to the high iron concentrations present in the IPB subsurface. Biodiversity was also assessed by DNA extraction and analysis with a phylogenetic oligonucleotide microarray for prokaryotes [4], and by cloning and sequencing of the PCR-amplified bacterial 16s rRNA gene. Members of the Gram-positive Firmicutes group of bacteria were detected by the oligonucleotide microarray and sequencing. Sequencing also revealed sequences similar to those of nitrate and sulphate reducing bacteria. Those results allowed us to build a preliminary model of the ecosystem and provided an initial insight into the biology of the deep subsurface of the Iberian Pyritic Belt.

[1] González-Toril (2003) Appl Environ Microbiol 69(8), 4853-65. [2] Amaral-Zettler (2002) Nature 417, 137. [3] Rivas (2008) Anal Chem, 80, 7970-9. [4] Garrido (2008) Environ Microbiol 10, 836-50.