Evolutionary Mechanisms and Dynamics of Extreme Acidophiles

CAROLINA GONZÁLEZ[1,2], GONZALO NEIRA[1], EVA VERGARA[1], DIEGO CORTEZ[1], JORGE VALDÉS[1,2] AND DAVID HOLMES[1,2]*

[1]Center for Bioinformatics and Genome Biology, Fundación Ciencia & Vida, Santiago, Chile
(*dsholmes2000@yahoo.com)
[2]Centro de Genómica y Bioinformática, Facultad de Ciencias, Universidad Mayor, Santiago, Chile

This presentation explores the evolution and genetic diversity of extremely acidophilic bacteria (grow at a pH of ≤3). They thrive in environments rich in concentrated sulfuric acid and unusually high levels of dissolved toxic heavy metals. Most are polyextremophilic chemolithoautotrophs. They are used in the commercial recovery of metals (biomining) and have been exploited for bioremediation of metal contaminated soils. They are also involved in the recycling of metals and nutrients in naturally occurring hyperacidic conditions such as surface and deep subsurface pyritic environments and acidic hot-springs. Further, their genomes can be plundered for clues of cellular metabolisms and bioenergetic pathways that might have evolved on early earth over 3.8 billion years ago. As such, they are of substantial interest to microbiologists, geochemists, geologists and planetary scientists,

Robust and coherent phylogenies were prepared from diverse examples of extant extreme acidophiles from very different early and late branching lineages distributed around the Tree of Life. Examination of these phylogenies, coupled with comparative genomics, allowed the inferred reconstruction of ancestral evolutionary trajectories. Models have been constructed that suggested how the ability to thrive in extremely acidic conditions can arise by the stepwise accumulation of mutations, acquisition of genes by horizontal gene transfer (HGT) and either a neutral ratchet of genetic material loss or adaptive genome streamlining. Analyses of amino acid substitution rates in key genes provide relative estimates of the timing of some of these evolutionary events.

The data also provided an inventory of genetic diversity, metabolic pathways and biogeochemical trait variations in a number of extreme acidophilic lineages. From this rich source of inventorial data, additional models were built of whole cell metabolisms and potential ecophysiological interactions.

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