A phylogenomic approach to understand genomic and metabolic diversity in extreme acidophilic environments

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Extreme acidic environments are characterized by a low pH, low abundance of organic carbon and high concentrations of heavy metals. We define “extreme acidophiles” as those organisms whose growth optimum is <pH 3.6. At present, the extreme acidophiles for which there is genome information belong to the Eubacteria and Archaea, although Eukaryotic microorganisms are abundant in some acidophilic environments.

These microorganisms have been extensively used in bioleaching, a technological process that use microorganisms to solubilize metals, principally copper, from ores. This process can result in the production of acid mine drainage (AMD). The genomics of bacteria and archaea from all natural and man-made acidic environments will be considered in this work although the focus will be on bioleaching microorganisms.

Since genomic and metagenomic information have been continuously released during the last years, promoting the experimental research on the biology of these microorganisms, little attention have been focused on the evolutionary nature of the strategies that these microorganisms use to cope with the challenges of extreme acidic environments. Among these challenges, we can mention the development of Iron and inorganic sulfur compounds based metabolism, strategies for heavy metal resistance and for the balance of the internal pH (neutral) with the external pH (< 3.6).

In order to investigate in more detail the evolutionary nature of the strategies used to survive under these extreme conditions we have taken a phylogenomic approach, which could provide some clues about the molecular
mechanisms that these microorganisms have developed through their evolutionary history.

The phylogenomic approach implicates the utilization of orthology detection methods in conjunction to metabolic and regulatory reconstruction systems in order to identify instances of gene novelty and diversification. In addition to these tools, comparative synteny maps and evolutionary profiles have been also applied to this study.

As a result of this approach we have identified organism specific genomic determinants with direct metabolic implications on the survival strategies of each representatives, potential evolutionary processes responsible for the generation of these molecular strategies and how these processes have been potentially transferred to non-closely related microorganisms founded in the same extreme acidic niche.

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