

**PROGRAMA FINAL
CONFERENCIAS
2ndo ISE30**

Conferencia de Apertura. 17H15-18H15 02/12/2019

GK922GK

Area: Ecología Microbiana

Dra. Purificación López García. France. puri.lopez@u-psud.fr

Unité d'Ecologie, systématique et évolution, CNRS, Université Paris-Sud/Paris-Saclay, Orsay, France.

Los limites de la Vida en la gradiente poliextrema del campo geotermal de Dallol.

Life limits at the polyextreme gradients of the Dallol geothermal field

Microbial life has adapted to various individual extreme conditions; yet, organisms simultaneously adapted to very low pH, high salt and high temperature are unknown. I will present evidence from combined environmental 16S/18S rRNA-gene metabarcoding, cultural approaches, fluorescence-activated cell sorting, scanning electron microscopy and chemical analyses supporting the existence of physicochemical barriers preventing active life along such unique polyextreme gradients in the Dallol-Danakil area (Ethiopia). We identify two physicochemical barriers to life in the presence of surface liquid water defined by: i) high chaotropicity-low water activity in Mg^{2+}/Ca^{2+} -dominated brines and ii) hyperacidity-salt combinations. We detect extremely diverse microbial life in the less polyextreme sites at the Dallol dome and Danakil depression surroundings. Microbial diversity was dominated by highly diverse ultrasmall archaea widely distributed across phyla with and without previously known hyperhalophilic members. We detect active silica encrustment/fossilization of cells but also abiotic biomorphs of varied chemistry, raising warnings for the interpretation of morphological biosignatures on Earth and beyond. In this framework, I will comment on recent claims about the occurrence of active life (one member of the Nanohaloarchaeota) in the hyperacidic and hypersaline Dallol ponds. I will show evidence suggesting that that finding corresponds to contamination from the salt pan area combined with misinterpretation of abiotic biomorphs as fossilized microbes. Our results point to the absence of life from some polyextreme sites in the presence of liquid surface water on Earth and should help to circumscribe habitability.

Conferencia Magistral 1. 09H00-10H00 03/12/2019

DB488TD

Area: Virus

Dra. Beatriz Díez. Chile. bdiez@bio.puc.cl

Molecular Genetics and Microbiology Department, Pontificia Universidad Católica de Chile, Santiago, Chile; Center for Climate and Resilience Research (CR)2, Chile.

Desvelando la identidad viral y su asociación con hospederos termófilos de tapetes fototróficos

Unveiling viral identity and their association with thermophilic hosts of phototrophic mats.

Extreme environments represent ideal natural models to understand the principles of microbial ecology. We investigated the identity and biogeography of viruses and their interactions with the microbial communities in hydrothermal systems through meta-omics. The mining of viral sequences from cellular metagenomes and metatranscriptomes, shown that a large fraction of the active viral communities in neutral pH hot springs phototrophic mats are predominantly composed of Caudovirus such as cyanophages, which are infecting and potentially controlling relevant communities for the biogeochemical cycles. Metagenomic assembly lead to the recovery of the first T7-like thermophilic cyanophage (CHP58), that was associated with the cyanobacteria *Fischerella* spp. by CRISPR spacers. Additionally, we found marked differences in the number of CRISPR loci and spacers diversity in *Fischerella*, as well as Single Nucleotide Variants (SNVs) in the TC-CHP58 proto-spacers at different temperatures, which reinforce the theory of a coevolution between natural viral populations and their cyanobacterial hosts.

Metagenome Assembled Genomes (MAGs), as well as natural and mitomycin C induced viral communities from thermophilic phototrophic mats were interrogated for the presence of integrated temperate viruses. Our results suggest that most active and dominant bacterial taxa such as *Fischerella*, have as main predators the most abundant lytic viral populations. Meanwhile spontaneously or mitomycin C induced lysogenic viruses were associated to Proteobacteria and Firmicutes phyla, respectively.

Finally, a viral biogeographic pattern was observed for all existing viral metagenomes of hot springs, according to major ecological drivers (here, pH and temperature) by analysis of protein, gene and genome sequences. Protein sharing network of the global thermophilic viral communities showed high modularity, suggesting the gene flow restriction between hot springs and a high local richness, mostly due to the existence of specific virus-host pairs that are locally structured influenced by the environmental conditions that primarily affect the structure of the host community.

All these sponsored by: FONDECYT 1105171, 1190998 (CONICYT, Chile); FONDAP 15110009 - Center for Climate and *Resilience* Research (CR)2 (CONICYT, Chile).

Conferencia Magistral 2. 11H15-12H15 03/12/2019

TP435JD

Area: Ecología Microbiana

Dra. Patricia Valdespino. México/Estados- Unidos. pancronica@gmail.com
Berkeley Synchrotron Infrared Structural Biology Imaging Program,
Lawrence Berkeley National Laboratory

Biogeoquímica al extremo: integrando la estructura y función de ensamblajes microbianos extremófilos en distintas escalas.

Biogeochemistry at the extremes: integrating structure and function of microbial extremophile assemblages across scales.

Microbes have been responsible for most of Earth's biogeochemical cycling. Their adaptation and/or resilience to environmental change will shape the future of ecosystems function. More specifically, microbial capabilities for carbon, nitrogen and phosphorus cycling, and their survival strategies including the production of metabolites, might change as a response to environmental change. Extremophiles provide useful models to study these processes.

While we have started to trace biogeochemical transformations from genes to biomes, the gap in the middle constitutes a black box that will require interdisciplinary efforts in order to be clarified. Our knowledge of physical chemistry, cell physiology, structural biology, ecological interactions and evolution should be integrated to understand and predict ecosystem function in the countdown of planetary change. To address these research questions, in this presentation I will attempt to leap across scales (presenting explorations from nanometric to ecosystem scale) to better understand the role of microbes in biogeochemical transformations.

Conferencia Magistral 3. 14H30-15H30 03/12/2019

GK215MG

Area: Ecología Microbiana

Dr. David S. Holmes. Chile. dsholmes2000@yahoo.com

Center for Bioinformatics and Genome Biology, Fundación Ciencia & Vida, Chile;
Centro de Genómica y Bioinformática, Universidad Mayor, Chile.

La Genómica Integrativa Aclara la Evolución de Hyper-acidófilos.

Integrative Genomics Sheds Light on the Evolution of Hyper-acidophiles.

This presentation explores the evolution and genetic diversity of hyper-acidophilic Bacteria and Archaea (grow at a pH of ≤ 3). An interactive database of more than 150 publicly available acidophile genomes was constructed and used to identify the lowest pH/highest temperature growth environments occupied by acidophiles and to map onto the Tree of Life the distributions of acidophile phenotypes such as methane/hydrogen/sulfur/iron energy pathways, CO₂ fixation and aerobic versus anaerobic metabolisms. Detailed robust and coherent phylogenies were generated from diverse examples of hyper-acidophiles from very different early and late branching microbial lineages distributed around the Tree of Life. Examination of these phylogenies, coupled with comparative genomics identified genes and mechanisms involved in acid resistance and allowed the reconstruction, by inference, of their ancestral evolutionary trajectories, including how acidophilicity can be acquired via recombination and horizontal gene transfer. Surprisingly, a potential link between the coevolution of acidophilicity and thermo-tolerance was discovered.

Genomic sequence-based (e.g. MSLA) and non sequence-based (e.g. ANI) phylogenetic analyses of hyper-acidophiles provided a rich source of data that addresses the fundamental question of whether microbial genetic diversity exists as a continuum or is divided into discrete clusters (species).

Acknowledgements: This work was supported by the Programa de Apoyo a Centros con Financiamiento Basal AFB 170004 to Fundación Ciencia & Vida and Fondecyt 1181717.

Conferencia Magistral 4. 09H00-10H00 04/12/2019

KG263QS

Area: Biotecnología

Dr. Edgardo Donati. Argentina. donati@quimica.unlp.edu.ar
CINDEFI (CONICET, UNLP), Faculty of Sciences, National University of La Plata, La Plata, Argentina.

Aplicaciones biotecnológicas de extremófilos provenientes de áreas geotermales

Biotechnological applications of extremophiles from geothermal areas

Geothermal areas are ecosystems inhabited by unique populations of microorganisms. Our research team investigated the microbial communities in different extreme environments including geothermal zones. Some of these areas showed high concentrations of certain metals and it was expected that microorganisms that thrive in such harsh environmental conditions have poly-resistance mechanisms. Strategies used by these microorganisms exhibiting tolerance or resistance to metals could constitute the basis for using such biota in different biotechnological applications that may have to deal with high metal content. Interactions metal-microorganisms is limited exclusively to mobilization, immobilization, and/or redox-mediated transformation of the metallic species. Microbial metal mobilization can be used to release (and eventually recover) metals from low-grade mineral ores, solid wastes, ashes, sludge, and even exhausted materials among others. Alternatively, metals can be immobilized in order to detoxify polluted water via mechanisms that are similar to those used to mobilize metals (pH and Eh changes plus complexation) but producing the opposite effect (*i. e.*, immobilization). Furthermore, accumulation in the microbial cells, adsorption (enzymically mediated or passive) onto the microbial surface, and precipitation through combination with specific metabolites released into the environment can also produce an immobilization of the metals. Finally, changes in the oxidation state of metals catalyzed by microorganisms not only can lead to modifications in the solubility facilitating the mobilization or immobilization but also can produce fewer toxic metallic species. In this presentation results on metal tolerance of microbial consortia from geothermal zones in Argentina, the characteristics of some microorganisms isolated there and their applications in bioremediation and waste treatment will be discussed.

Conferencia Magistral 5. 11H15-12H15 04/12/2019

NT816SR

Area: Biotecnología

Dra. Susana Castro. Uruguay. s.castro.sow@gmail.com

Facultad de Ciencias, Universidad de la República, Montevideo, Uruguay.

Uso del material genético de origen antártico para el desarrollo de productos biotecnológicos.

Antarctic genetic material: current and potential applications.

Antarctica is a pristine place, with climatic conditions that are considered extreme for human life. These conditions include low temperatures and high exposure to UV-irradiation, among others. Microbes that thrive in this environment have developed many strategies to cope with, e.g. psychrophilic and psychro-tolerant microbes produce enzymes with high catalytic constant at low temperature (psychrophilic enzymes) compared with enzymes produced by mesophilic microbes; these enzymes show biochemical properties compatible with their use in many industrial processes. Also, Antarctica is a good place for the isolation of UV-resistance microbes that produce highly efficient mechanisms of DNA-repair. UV-irradiation induces the production of DNA-photoproducts that may halt RNA-polymerase; among the UV-resistance mechanisms, microbes produce the enzyme photolyase that directly reverses the production of photoproducts. In this scenario, our team works to answer the following questions: what potential uses psychrophilic enzymes have in the industries of detergents, nutraceuticals, and biofuels? What potential uses have the photolyases produced by the UV-resistant Antarctic microbes, with a focus on the cosmetic and pharmaceutical industries? We showed that the Antarctic genetic material is an important source for the development of many biotechnological goods, such as detergents, cosmetic creams, and bioethanol, among others.

Conferencia Magistral 6. 14H30-15H30 04/12/2019

HC151FP

Area: Hongos

Dr. Ramón Batista. México. rabg@uaem.mx

Centro de Investigación en Dinámica Celular, Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, México.

Transcriptómica de hongos halófilos: Fisiología y aplicaciones biotecnológicas.

Transcriptomics of halophilic fungi: Physiology and Biotechnological applications.

Las respuestas a nivel molecular que median las adaptaciones fisiológicas de hongos que crecen óptimamente en condiciones hipersalinas (>1M NaCl) han sido abordadas en un número reducido de sistemas fúngicos. Sin embargo, nuevos estudios transcripcionales son necesarios para sistematizar el conocimiento sobre las dinámicas de expresión génica en los hongos halófilos. *Aspergillus sydowii* y *Aspergillus destruens* son hongos halófilos que en nuestro grupo de trabajo usamos como modelos de estudio, no solo para el análisis a nivel molecular de las respuestas a halofilia, sino porque tienen una extraordinaria capacidad para remover compuestos xenobióticos y/o degradar lignocelulosa en condiciones de alta salinidad. Estudios de RNA-seq en ambas especies de *Aspergillus* han permitido analizar y comparar con otros sistemas fúngicos la expresión diferencial de genes involucrados en halofilia, y a su vez, proponer los mecanismos que permiten a estos hongos crecer de manera exitosa en ambientes con baja actividad de agua por la presencia de cloruro de sodio. Por otra parte, los análisis de los perfiles de transcripción en estos modelos también han permitido establecer las bases moleculares de las estrategias de biodegradación de xenobióticos, como hidrocarburos policíclicos aromáticos, en presencia de elevadas concentraciones de cloruro de sodio. Además, estos hongos muestran características xerófilas, pueden tolerar concentraciones de cloruro de magnesio hasta 2M. Hasta el momento se desconoce prácticamente las respuestas moleculares de hongos creciendo en condiciones de xerofilia por adición de sales inorgánicas. Nuestros estudios aportan evidencias novedosas de cuáles son las principales estrategias adaptativas a nivel molecular de estos hongos para crecer en medios halófilos y xerófilos, así como algunas de sus potencialidades para el tratamiento de agua contaminadas con hidrocarburos, fenoles, fármacos y biosólidos municipales.

Conferencia Magistral 7. 09H00-10H00 05/12/2019

NF252MP

Area: Hongos

Dra. Vívian Nicolau, Brazil. viviannicolau@yahoo.com.br

Laboratório de Microbiologia Polar & Conexões Tropicais, Departamento de Microbiologia, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Brasil.

Pueden muestras del continente Antártica ser una fuente de hongos potencialmente oportunistas para humanos?

Can samples from Antarctica continent be a source of potential human opportunistic fungi?

Fungi are an important component of the microbial communities resident in different environments and substrates of Antarctica and have shown different ecological roles as symbionts, saprobes, and potentially pathogens. Some studies have shown that there is a group of some filamentous fungi that are phylogenetically close to opportunistic pathogenic and mycotoxigenic taxa and showed potential physiologic virulence characteristics *in vitro*. Fungal species display different morpho-physiological and biochemical strategies to adapt and survive in environments with extreme temperatures, low nutrient availability, prolonged desiccation, and solar irradiation. The resilience and adaptation arising from the high genetic plasticity of some fungi present in the extreme environments may result in their ability to infect plants and animals with deficiencies in their defence barriers. Characteristics like capability of grow at 37 °C and/or different pH, display macro- and micro morphological polymorphism, display haemolytic and phospholipase activities, produce tiny spores and show resistance to amphotericin B are some of virulence factors *in vitro* that we can find when the diversity of cultivable fungi from samples of Antarctica is accessed. The most commonly taxa with physiologic virulence characteristics *in vitro* isolated from Antarctica were *Penicillium chrysogenum*, *P. tardochrysogenum* (rocks) and *Aspergillus fumigatus* (ornithogenic soil). *Aspergillus* species are capable of causing infection in immunocompromised patients which *A. fumigatus* has great importance because is often reported as the main cause of aspergillosis. Considering the results obtained with isolates of *A. fumigatus* from Antarctic ornithogenic soil and the fact of the number of cases of systemic fungal infections has increased in immunocompromised patients, we decided to performed *in vivo* assays. The recent results allowed a better understanding of the real risk of potential pathogens spreading to other regions of the planet and the consequences for people, mainly to those with disturbed immune systems.

Conferencia Magistral 8. 11H30-12H30 05/12/2019

RK992MF

Area: Ecología Microbiana

Dra. Lea Cabrol. France. lea.cabrol@mio.osupytheas.fr

Mediterranean Institute of Oceanography (MIO) UMR 7294 - Institut de Recherche pour le Développement (IRD) - OCEANOMED- Campus Universitaire de Luminy, Marseille, France

Microbial methane oxidizers in permafrost thawing ponds, Siberia

High-latitude ecosystems are strongly affected by climate change. Accelerated thawing of permanently frozen soils (permafrost) generates ponds, lakes and wetlands, which are major sources of biogenic methane emissions. With its high warming potential, methane constitutes a positive feedback on global warming. Global changes may disrupt the methane cycle by affecting the metabolic pathways, kinetics, abundances and community composition of the microbial key players involved in methane production and consumption. Surveying the microbial diversity and functionalities in these ecosystems is essential for a better understanding of their potential feedback to climate change. In this study, methane cycling was investigated in four glacial lakes under thermokarst influence in Igarka, Northern Siberian Arctic (discontinuous permafrost). Biogeochemical analyses (dissolved gases concentration, stable isotopes) along the water column profiles demonstrated that methane oxidation occurred mainly in the anoxic layer of the lakes. In some cases, it could totally mitigate the methane produced deeper in the lake sediment. DNA was extracted from superficial sediment and water samples at different depths. The quantification of *mcrA* and *pmoA* gene (functional marker of methanogeny and methanotrophy) and the analysis of bacterial and archaeal diversity by 16S amplicon sequencing (Illumina MiSeq) revealed that the same *Methylomonadaceae*-members, including *Methylobacter* and *Crenothrix*, were the major contributors of methane oxidation in the anoxic water of the four lakes under study. This result raises the question of how these supposedly aerobic methanotrophs can carry out an oxic reaction in fully anoxic waters. Our study highlighted the importance of potential metabolic partners identified in these anaerobic methane oxidation (AOM) layers and co-occurring with the methanotrophs, such as iron-reducers (*Rhodoferrax*, *Geothrix* and *Geobacter*) and iron oxidizers (*Galionella*). The reduction of iron oxides might consume the electrons resulting from methane oxidation. This study provides insight into an anaerobic oxidation process highly relevant for methane emission mitigation.

Conferencia Magistral 9. 14H30-15H30 05/12/2019

JL956LK

Area: Ecología Microbiana

Dr. Francisco Rodríguez-Valera. España. frvalera@umh.es

Evolutionary Genomics Group, Universidad Miguel Hernandez, San Juan de Alicante, Spain and Moscow Institute of Physics and Technology (MIPT), Dolgoprudny 141701, Russia.

***Haloquadratum*, *Salinibacter* and *Spiribacter*, three halophiles, three metagenomic stories**

The major revolutions that took place at the end of the past century and the beginning of the new one nurtured by the molecular approach (rRNA genes) and the high throughput sequencing (cheap and easy genomes and metagenomes) have had a profound influence in our understanding of hypersaline environments. In a way they have been like a scale model of the revolution that is taking place in Microbiology at large. The existence of square cells that turned out to be the dominant archaeon in saturated brines was brought up by 16S rDNA sequencing of solar saltern DNA that latter on allowed the isolation of *Haloquadratum walsbyi* in pure culture. This peculiar microbe dominates neutral saturated brines worldwide and in spite of its sequencing as genomes and metagenomes still carries a large load of unexplained mysteries starting from its own massive dominance of habitats in which many other microbes can grow successfully. Its strategies to succeed might shed light on other similarly successful microbes such as *Pelagibacter* in the surface ocean. A by-product of the efforts to isolate *Haloquadratum* was the unexpected discovery and subsequent isolation and genome sequencing of *Salinibacter* an interesting example of convergent evolution in which a bacterium, likely by the acquisition of several archaeal properties (like having carotenoids in the membrane or several rhodopsins, some typically archaeal such as halorhodopsin) has also succeeded in colonizing saturated brines and being relatively successful, although its actual specific habitat remains unclear. Latter on, through extensive metagenomic studies carried out in differently concentrated brines of solar salterns we still discovered another yet hidden microbe: *Spiribacter* a truly moderate halophile thriving at intermediate salinities and sharing features with *Salinibacter* such as the salt-in strategy and the presence of xanthorhodopsin. Still, a last challenge remains, the nanohaloarchaea found in saturated brines of different pH.

Conferencia de Cierre. 17H45-18H45 05/12/2019

JC932FQ

Area: Ecología Microbiana

Dra. Cristina Dorador. Chile. criordor@gmail.com

Laboratorio de Complejidad Microbiana y Ecología Funcional, Departamento de Biotecnología, Facultad de Ciencias del Mar y Recursos Biológicos, Centre for Biotechnology and Bioengineering, Universidad de Antofagasta, Antofagasta, Chile.

Cambio global, Antropoceno y microorganismos: un llamado urgente a la conservación de ambientes extremos

Global change, Anthropocene and microorganisms: an urgent call for the conservation of extreme environments

El Desierto de Atacama ocupa una vasta extensión territorial en el norte de Chile con distintos gradientes altitudinales y latitudinales (2 en el Altiplano). La vida microbiana (Bacteria, Archaea, Eukarya y virus) se ha estudiado en distintos hábitats incluyendo suelo hiperárido, interior de rocas, salares, volcanes, aguas termales, bofedales, entre otros, donde es frecuente observar una alta diversidad microbiana y la presencia de microorganismos con adaptaciones específicas a variados estresores ambientales. Los microorganismos son claves para la mantención de la trama trófica, junto con la mitigación y adaptación al cambio climático y realizan distintos servicios ecosistémicos, incluyendo ciclaje de nutrientes y producción de compuestos bioactivos. Actualmente los hábitats microbianos del Desierto de Atacama están bajo distintas presiones antrópicas y otras vinculadas probablemente al calentamiento global. La intensiva extracción de agua y salmueras desde salares estaría afectando la mantención de los tapetes microbianos y junto con ello, el resto de la trama trófica. Del mismo modo, salmueras de cloruro de litio serían nuevos hábitats para Bacteria y Archaea. El uso de nuevas tecnologías de secuenciación de ADN ha permitido profundizar en la diversidad y función de las comunidades microbianas reflejando la complejidad de interacciones bióticas y abióticas. Este nuevo conocimiento es crucial para proponer parámetros ambientales de conservación microbiana, las cuales se vinculan directamente con la conservación del hábitat. Considerando el carácter poliextremo de estos ambientes junto con su hiperdiversidad, se propone al Desierto de Atacama como Patrimonio Microbiológico del Planeta.