Comparative genomics of the oxidative stress response in acidophilic microorganisms

Cárdenas, J.P.\textsuperscript{1,2}, Levicán, G.\textsuperscript{3}, Holmes, D.S.\textsuperscript{1,2}, Quatrini, R.\textsuperscript{1,2}

Center for Bioinformatics and Genome Biology, Fundación Ciencia & Vida, Santiago, Chile\textsuperscript{1}, Facultad de Ciencias Biológicas, Universidad Andrés Bello, Santiago Chile\textsuperscript{2}, Facultad de Química y Biología, Universidad de Santiago de Chile\textsuperscript{3}.

Acidophilic microorganisms inhabit environments with unusually high concentrations of iron, copper and heavy metals, which can potentially cause oxidative stress. Reactive oxygen species (ROS) damage proteins, nucleic acids, lipids and other macromolecules and thus have deleterious effects on cell growth and survival. Many of these acidophilic microorganisms are chemolithotrophs with unusually high oxygen consumption rates that may exacerbate the problem of oxidative stress. Although some knowledge has been gained in recent years regarding the oxidative stress response in a few acidophiles, the general strategies used by them to face ROS challenges are still inadequately understood.

Comparative genomics and multiple bioinformatic tools were used to explore 50 sequenced genomes of acidophilic bacteria and archaea in an attempt to reconstruct their individual oxidative stress responses and to look for conserved and novel strategies.

These analyses revealed that acidophiles tend to lack genes encoding typical oxidative stress response regulators (OxyR, SoxRS, OhrR and Spx) and have an underrepresentation of classical ROS consumption enzymes (e.g. catalases) compared to phylogenetically related neutrophiles. In contrast, acidophiles have a well represented gene repertoire of repair systems for DNA, protein and lipids. Phylogenetic studies suggest that some of these genes are indeed inherited in a niche-specific fashion. In addition, these analysis also show that members of the Fur regulator family have several copies in most acidophiles which form part of well defined clades that include well characterized Irr and PerR proteins from neutrophiles. These results suggest that Fur orthologs are potential candidates for oxidative stress regulation in acidophiles.

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