

**PROGRAMA FINAL
PRESENTACIONES ORALES
2ndo ISE30**

PO-01

10h00-10h30

03/12/19

HB232ND
Area: Bacterias

Biología de los RNA en microorganismos acidófilos

RNA biology in acidophilic micororganisms

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Nuestro laboratorio ha analizado diferentes aspectos de la participación de los RNA en el proceso de traducción de la información genética en *Acidithiobacillus ferrooxidans*. En este trabajo presentarán nuestros hallazgos relacionados con el estudio de algunos de los componentes involucrados en diferentes etapas del proceso de traducción y las novedades que estos hallazgos implican en la biología de los RNA en este microorganismo. El genoma de *A. ferrooxidans* contiene dos operones para genes de rRNA con una organización similar a la mayoría de las bacterias. Sin embargo un gen para una tirosil-tRNA sintetasa (TirRS) y otro para una GluRS tienen una alta similitud en estructura y organización con genes equivalentes de bacterias Gram positivas. En la TirRS la similitud con Gram positivas se extiende a la región 5' no traducida del mRNA que, se predice, se pliega como un posible riboswitch que demostró ser funcional. Por otro lado, pudimos determinar que en *A. ferrooxidans* existen dos genes que codifican para GluRS y ninguno para GlnRS. Estas enzimas tienen especificidad diferente por los cuatro tRNAGlu codificados en el genoma. Dos de estos genes están codificados en un elemento genético móvil que contiene un "cluster" con 37 genes de tRNA. La presencia de genes de tRNA en un elemento genético móvil hace pensar que proviene de transferencia génica horizontal. Por otro lado hemos abordado el estudio de los sRNA que regulan la traducción en esta bacteria. Mediante un estudio masivo por herramientas de predicción bioinformáticas y de secuenciación masiva de RNAs se detectaron varios posibles sRNA. Se analizaron funcionalmente algunos de los que respondían a estrés oxidativo. Se identificó y analizó un sRNA que responde a peróxido de hidrógeno y que es exclusivo de bacterias acidófilas. Otros estudios también han identificado sRNAs de acidófilos incluso algunos codificados en elementos genéticos móviles. De esta información sugerimos que al menos parte de la maquinaria de traducción de la información genética de *A. ferrooxidans* se ha adquirido por transferencia horizontal de genes.

Fondecyt 1150834 y 1190552 a OO y1170799a GL

PO-02

12h15-12h45

03/12/19

HK585JC

Area: Genómica y Evolución

Los tapetes microbianos como testigos de grandes transiciones metabólicas en la Tierra primitiva

Microbial mats recapitulate major metabolic transitions of the early Earth

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Phototrophic microbial mats have dominated terrestrial ecosystems during most of Earth's history. ~2.5 billion years ago, they largely contributed to the Great Oxidation Event, the massive oxygenation of our atmosphere. Using metagenomic data, we have determined the taxonomic diversity and gene co-occurrence networks of the complex microbial communities found in microbial mats of the Atacama desert (Chile) growing in a very steep redox gradient [1]. By applying a space-for-time approach to study the dominant metabolisms in these mats exposed to different oxygen concentrations, we infer that anoxygenic photosynthesis was present in the environmental conditions that reigned during the early Precambrian but, in contrast with common assumptions, it was not dominant and was accompanied by other autotrophic metabolisms. Anoxygenic photosynthesis seems to have become widespread in parallel with oxygenic photosynthesis and aerobic respiration. This space-for-time approach also suggests that the Wood-Ljungdahl carbon fixation pathway was dominant in the early Earth microbial mats and that the Calvin cycle likely evolved later to become the major carbon fixation mechanisms in present days. [1] Gutiérrez-Preciado *et al.*, Nature Ecol. Evol., 2018, 2:1700-1708.

PO-03

15h30-16h00

03/12/19

QB159KQ

Area: Ecología Microbiana

Distribución de rutas de fijación de carbono en la microbiota asociada a las evaporitas de yeso del Sala de Llamara

Distribution of the carbon fixation pathways in the microbiota inhabiting the gypsum evaporites at Salar de Llamara

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The endorheic basins in the Central Depression of Northern Chile are interesting depositional environments of continental evaporites. Inside the frame of the environmental baseline studies of Salar de Llamara, the microbial and metabolic diversity were assessed together with the geochemical, limnological and hydrological aspects. We collected core samples of the evaporites and isolated colored layers for DNA extraction and metagenome sequencing. Interestingly, more than 30% of the sequences retrieved have not close neighbors in available databases, which reveals a high degree of novelty. *Proteobacteria*, *Plantomycetes* and *Cyanobacteria* dominate the microbial communities. The similarity observed among all the samples (>50 and >80% considering taxonomic and functional sequence assignation, respectively) allow us to infer a functional redundancy as was already reported in similar open systems. We explored the key microbial populations and functional genomic resources available to fix carbon in the ecosystem by bioinformatics analysis of the metagenomes. Interestingly, genes associated to the Reductive pentose phosphate cycle (CBB), the Reductive Tricarboxylic Acid Cycle (RTCA) and variants of the carbon fixation pathway using reduced C1 compounds (like reductive acetyl-CoA pathway known as Wood-Ljungdahl, WL) are present in the green layer. The predominant one is the WL pathway represented by the Carbon monoxide dehydrogenase (CODH) coding gene. In addition, the WL coding genes are associated to members of Alpha, Gammaproteobacteria and Bacteroidetes in those metagenomes. Moreover, the CBB coding genes are mostly associated to representatives of Cyanobacteria and an unidentified Alphaproteobacteria, and the RTCA coding genes to Bacteroidetes, Blaneolaeta and Archaea. A relevant difference between C1 carbon fixation pathways and the others (CBB and RTCA) is that C1 are also used for several other metabolic goals as energy conservation and the recycling of reduced electron carriers. On the contrary, the non-C1 carbon fixation pathways are mostly used for autotrophic growth. The capacity to oxidize CO aerobically and the lack of functional autotrophic carbon fixation was previously observed and was interpreted as a strategy for supplementing heterotrophy with the use of inorganic compounds. That mixed metabolic scheme (heterotrophy plus lithotrophy) seems to represent a successful strategy in those extreme environments as well as bacterial photoheterotrophy.

PO-04

17h15-17h45

03/12/19

DT142CD

Area: Biotecnología

Estudio de los mecanismos de adaptación de una enzima microbiana de origen Antártico

Study of the adaptation mechanisms of a microbial enzyme of Antarctic origin

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En la actualidad, es ampliamente aceptado que durante la evolución, los organismos que habitan en la Antártida sufrieron diversas adaptaciones para poder prosperar en este ambiente extremo. Dentro de esas adaptaciones, las enzimas que comandan el metabolismo debieron modificarse para poder funcionar en condiciones extremas, particularmente, a bajas temperaturas. El estudio de las enzimas adaptadas al frío de origen Antártico es un campo de enorme interés que ha sido poco explorado, por lo que aún no es totalmente claro como es que estas enzimas logran funcionar a bajas temperaturas. Por otro lado, la mayoría de los estudios realizados en enzimas adaptadas al frío no consideran el efecto de estas adaptaciones sobre la actividad y la especificidad de sustrato de la enzima, lo que podría dar una visión evolutiva más general de estas adaptaciones. En este trabajo, mostramos los estudios realizados por nuestro grupo interdisciplinario durante los últimos años para entender el mecanismo de funcionamiento de una enzima de origen Antártico. Estos estudios han contemplado tanto a la enzima nativa, como a una versión mutante de la misma. En ambas proteínas, hemos realizados diversas mediciones bioquímicas, biofísicas, y de dinámica molecular. Los resultados obtenidos hasta ahora nos indican que al igual que en otras enzimas adaptadas al frío, la flexibilidad de la enzima parece estar en el centro de su adaptación térmica. Más importante, nuestros resultados indican que cambios en la adaptación térmica de la enzima conllevan cambios radicales en su especificidad de sustrato, sugiriendo que ambos fenómenos tienen orígenes comunes.

Este trabajo fue financiado parcialmente por el proyecto INACH RG_03-14, y DICYT-USACH.

PO-05

10h00-10h30

04/12/19

MD666RN
Area: Hongos

Producción de compuestos nitrados por hongos antárticos del género *Pseudogymnoascus*

Production of nitrated compounds by Antarctic fungi of the genus *Pseudogymnoascus*

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Los hongos filamentosos de origen antártico poseen un gran potencial para la producción de metabolitos secundarios con propiedades de interés biotecnológico. Sin embargo, son muy pocos los metabolitos aislados e identificados desde cepas fúngicas antárticas. Uno de los géneros fúngicos predominantes en la Antártica es *Pseudogymnoascus*. Extractos obtenidos desde un gran número de cepas del género *Pseudogymnoascus*, aisladas de diversos ambientes antárticos, han mostrado una notable actividad como antibacterianos, antifúngicos, citotóxicos y antivirales. A pesar de este destacable potencial, es muy poco lo que se conoce de la química de los metabolitos producidos por estos hongos. En los últimos años, nuestro grupo de investigación ha estado interesado en la caracterización química de los metabolitos de hongos antárticos del género *Pseudogymnoascus*. Mediante técnicas que involucran el fraccionamiento de extractos de *Pseudogymnoascus* obtenidos desde cultivos sólidos y líquidos, el uso de diferentes técnicas cromatográficas, y la elucidación estructural mediante técnicas espectroscópicas, hemos determinado la estructura química de varios metabolitos de estos hongos. Notablemente, los principales compuestos aislados hasta el momento son compuestos nitrados, los que incluyen estructuras químicas tan disímiles como éteres bifenílicos, dicetopiperazinas, y fenilmetilamidas. La cantidad y variedad estructural de los compuestos nitrados detectados en estas cepas contrasta fuertemente con los escasos compuestos nitrados obtenidos hasta la fecha desde otros hongos. En definitiva, nuestros resultados sugieren que las cepas antárticas de *Pseudogymnoascus* han desarrollado adaptaciones metabólicas específicas para producir compuestos químicos nitrados. A nivel biológico, esto abre interesantes preguntas de investigación respecto a la función biológica y/o ecológica de estos metabolitos nitrados en hongos antárticos.

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PO-06

12h15-12h45

04/12/19

LP122ML

Area: Biotecnología

Respuesta a sal en la cepa *Exiguobacterium* SH31 y su potencial uso en promover el crecimiento de plantas bajo estrés salino

Salt response in *Exiguobacterium* sp. SH31 and its potential use in promoting plant growth under saline stress

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Members of *Exiguobacterium* genus have been isolated and characterized from various environments, indicating high levels of plasticity and adaptability. To date, the tolerance to salinity and osmotic pressure have been poorly studied in these microorganisms. In this work, we used the halotolerant strain *Exiguobacterium* SH31 previously isolated from the Salar de Huasco (Altiplano Chileno), an environment known for presenting a wide range of salinities and poly-extremophilic conditions. Using different physiology, genomic and transcriptomic approaches, we determined that the bacterium is able to grow properly in a NaCl concentration of up to 50 g/L, however, the best growth rate was observed at 25 g/L. Moreover, we determine that motility and biofilm formation are affected in front an increase in salinity. At genomic level, we report the presence of 15 genes related with osmoadaptive processes. Some of these genes, such as *opuBA* and *putP* (solute transport), *glnA*, *proC*, *gltA* and *gbsA* (solute synthesis) showed an induction in relative expression under NaCl condition. On the other hand, some halotolerant strains of this genus have shown possible biotechnological applications including the promotion of plant growth. Preliminary results have shown that strain SH3 improve the germination percentage in lettuce seeds (*Lactuca sativa* L.) subjected to 150 mM NaCl. In addition, strain SH31 showed positive effects in *in vitro* assays using *Arabidopsis thaliana* as plant model. Therefore, *Exiguobacterium* SH31 could be considered as a bacterial strain with potential to improve plant growth under conditions of saline stress.

FONDECYT 1160315 y 11100414, Universidad Andrés Bello Nucleo DI-3-17/N UNAB y proyecto CONICYT N° R16A10003

PO-07

15h30-16h00

04/12/19

TH528LS

Area: Bacterias

Composición de las comunidades bacterianas y el compendio de genes de respuesta a arsénico y estrés global en el Salar de Huasco: estudio metagenómico de cinco nichos

Metagenomic assessment of bacterial community composition and arsenic / stress related gene abundance of five Salar de Huasco niches under an As gradient

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Polyextremophilic bacteria can thrive in environments with multiple stressors. Salar de Huasco (SH) is one poly-extreme habitat where these bacteria can be found. Here, they are exposed to several factors such as high atmospheric pressure, UV radiation and salinity; changing temperatures and the presence of toxic compounds like arsenic (As). Here, we highlight arsenic stress as one of the main adverse factors in SH. Hence, we aimed to shed light on the effect of arsenic on the bacterial community composition of five different SH sites that present a gradient of this metalloid. Also, we addressed the distribution and abundances of genes related to As metabolism and stress tolerance on these five different niches. Our research group sampled five different SH sites with an As gradient (9 to 321 mg/kg: sediment). Moreover, through a shotgun metagenomic approach, we describe bacterial community composition with greater sensitivity and found a clear dominance exerted by the *Proteobacteria* and *Bacteroidetes* phyla in different proportions. Interestingly, the phyla *Cyanobacteria*, *Chloroflexi* and *Acidobacteria* showed a highly variable distribution among the sites. On the other hand, the abundance of As and stress response genes inevitably follow the metalloid concentration gradient. In particular, approximately 60% of the detected sequences for As metabolism belong to extrusion mechanism, being *arsJ* and *arsP* apparently related to sites with greater presence of As. Additionally, As respiration mechanism was the one which presented most variation among the sites. Whereas, abundance of global stress markers increased following the As gradient. Therefore, we conclude that bacterial communities from SH are very variable and appear to be adapted/shaped using a broad set of genes to physiologically overcome the particular and contrasting environmental conditions in which they inhabit and As generate great pressure that could be driving these changes.

CPS: CONICYT FONDECYT 1160315, ECOS-CONICYT 170023 and Núcleo-UNAB DI-3-17/N.
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CPE: CONICYT National Doctoral Fellowship 2015.

PO-08

10h00-10h30

05/12/19

BQ569FL

Area: Bacterias

Response of sessile and plancktonic cells of the extreme acidophilic *Acidithiobacillus ferrooxidans* to high copper concentration

Response of sessile and plancktonic cells of the extreme acidophilic *Acidithiobacillus ferrooxidans* to high copper concentration

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Acidithiobacillus ferrooxidans is a chemolithoautotrophic acidophile used in industrial biomining to recover elements such as copper or gold. It grows at high metals concentrations both in a plancktonic (P) form in liquid media or in a sessile (S) style attached to different mineral substrates by a monolayer biofilm. The presence of toxic metals may trigger different physiological responses depending on the microorganism lifestyle. To explore this idea, *A. ferrooxidans* ATCC 23270 was grown on solid elemental sulfur prills submerged in the salts of 9K medium (5% weight/volume) at pH 2.5. This allows to compare simultaneously both life styles. Both kinds of cells were adapted to grow at 40 mM copper for 4 days and then separated by centrifugation to analyze their respective total protein changes by using an iTRAQ quantitative proteomics (PCu/SCu). Also a transcriptional analysis (qRT-PCR) of selected genes was done. A total of 139 proteins changed their abundance levels when the proteome of both types of populations grown in the presence of the metal were compared. Eighty eight proteins showed higher levels and 51 lower amounts. As we reported recently, metal-exposed *A. ferrooxidans* cells grown in ferrous iron showed higher levels of cell membrane biogenesis proteins and efflux copper proteins such as CusABC systems. As an example of the several proteomic changes seen in both cell types grown in sulfur, copper-adapted plancktonic cells had increased amounts of surface proteins such as LptA (LPS-transport protein) and TadB (surface attachment protein) when compared to the levels seen in copper-adapted sessile cells. Furthermore, increased TetH (tetrathionate hydrolase) levels (protein and its mRNA) and decreased levels of an ATP synthase subunit (AtpG) suggest a metabolic difference between both lifestyles of the acidophile. In addition, an increased transcriptional level of *MurF*, involved in peptidoglycan synthesis was also seen. The results suggest a possible role of the envelope composition in trapping the toxic metals before their entrance to the cell. The decrease of CusABC protein levels in the plancktonic copper adapted bacteria compared with the sessile ones is in agreement with the possible role of the bacterial surface to prevent metal toxicity.

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PO-09

12h30-13h00

05/12/19

TR218JK

Area: Biotecnología

Hacia el entendimiento del estilo de vida en biopelículas de *Acidithiobacillus* sp. Estudios de proteómica y microscopia de alta resolución

Insights about biofilm lifestyle of *Acidithiobacillus* sp. on metal sulfides. Proteomics and high throughput imaging studies

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Acidithiobacillus species are able to leach metal sulfides such as Pyrite (FeS₂) and Chalcopyrite (CuFeS₂). Under these conditions, a certain part of the cell population remain planktonic and another one forms biofilms on the surface. These metal sulfides, generate extracellular reactive oxygen species (ROS) upon exposure to acidic water. Oxidative stress management is important in acidophilic leaching microorganisms, especially when forming biofilms on metal sulfides. The responses upon exposure to pyrite are not well understood in acidophiles. Shot-gun proteomics was used to compare proteomes of cells grown with iron(II)-ions against biofilm cells, grown for five days in presence of pyrite as sole energy source. In total 1157 proteins were identified. 213 and 207 ones were found to have increased levels in iron(II)-grown or pyrite-biofilm cells, respectively. In total, 80 proteins involved in ROS degradation, thiol redox regulation, macromolecule repair mechanisms, biosynthesis of antioxidants, as well as metal and oxygen homeostasis were found. Forty two of these proteins had no significant changes in abundance, while 30 proteins had increased levels in pyrite-biofilm cells. Proteins associated with inorganic sulfur compound (ISC) oxidation were among the latter. New insights in ROS mitigation strategies are presented for *A. ferrooxidans* biofilm cells. Furthermore, proteomic analyses provide insights in adaptations of carbon fixation and oxidative phosphorylation pathways under these two growth conditions. In order to study biofilm formation, an already existing method for direct quantification of the mineral-attached cell population on pyrite particles in bioleaching experiments by coupling high-throughput, automated epifluorescence microscopy imaging of mineral particles with algorithms for image analysis and cell quantification is being employed. This avoids human bias in cell counting and imaging. New improvements to this method will be presented.

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