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ECOLOGÍA MICROBIANA DE SUELOS - ECOLOGÍA MICROBIANA DE AMBIENTES ACUÁTICOS - ECOLOGÍA MICROBIANA DE COMUNIDADES MIXTAS - EXTREMÓFILOS - FAGOS Y VIRUS - ECOLOGÍA MICROBIANA SINTÉTICA - MICROBIOMA HUMANO Y SALUD - MICROBIOMAS ASOCIADOS A HUÉSPEDES ANIMALES - MICROBIOMAS ASOCIADOS A PLANTAS - EFECTOS AMBIENTALES SOBRE COMUNIDADES MICROBIANAS - MÉTODOS APLICADOS EN ECOLOGÍA MICROBIANA Y HERRAMIENTAS COMPUTACIONALES - BIOTECNOLOGÍA MICROBIANA

ISMELAT Bogotá - Colombia 2021

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PROGRAM - Day 1 – July 27, 2021

Schedule GTM-5	Room A: Microbiomes associated with animal hosts	Room B: Environmental effects on microbial communities	Room C: Phages and viruses
10:00 – 10:30	**Opening remarks**		
10:30 – 11:30	Keynote lecture 1: **Redirecting the scientific system to combat the SARS-CoV-2 pandemic** Gonzalo Moratorio Ph.D. Instituto Pasteur de Montevideo Uruguay		
11:30 – 12:00	A1: **Insects are empowered by microbes** Javier A. Ceja-Navarro Ph.D. Lawrence Berkeley National Laboratory U.S.A.	B1: **Taxonomic, functional and environmental interactions in hot springs microbial mats** Beatriz Díez Ph.D. Universidad Católica de Chile Chile	C1: **Human gut phages and their role as modifiers of microbial communities** Alejandro Reyes Ph.D. Universidad de Los Andes Colombia
12:00 – 12:30	A2: **The gut microbiota of honey bees** Karina Antúnez Ph.D. Instituto de Investigaciones Biológicas Clemente Estable Uruguay	B2: **Composition, diversity and functional analysis of long-term hydrocarbons-contaminated soil microbiome** Irma Morelli Ph.D. Universidad Nacional de La Plata Argentina	C2: **Bacteriophage-mediated manipulation of the gut microbiome** Josué Castro Ph.D. University of Copenhagen Denmark
12:30 – 12:50	Break		
12:50 – 13:10	A3: **Unveiling the neglected fraction of the ruminal microbiome at the intersection of culturing and molecular approaches** Alejandro Caro-Quintero Ph.D. Universidad Nacional de Colombia Colombia	B3: **Composition and health impact of city public transport microbiomes** María Mercedes Zambrano Ph.D. Corporación Corpogen Colombia	C3: **Bacteriophages as a precision tool for controlling undesired microbiota partners** Martha Vives Ph.D. Universidad de Los Andes Colombia
13:10 – 13:30	A4: **Prokaryotic, fungal, and unicellular eukaryotic core communities across three sympatric marine sponges from the southwestern atlantic coast are dominated largely by deterministic assemblage processes** Cristiane Hardoim Ph.D. State University of São Paulo Brazil	B4: **Pollution and bioremediation drives the microbial communities in soils and water** Michael Seeger Ph.D. Universidad Técnica Federico Santa María Chile	C4: **Metagenomic CRISPR reconstruction disentangle bacteria-phage dynamics** Leandro Guerrero Ph.D. Instituto de Investigaciones en Ingeniería Genética y Biología Molecular Argentina
13:30 – 14:30	Keynote lecture 2: **Linking the gut microbiome and metabolome to understand dietary response** Rob Knight Ph.D. Universidad de California - San Diego USA		
14:30 - 16:30	Poster session – Day 1		

PROGRAM - Day 2 – July 28, 2021

Schedule **GTM-5**	**Room D:** **Microbial biotechnology**	**Room E:** **Methods applied in microbial ecology and computational tools**	**Room F:** **Extremophiles**
10:00 – 11:00	Keynote lecture 3: **Codiversification of gut microbiota with humans** Ruth Ley Ph.D. Instituto Max Planck Germany		
11:00 – 11:30	D1: **Biotechnological potential of insect gut microbiome** Paola Talia Ph.D. Instituto de Tecnología Agropecuaria Argentina	E1: **Quantitative prediction of complex functions in constructed ecosystems using machine learning** Ulisses Nunes da Rocha Ph.D. The Helmholtz-Centre for Environmental Research Germany	F1: **Microbial diversity in deep-sea habitats of the Southwestern Atlantic** Vivian Helena Pellizari Ph.D. University of Sao Paulo Brazil
11:30 – 12:00	D2: **The microbes in our food and their potential to become health solutions** Gerardo Toledo Ph.D. Solarea Bio Inc. U.S.A.	E2: **Indexing the genomic diversity of Archaea and Bacteria with MiGA, the Microbial Genomes Atlas** Luis Miguel Rodríguez Ph.D. University of Innsbruck Austria	F2: **Biodiversity in the Copahue geothermal region; a study case of biogeography and community structure of acidic and thermophilic extremophiles** María Sofía Urbieta Ph.D. Universidad Nacional de la Plata Argentina
12:00 – 12:20	**Break**		
12:20 – 12:40	D3: **Effect of inhibitors over the anaerobic digestion process based on the metabolic reconstruction of the process** María Francisca Villegas Ph.D. Universidad ICESI Colombia	E3: **PIME: capturing biological differences using prevalence**. Victor Pyrlo Ph.D. Federal University of Lavras Brazil	F3: **Recovering microbial genomes in Antarctic and subsurface ecosystems through metagenomics** Amanda G. Bendía Ph.D. Universidade de São Paulo Brazil
12:40 – 13:00	D4: **Genomic analysis of biodegradation pathways for furans and their relevance for bioconversion of lignocellulosic biomass** Danilo Perez-Pantoja Ph.D. Universidad Tecnológica Metropolitana Chile	E4: **Genomes comparative analysis in PGPR: Identifying genetic traits involved in plant-bacteria interaction under abiotic stress conditions** Claudio Córtes Vásquez Ing. Biotec. Centro de estudios Avanzados en Zonas Áridas (CEAZA) Chile	F4: **Tracking arsenic metabolism in the Salar de Huasco - Altiplanic environment, via genome-resolved metagenomics** Juan Castro-Severyn Ph.D. Universidad Católica del Norte Chile
13:00 – 14:00	Keynote lecture 4: **The human microbiome in a disruptive era** María Domínguez Ph.D. Universidad Rutgers USA		
14:00 - 16:00	Poster session – Day 2		

PROGRAM - Day 3 – July 29, 2021

Schedule **GTM-5**	**Room G:** **Synthetic microbial ecology**	**Room H:** **Microbial ecology of mixed communities**	**Room I:** **Plant-associated microbiomes**
10:00 – 11:00	Keynote lecture 5: **Structuring the soil microbiome by the cultivation of cover crops** Fernando Dini Andreote Ph.D. Universidad de São Paulo Brazil		
11:00 – 11:30	G1: **Rules of microbial community assembly in simple environments** Sylvie Estrela Ph.D. Yale University U.S.A.	H1: **Verrucomicrobiota degrade sulfated methyl pentoses during diatom blooms** Luis H. Orellana (Coto) Ph.D. Max Planck Institute Germany	I1: **Seed transmitted *Proteobacteria* from the core microbiome of juvenile angiosperm plants** David Johnston-Monje Ph.D. Universidad del Valle Colombia
11:30 – 12:00	G2: **Providing complex biological outputs by engineering division of labor in bacteria** Juan Nogales Ph.D. Centro Nacional de Biotecnología Spain	H2: **Bacterivory by mixotrophic phytoflagellates** Fernando Unrein Ph.D. Instituto de Investigaciones Biotecnológicas de Chascomús Argentina	I2: **The effect of domestication on the tomato rhizosphere microbiome** Alexandra Stoll Ph.D. Centro de estudios Avanzados en Zonas Áridas (CEAZA) Chile
12:00 – 12:20	Break		
12:20 – 12:40	G3: **A top-down enrichment strategy to guide the design of synthetic microbial consortia** Diego Jiménez Ph.D. Universidad de Los Andes Colombia	H3: **A proposed framework for the consolidation of a South America mycorrhizal database**. Jessica Duchicela Ph.D. Universidad de las Fuerzas Armadas - ESPE Ecuador	I3: **Harnessing the microbiome to control plant parasitic weeds** Francisco Dini Andreote Ph.D. Pennsylvania State University U.S.A.
12:40 – 13:00	G4: **Synthetic community invasion depends on secondary metabolite production in Bacillus subtilis** Carlos N. Lozano-Andrade cPhD Technical University of Denmark Denmark	H4: **Genome of a new Candidatus anammox bacteria assembled from the metagenome of two anammox reactors** Pía Oyarzúa cPhD Universitat Autónoma de Barcelona Spain	I4: **Simulated climate change in a semiarid shrubland decreased the phylogenetic diversity of arbuscular mycorrhizal fungal communities** María del Mar Alguacil Ph.D. Estación Experimental el Zaidín Spain
13:00 – 14:00	Selected posters - session		

PROGRAM - Day 4 – July 30, 2021

Schedule GTM-5	Room J: Soil microbial ecology	Room K: Microbial ecology of aquatic environments	Room L: Human microbiome and health
10:00 – 11:00	Keynote lecture 6: **The Art of Harnessing Dark Energy: Symbioses between Chemosynthetic Bacteria and Marine Invertebrates** Nicole Dubilier Ph.D. President of the International Society for Microbial Ecology - ISME Max Planck Institute Germany		
11:00 – 11:30	J1: **The rhizosphere microbiome as a tool for a sustainable agriculture** Lucas William Mendes Ph.D. Universidade de São Paulo Brazil	K1: **Mangrove Microbiome Initiative (MMI)** Alexandre Soares Rosado Ph.D. King Abdullah University of Science and Technology Saudi Arabia	L1: **A simpler niche? A microbial ecologist's guide to cervicovaginal microbiota in health and disease** Fillipa Godoy-Vitorino Ph.D. Universidad de Puerto Rico Puerto Rico
11:30 – 12:00	J2: **The ecology of bacterial invasions** Joana Falcao Salles Ph.D. University of Groningen The Netherlands	K2: **Differences in the microbial community structure in sediments from the Yucatan underground aquifer appear to be determined by physical and chemical characteristics posed by coastal and inland environments** Alejandra Prieto Davó Ph.D. Universidad Nacional Autónoma de México Mexico	L2: **A systems genetics approach to dissect interactions between gut microbes, metabolites and the host** Federico Rey Ph.D. University of Wisconsin-Madison U.S.A.
12:00 – 13:00	**Long Break**		
13:00 – 13:20	J3: **Using soil probiotics to improve the efficiency of phosphorus fertilizers in the tropic** German Estrada Ph.D. AGROSAVIA Colombia	K3: **Microbiome manipulation elicits metabolic and genetic restructuring and improves coral biology** Raquel Silva Peixoto Ph.D. King Abdullah University of Science and Technology Saudi Arabia	L3: **The Latinbiota Consortium: understanding composition and variation of human gut microbiota in Latin American populations** Gregorio Iraola Ph.D. Instituto Pasteur de Montevideo Uruguay
13:20 – 13:40	J4: **Spatial and temporal biogeographic distribution of soil bacterial community in cranberry soils** Thiago Gumiere Ph.D. Laval University Canada	K4: **Disentangling the bacterial metabolic interactions on Brazilian soda lakes** Simone Cota Ph.D. CENA/USP Brazil	L4: **Gut bugs matter to viroimmunotherapy: bacterial changes associated to the efficacy of Delta-24-RGDOX against glioblastoma** Natalie M. Meléndez-Vázquez cPhD University of Puerto Rico USA
13:40 – 14:30	**Round Table Discussion: *Science and Society in Latin America***		
14:30 – 15:30	Closure**: Microbial ecology in a changing world: public policy, interdisciplinarity and outreach** Cristina Dorador Ph.D. Universidad de Antofagasta Chile		

POSTER PROGRAM

TUESDAY POSTER SESSION – DAY 1

Code	Name	Affiliation	Title	Room
A3	Bruno Francesco Rodrigues de Oliveira	Federal University of Rio de Janeiro (Brazil)	One from the mother, the other from the daughter: a genomic survey of two Vibrio strains isolated from different life stages of the marine sponge *Plakina cyanorosea*	**Room 1a**
A4	Karla Cautivo-Reyes	Murdoch University (Australia)	*Clostridium difficile* in Western Australian native animals: Prevalence and molecular epidemiology.	
A5	Leslie M. Montes-Carreto	Universidad Autónoma del Estado de Morelos (México)	Gut microbial community and their potential role in the Volcano rabbit (Romerolagus diazi)	
A6	Juliana María Ruiz Barrionuevo	Facultad de Ciencias Naturales e Instituto Miguel Lillo, Universidad Nacional de Tucumán (Argentina)	Biological effects and differences on the gut microbiome of *Galleria mellonella* larvae consuming plastics	
A7	Luis Acevedo-Márquez	University of Puerto Rico, Medical Sciences Campus (US)	Specific Pathogen Free and Conventional primates differ in microbiota composition and diversity	
A8	Diego Dierick	Universidad de Costa Rica (Costa Rica)	Exploring the gut microbial community associated with herbivorous hosts in Costa Rica	
A9	Jesús Mateo Amillano Cisneros	Universidad Michoacana de San Nicolás de Hidalgo (México)	Efectos de probióticos y prebióticos en el crecimiento y la microbiota intestinal del pez blanco *Chirostoma estor* endémico del altiplano mexicano.	
A11	Marileyxis López	Universidad Mayor (Chile)	Characterization of dinoflagellate communities in marine sponges and seawater in Fildes Bay, Antarctic Peninsula	
A20	Osiris Gaona	Universidad Nacional Autónoma de México (México)	Characterization of the intestinal microbiome of *Tapirus bairdii* from the Yucatan Peninsula, Mexico	**Room 2a**
A21	Ruth Hernández	Universidad de los Andes (Colombia)	Studying the bacterial diversity of the rumen at high resolution	
B2	Luanny Fernandes	Universidade Federal Fluminense (Brazil)	The influence of the Doce river mouth on the microbiome of nearby coastal areas three years after the Fundão Dam failure, Brazil.	
B3	Nailah Ahmed	Universidade de São Paulo (Brazil)	Metagenome-assembled genomes from glacier retreat areas in King George Island	
B4	Maria Camila Escobar Restrepo	Amazonian Scientific Research Institute SINCHI (Colombia)	Taxonomic bacterial composition and Hg-functional genes change according to mercury distribution across a transect of the Caquetá River in Colombia Amazon region	
B5	Florencia Bertoglio	Instituto de Investigaciones Biológicas Clemente Estable (Uruguay)	Bacterias acuáticas como indicadores de cambio ambiental en lagos de la Península Fildes (Antártida)	
B6	Martín Saraceno	IEGEBA – UBA/CONICET (Argentina)	Estudio de condicionantes urbanos y ambientales sobre la ocurrencia de patógenos en una red hidrológica de arroyos con un elevado grado de contaminación	
B7	Francisco L. Massello	CINDEFI (Argentina)	Análisis de ocurrencia de filotipos tras la exposición a metales pesados en enriquecimientos de una muestra ambiental del Río Agrio, Argentina	

B17	Vivana Starevich	CINDEFI - CONICET - UNLP (Argentina)	Estudio de la actividad degradadora anaeróbica de hidrocarburos en sedimentos de agua dulce con hidrocarburos	**Room 3a**
B18	Lorraine Vélez-Torres	University of Puerto Rico - Medical Sciences Campus (US)	Effect of Hurricane María on Fungal Communities in Water-Exposed Homes in San Juan, Puerto Rico	
B19	Eduardo J. Aguilar Rangel	Universidad Nacional Autónoma de México (México)	Ecological and evolutionary correlation of *amo* genes	
B20	Dinka Ivulic	Universidad de Chile (Chile)	Comunidades bacterianas en aerosoles ambientales en granjas de pollos Broiler	
B21	Clovis Daniel Borges	University of São Paulo (Brazil)	A multidimensional approach in modulating mammal exclosure to determine plant-microbial interactions and greenhouse gas emissions in the Atlantic Forest	
B23	Esteban Palacio Pérez	Universidad EIA (Colombia)	Biomasa microbiana y respiración basal en turba de humedales de alta montaña en la Cuenca Alta del Río Claro en el Macizo Volcánico Ruiz-Tolima	
B25	Luisa Alzate-Ruiz	Rothamsted Research (UK), El Bosque University (Colombia)	*In silico* analysis for identification of microbial profiles linked to potential Chromium (VI) remediation.	
D3	Francisco L. Massello	CINDEFI (Argentina)	Biosorción de cadmio y cinc por dos especies del género *Bacillus* provenientes de la región volcánica Caviahue-Copahue, Argentina	**Room 4a**
D4	Micaela Gallicet	Centro de Investigación y Desarrollo en Fermentaciones Industriales (CINDEFI) – CONICET (Argentina)	The application of natural muds and their extreme microbial communities in the remediation of heavy metals	
D5	Aixa Sarmiento Tovar	Universidad de La Sabana (Colombia)	Bioproduction and bioactivity of *Streptomyces* pigments isolated the Guaviare and Arauca rivers (Colombia)	
D6	Jéssyca Silva	Universidade Federal do Rio de Janeiro (Brazil)	Biosurfactant and bioemulsifier activities from marine sponge-associated bacteria collected in Rio de Janeiro, Brazil	
D7	Carolina Rubiano Labrador	Universidad Tecnológica de Bolívar (Colombia)	Cartagena mangroves: reservoir of bacteria with biotechnological potential	
D8	Vitoria Barros	Universidade Federal do Rio de Janeiro (Brazil)	Potencial de leveduras marinhas na produção de biosurfactantes	
D9	Ana Agnello	Centro de Investigación y Desarrollo en Fermentaciones Industriales (CINDEFI) – CONICET-UNLP (Argentina)	Biological contribution of composting and phytotechnologies to manage solid wastes of petroleum industry after chemical oxidation	
D10	Stephanny Sánchez-Vargas	Universidad Nacional de Costa Rica (Costa Rica)	Antimicrobial activity of mangrove-associated fungi from the Tropical Pacific of Costa Rica	
D19	Jonathan Fortt	Universidad Católica del Norte (Chile)	Efecto de cepas nativas del norte de Chile sobre los mecanismos implicados en la tolerancia a estrés salino e hídrico en plantas de lechuga.	**Room 5a**
D20	Cecilia Ghiazza	Facultad de Química, Universidad de la República (Uruguay)	Dinámica y persistencia de indicadores de contaminación fecal microbianos y virales en lodos y biosólidos de Plantas de Tratamiento de Aguas Residuales	
D21	Nelly Diaz	CorpoGen (Colombia)	Formulation of an Alternative medium for the growth of the cellulolytic fungus *Trichoderma* spp.	
D24	Angeline Saadoun	Instituto de Investigaciones Biológicas Clemente Estable (Argentina)	Desarrollo de consorcios microbianos para la biorremediación de suelos y aguas contaminadas con hidrocarburos provenientes de combustibles fósiles	
D25	Milko Jorquera	Universidad de La Frontera (Chile)	Salt–induced stress tolerance during wheat seed germination is improved when *Variovorax sp*. strain P1R9 is applied as part of bacterial consortia	
D26	ximena Báez	Universidad Técnica Federico Santa María (Chile)	Bioinformatic analysis of oxidative stress genes and salt stress genes in hydrocarbon degrading strains Rhodococcus sp. ICBD2 and *Acinetobacter radioresistens* DD78	
D27	Constanza Macaya Ramos	Universidad Técnica Federico Santa María (Chile)	Protective role of choline in *Acinetobacter radioresistens* DD78 during hydrocarbons degradation under saline conditions	
D28	Jeysson Sanchez-Suárez	Universidad de La Sabana (Colombia)	Discovering *Eunicea fusca*-derived actinobacterial isolates with a potential photoprotective capability	

D37	Maria Clara De La Hoz Romo	Universidad de La Sabana (Colombia)	Evaluación de la actividad antibacteriana de extractos de actinobacterias marinas frente a *Staphylococcus epidermidis*	**Room 6a**
D38	Julian Wissner	University of Stuttgart (Germany)	A customized toluene dioxygenase platform for the production of cis-1,2-dihydrocatechol in *Escherichia coli* BW25113 lacking glycerol dehydrogenase activity	
D40	Silvio Lopez	Universidad Antonio Nariño (Colombia)	*Bacillus thuringiensis* Parasporin-6 associations in the context of uterine cancer	
F1	Kattia Nuñez-Montero	Universidad de La Frontera (Chile)	An antarctic Rahnella inusitata showed polyextreme adaptability and cold-active β-galactosidase enzymes based on genomic analysis.	
F2	Montserrat Arciénaga	Universidad Nacional de La Plata (Argentina)	Drenajes ácidos en pasivos mineros de la Puna Argentina: microorganismos responsables y su inhibición	
F3	Juan Castro-Severyn	Universidad Católica del Norte (Chile)	Tracking arsenic metabolism in the Salar de Huasco - Altiplanic environment, via genome-resolved metagenomics.	
F4	Cecilia Bernardelli	Facultad de Ciencias Exactas, UNLP, Argentina y CINDEFI, Conicet (Argentina)	Biogeoquímica en el Río Amarillo: rol de microorganismos autótrofos y heterótrofos	
F5	Maira Nayeli Luis Vargas	Universidad Nacional Autónoma de México (México)	Análisis de las comunidades procariontes de tapetes microbianos y estructuras órgano-sedimentarias asociadas de cuevas pseudokársticas en la Sierra del Chichinautzin, México.	
F6	Kimberly Agüero	Universidad Nacional de Costa Rica (Costa Rica)	Diversidad y distribución del filo *Chloroflexi* en tapetes microbianos de 14 fuentes termales de Costa Rica	**Room 7a**
F7	Eliza Jara-Negrete	University of Liège (Bélgica) - Pontificia Universidad Católica del Ecuador (Ecuador)	First steps in the quest for actinobacteria in Ecuadorian Amazon oil-ponds	
F8	Rodolfo Menes	Universidad de la República (Uruguay)	*Frigoflavimonas asaccharolytica* gen. nov. sp. nov., isolated from Antarctica	
F10	Nicolas Napolitano	CONICET (Argentina)	CRISPR-CAS tipo IVB en *Rhodococcus* sp. cepa ADH, una actinobacteria aislada de la Antártida	
F11	Jaime Alcorta	Pontificia Universidad Católica de Chile (Chile)	Novel hot spring cyanobacterial genomes from metagenomes unveil genetic adaptations to the high temperature environment	
F12	Rocío J Alcántara-Hernández	Institute of Geology, National Autonomous University of Mexico (UNAM)	In the dark: microorganisms of microbial mats and terrestrial stromatolites in lava tubes.	
F13	Bárbara Robles	Pontificia Universidad Católica de Valparaíso (Chile)	Análisis del metagenoma de una poza hidrotermal del sistema Lirima, Chile: una nueva fuente de compuestos promotores del crecimiento vegetal	
F14	Hermes Hernán Bolívar-Torres	Universidad Nacional Autónoma de México (México)	Genomic diversity of thermoacidophile bacteria from los azufres geothermal field and their implications in biotechnology and astrobiology.	
I1	Nguyen Esmeralda López Lozano	Instituto Potosino de Investigación Científica y Tecnológica (México)	The seed-associated microbiome of four cactus species from Southern Chihuahuan Desert	**Room 8a**
I2	Diego Garfias Gallegos	Langebio-Cinvestav (Argentina)	Genomics of cycads' coralloid-root bacterial microbiome suggests adaptation from bacterial symbionts allowing holobiont to thrive in contrasting environments	
I3	Vanessa Reyes Loaiza	Universidad Javeriana – Sede Cali (Colombia)	Análisis del microbioma endófito bacteriano radicular y su relación con el comportamiento hospedero-dependiente de la bacteria endófita diazotrófica SOG26 durante la interacción con las especies *Oryza glumaepatula* y *Arabidopsis thaliana*	
I4	Ciro Félix	Universidade Federal de Alagoas (Brazil)	Elevada beta-diversidade nas comunidades de leveduras cultiváveis em folhas e frutos de *Bromelia sp.* na Floresta Tropical Seca no Nordeste do Brasil	
I5	Darlyng Pontigo	Universidad de Santiago de Chile (Chile)	Caracterización química de sobrenadantes de un aislado de cianobacterias con efecto promotor del crecimiento de la gramínea *P. australis*	
I6	Victor Daniel Firmino dos Santos Tavares	Universidade Federal de Alagoas (Brazil)	Comunidade de leveduras do filoplano e a predileção por hábitos de vida em *Bromeliaceae*	

I7	Mateo Córdoba Agudelo	Universidad de Antioquia (Colombia)	Análisis de comunidades bacterianas rizosféricas asociadas a dos genotipos de *Persea americana* cv. Hass, en dos localidades del Departamento de Antioquia, Colombia.	**Room 8a**
I8	María del Mar Alguacil	Estación Experimental del Zaidín (España)	Simulated climate change in a semiarid shrubland decreased the phylogenetic diversity of arbuscular mycorrhizal fungal communities	
J1	Valentín Pérez-Hernández	Tecnológico Nacional de México/Instituto Tecnológico de Tuxtla Gutiérrez, Chiapas (México)	Aerobic methanotrophic bacteria in saline-alkaline soil of the former lake Texcoco, Mexico	**Room 9a**
J3	Sergio Pardo-Diaz	AGROSAVIA (Colombia)	Inoculation with endophytic PGPB improves plant growth and quality, and modulates the rhizosphere bacterial community of an intercropping system	
J4	María Serrano	Universidad Simón Bolívar (Colombia)	The effect of agricultural practices on the soil microbiome in Colombian Caribbean tropical dry forest	
J5	Karen Santaren	Universidade Federal do Rio de Janeiro (Brazil)	Greenhouse gases fluxes associated with the compositional and functional dynamics of bacterial communities in response to rain on pasture soils	
J6	Laura Rengifo Cajias	Universidad del Rosario (Colombia)	Fungal root endophytes of tropical pioneer plants from a premontane forest in Colombia	
J7	Juan David Sánchez Tello	Universidad del Rosario (Colombia)	How ectomycorrhizal communities vary from natural to urban ecosystems: *Quercus humboldtii* as a study case in the tropical Andes	
J9	Micaela Boenel	IPATEC – COMAHUE – CONICET (Argentina)	Levaduras y actinobacterias rizosféricas tolerantes a salinidad y sequía de la estepa Patagónica	
J10	Lorena Rodríguez-Orduña	Tecnológico de Monterrey (México)	Comparative genomics of environmental isolates of *Nocardia* and *Streptomyces* from contrasting environments	
J19	Georgina Conti	Universidad Nacional de Córdoba (Argentina)	Los hongos micorrícicos arbusculares aumentan la fertilidad del suelo en agroecosistemas: resultados desde una aproximación meta-analítica	**Room 10a**
J21	Pedro Feria	Universidad Nacional de Colombia – Sede Medellín (Colombia)	Characterization of a high cadmium accumulation soil bacterium isolated in *Theobroma cacao* crops with geogenic cadmium levels	
J22	Laura Natali Afanador Barajas	Centro de Investigación y de Estudios Avanzados del IPN, CINVESTAV (México)	Efecto de la aplicación de un biofertilizante sobre estructura de la comunidad bacteriana del cultivo de maíz (*Zea mays* L.)	
J23	Deisi Navroski	University of São Paulo (Brazil)	Monitoring soil microbiota in a forest restoration chronosequence in the Atlantic Forest	
J28	César Marín	Institute of Botany, The Czech Academy of Sciences (Czech Republic)	Chilean blind spots in soil biodiversity and ecosystem function research	
J25	Daymara Sánchez Castro	Universidad de La Habana (Cuba)	Solubilización y mineralización de fósforo por cepas del género *Bacillus*.	
J26	Aline Giovana da França	Luiz de Queiroz College of Agriculture - ESALQ/USP (Brazil)	Soil microbial communities' responses to deforestation and reforestation processes in the Eastern Amazon	
J27	Siu Mui Tsai	Center for Nuclear Energy in Agriculture/University of Sao Paulo, (CENA/USP) (Brazil)	The conversion burnt-to-green harvest in sugarcane promotes microbial functional diversity and soil organic matter resilience	
K5	Anna Luiza Bauer Canellas	Federal University of Rio de Janeiro (Brazil)	Diving into the unknown: identification of antimicrobial resistance hotspots in a tropical urban estuary	**Room 11a**
K6	Camila Castillo-Vilcahuaman	Universidad Peruana Cayetano Heredia (Perú)	Caracterización de las comunidades microbianas del río Rímac utilizando 16S rRNA metabarcoding	
K7	Lucas Ferreira	University of São Paulo (Brazil)	Characterization of plastisphere associated with plastic polymers during biofilm succession in the coastal Southwest Atlantic of Brazil	
K8	Ana Carolina Butarelli	University of São Paulo (Brazil)	Diversity of culturable methane-oxidizing bacteria from deep sediments of the Southwest Atlantic Ocean	
K9	Rocio Azcatl	Centro de Investigación Científica y de Educación Superior de Ensenada, Baja California (México)	Síntesis de halometanos en la cuenca del Sur de California: ¿Qué papel juegan las distintas variables bióticas y abióticas en este sistema?	

K10	Jonathan Parra	University of Strathclyde (UK)	A multi-omics approach to assess the chemical ecology of *Pseudonocardia* spp. from marine sediments	**Room 11a**
K11	Layla Mayer Fonseca	Universidade Federal de Juiz de Fora (Brazil)	Bacteria and seston in tropical reservoirs from different latitudes present similar carbon to nutrients ratio	
K12	Catherine Opitz Rios	Universidad San Sebastián (Chile)	Microbial signature in urban wetlands of Llanquihue and Puerto Montt, Chile	
K21	Kimberly Guapi	Pontificia Universidad Católica del Ecuador (Ecuador)	Caracterización fenotípica de microalgas y cianobacterias del perifiton de los ríos aportantes del embalse altoandino Succus, Cordillera Real del Ecuador	**Room 12a**
K23	Julieta Bianchelli	Universidad Nacional del Noroeste de la provincia de Buenos Aires (Argentina)	Temporal dynamics of *Legionella* (*Proteobacteria, Legionellaceae*) in a Pampean shallow lake	
K24	Alberto N. Arroyo	Centro de Investigación Científica y de Educación Superior de Ensenada (México)	Patrones de distribución de metabolismos fotoheterotróficos en comunidades microbianas del mar Mediterráneo	
K25	Icaro Zapparoli	Federal University of São Carlos – UFSCAR (Brazil)	Fluorescent dissolved organic matter produced by freshwater phytoplankton axenic cultures	
K26	Facundo Lepillanca	Instituto de Investigaciones Biológicas Clemente Estable (Argentina)	Predicción de la abundancia de células tóxicas de colonias de *Microcystis* spp. mediante remote sensing	
K27	Laura Velandia Pérez	Grupo de investigación Manejo Integrado de Ecosistemas y Biodiversidad XIUA, Universidad Pedagógica y Tecnológica de Colombia (Colombia)	Relación entre la abundancia del bacterioplancton y la presencia de trucha arco iris, experimentación *in situ*	
K28	Nohora Millán	Universidad Jorge Tadeo Lozano (Colombia)	Bacterias epífitas y endófitas aisladas de macroalgas marinas de la especie *Ulva lactuca.*	
K29	Gabriela Martínez de la Escalera	Instituto de Investigaciones Biológicas Clemente Estable (Argentina)	Selección de genotipos tóxicos de *Microcystis* en ecosistemas eutróficos: temperatura, turbidez y conductividad como variables más relevantes	
K38	María Bejarano Suta	Universidad Militar Nueva Granada (Colombia)	Detección de genes de nitrito y óxido nitroso reductasa en bacterias desnitrificantes del humedal Santa María del Lago.	**Room 13a**
K40	Patricio Flores	Universidad Mayor (Chile)	Identification of Secretion Systems in bacterial strains isolated from Antarctic Sponges.	
K41	Carolline Fazolato	Federal University of Rio de Janeiro – UFRJ (Brazil)	Assessment of oil degrading multi-domain microbial consortium immobilized in calcium alginate applied in adaptable mesocosms	
K42	Mariela Guajardo	Universidad Mayor (Chile)	De novo transcriptome comparison of *Minidiscus* spp. from the English Channel and Antarctica coastal waters.	
K43	Alice Moura Emílio	University of Sao Paulo (Brazil)	Diversity and distribution of ammonia-oxidizing archaea in Santos Basin	
K45	José Carlos Parada Fabián	Universidad Nacional Autónoma de México (México)	Diversidad microbiana aislada de sedimentos y esponjas presentes en cenotes de la península de Yucatán con potencial biotecnológico	
K46	Patricia Águila-Torres	Universidad Austral de Chile (Chile)	Microplastics associated to bacterial communities from surface seawater of the Northern Chilean Patagonia	
K47	Natalia Segura	Universidad de la Salle (Colombia)	Relación del ensamblaje fitoperifítico con tres sustratos naturales en un tramo del Río Dulce – Sasaima, Cundinamarca.	
L6	Natalie M. Meléndez-Vázquez	University of Puerto Rico, Medical Sciences Campus (US)	Gut bugs matter to viroimmunotherapy: bacterial changes associated to the efficacy of Delta-24-RGDOX against glioblastoma	**Room 14a**
L8	Laura Salazar-Jaramillo	Vidarium-Centro de investigación en nutrición, salud y bienestar (Colombia)	Evaluation of two DNA markers for improving the resolution of microbial diversity in a Colombian population	
L9	Juan Pablo Cárdenas	Center for Genomics and Bioinformatics, Universidad Mayor (Chile)	New insights into taxonomic and genetic diversity of the Blautia genus, found by a phylogenomic approach	

L10	Frances Vázquez-Sánchez	Comprehensive Cancer Center, University of Puerto Rico (US)	Differential Microbiota of HPV and Non HPV related Penile Cancer	**Room 14a**
L11	Luz Oleyda Tapasco Tapasco	Universidad de Caldas (Colombia)	Modulación de la microbiota intestinal mediante protocolo de hidroterapia de colón en mujeres jóvenes con sobrepeso	
L12	Andrés Balbín Hernández	Universidad de Costa Rica 8Costa Rica)	Situación de la investigación en microbioma humano en América Latina: una revisión bibliométrica 2015-2020	

WEDNESDAY POSTER SESSION – DAY 2

Code	Name	Affiliation	Title	Room
A12	Lymarie Díaz Díaz	University of Puerto Rico, Río Piedras (US)	Microbial community profiles associated with the sea cucumber *Holothuria glaberrima*'s regenerating gut.	**Room 1b**
A13	Lina Marcela Botero Rute	AGROSAVIA (Colombia)	Mejoramiento de la cultivabilidad de bacterias anaerobias ruminales mediante el uso de una estrategia de cultivo alternativa.	
A14	Loreley Castelli	Instituto de Investigaciones Biológicas Clemente Estable (Uruguay)	Impacto del herbicida glufosinato de amonio, en la microbiota intestinal e inmnunidad de las abejas melíferas	
A15	Luciana Raggi	Instituto de Investigaciones Agropecuarias y Forestales, Universidad Michoacana de San Nicolás de Hidalgo (México)	Microbiota dynamics in a unique intestinal teleost model: *Chirostoma estor*	
A16	Nickole Villabona	Universidad de los Andes (Colombia)	First gut microbiota Characterization of Neotropical Bees	
A17	Emanuel Martínez-Ugalde	Centro de Ciencias Genómicas, Universidad Nacional Autónoma de México (México)	*Ambystoma altamirani* skin microbiome is highly influenced by host developmental stage and seasonality but not by pathogen presence.	
A18	Antonia Ramos	Universidad de Chile (Chile)	Functional zebrafish microbiome as revealed by global proteomic profiling of control and infected larvae	
A19	Diego Rojas	Centro Nacional de Innovaciones Biotecnológicas, Universidad de Costa Rica (Costa Rica)	*Micrococcales* dominate the microbiome in sloths hair and may act as a defense mechanism against bacterial pathogens	
B8	Wellington Felipe Costa	Federal University of Rio de Janeiro (Brazil)	Association of gram-negative bacilli harboring extended-spectrum beta-lactamases with fecal contamination in waters from an urban tropical estuary	**Room 2b**
B10	Karina Verdel-Aranda	Tecnológico Nacional de México, Instituto Tecnológico de Chiná (México)	Study of bacterial diversity for bioprospecting on Calakmul wetlands using comparative genomics and metagenomics	
B11	Bruno Nascimento	Universidade Federal de Alagoas (Brazil)	Diversidade de *Aureobasidium* spp. em bromélias de umaregião semiárida no Nordeste do Brasil	
B12	Alejandra Arenas Taborda	Universidad de Antioquia (Colombia)	Recambio del ensamblaje de myxomycetes a lo largo de un gradiente altitudinal y de humedad en Costa Rica	
B13	Aracely Zambrano-Romero	Instituto de Microbiología. Universidad San Francisco de Quito (Ecuador)	Microbial dynamics in an engineered sulfate reducing environment during the bioprecipitation of copper and zinc	
B14	Valentina Machin	Universidad de la República (Uruguay)	Diversidad de arqueas metanogénicas en sedimentos lacustres antárticos y efecto de la temperatura sobre la actividad potencial	
B15	Carla Barbosa	Universidad de Chile (Chile)	Effect of Hydrogeochemistry on Microbial Communities in Hot Springs from Geothermal Areas	
B16	Andres Cumsille	Universidad Técnica Federico Santa María (Chile)	Comparative genomics in the Genus *Brevibacterium*	

C1	Daniel Nariño Rojas	University of York (UK)	The efficacy and evolution of phage therapy in model cystic fibrosis lung environment	**Room 3b**
C2	Virginia Patricia Bustos	Centro de Ciencias Genómicas UNAM (México)	A search for phages and prophages in the rhizosphere of common bean (*Phaseolus vulgaris*).	
C3	Víctor González	Centro de Ciencias Genómicas UNAM (México)	New lineage of single stranded DNA virus that infects the symbiotic bacteria *Rhizobi*	
C4	Julia Plewka	University Duisburg-Essen (Germany)	Globally ubiquitous viruses in oil reservoirs refute burial and isolation theory	
C5	Rosa I. Santamaría	Centro de Ciencias Genómicas, Universidad Nacional Autónoma de México (México)	Genomic relationships between phages and prophages of the symbiotic bacteria *Rhizobium.*	
C7	Santiago Hernández Villamizar	Universidad de los Andes (Colombia)	La anaerobiosis como factor influyente en la interacción fago-hospedero	
D1	César Aguilar	Purdue University (USA)	Convergent evolution of *Streptomyces* protease inhibitory activities via divergent peptide condensation mechanisms	
D2	Laura Silva	Universidad de La Sabana (Colombia)	Bioactivity of colored extracts from *Streptomyces* with potential cosmetic application	
D11	Eliana Marcela Soto Rueda	Universidad Nacional de Córdoba-Centro de Investigación en Ciencias de la Tierra- CONICET (Argentina)	Toxicidad y acumulación de arsénico en cultivos de *Rivularia halophila*, cianobacteria aislada de la Laguna Negra (Catamarca- Argentina).	**Room 4b**
D12	Iván Ávila-León	Universidad Antonio Nariño (Colombia)	Estudio del potencial biotecnológico del hongo *Trichoderma* sp, para degradar compuestos fenólicos, empleando lignina como fuente de carbono	
D13	Michel Geovanni Santiago-Martínez	Pennsylvania State University (USA)	Metabolic regulation of gluconeogenesis and glycolysis in the marine archaeon *Methanosarcina acetivorans*	
D14	Susana Ochoa Agudelo	Colegio Mayor de Antioquia (Colombia)	*Pseudomonas* spp. aislados de aguas contaminadas con plomo, productor de sideróforos y screening de la actividad enzimática microbiana	
D15	Roberta Merguizo	Biosciences Institute, Coastal Campus of São Vicente, São Paulo State University – UNESP (Brazil)	DCPIP (Colorimetric method), determination of the ability of *Bacillus licheniformis* to biodegrade diesel S10 and AFFF - Aqueous Film-Forming Foam	
D16	Laura Chaparro	Universidad Libre (Colombia)	*Aspergillus* sp. y *Mucor* sp. como potenciales hongos degradadores de hidrocarburos	
D17	Miguel Beltrán	Universidad de la Salle (Colombia)	Interacción entre el extracto de *Azadirachta indica* y el hongo *Metarhizium anisopliae* para el control biológico de *Anopheles albimanus* un vector de la malaria	
D18	Valeria Gómez Marín	CorpoGen (Colombia)	Screening of actinobacteria isolated from lichens for antimicrobial, cellulolytic and proteolytic activity	
D29	Mario Sepúlveda	Universidad Técnica Federico Santa María (Chile)	Diversity of polyhydroxyalkanoate synthases in bacteria of the order *Burkholderiales*	**Room 5b**
D30	Esli Lobaina	Universidad Técnica Federico Santa María (Chile)	Characterization of native *Trichoderma* strains from Valparaiso Region, Central Chile	
D31	Erika Martínez Ruiz	Technische Universität Berlin (Germany)	Genome analysis of two manganese-oxidizing bacteria suggests enzyme-mediated processes for manganese oxidation required for cylindrospermopsin transformation	
D32	María Fernanda Rodríguez Fonseca	Universidad de La Sabana (Colombia)	Evaluation of polyvinyl chloride biodegradation by freshwater-derived *Streptomyces* strains	
D33	Eliana Nervi	Laboratorio de Biotecnología, Facultad de Ingeniería, Universidad ORT (Uruguay)	Isolation and characterization of glyphosate-degrading bacteria (GDB) isolated from Uruguayan soils	
D34	Leonardo Zamora-Leiva	Departamento de Química, Centro de Biotecnología Dr. Daniel Alkalay Lowitt, Universidad Técnica Federico Santa María (Chile)	Integration of bioinformatic tools in an automatized workflow for the search of novel biosynthetic gene clusters	

D35	Paola Talia	CONICET/INTA (Argentina)	Cloning, expression and evaluation of a GH10 alkali xylanase from termite gut microbiomes	**Room 5b**
D36	Ileana Sánchez Ortiz	Centro de Ingeniería Genética y Biotecnología de Camaguey (Cuba)	*Pseudoxanthomonas indica* cepa H32 como biofertilizante eficiente para los cultivos agrícolas de acelga, zanahoria y rábano	
E1	Luz Adriana Pedraza Herrera	Universidad Nacional de Colombia (Colombia)	Comparative genomics reveals *Bacillus velezensis* genes and their importance in the ecological relationship with plants	**Room 6b**
E3	Daniel Osorio	Universidad de Antioquia (Colombia)	Estandarización de una PCR en tiempo real para la detección de *Ralstonia solanacearum* filo IIB4 a partir de muestras de suelo rizosférico	
E4	Rafael Barty Dextro	Universidade de Sao Paulo – USP (Brazil)	Exploring microbial production of mycosporine-like amino acids in metagenomes from soda lakes of Brazilian Pantanal	
E5	María Clara Arrieta Echeverri	Universidad EAFIT (Colombia)	Microbial chemical ecology of water kefir grains fermentation	
E7	Mauricio Junior Machado	Superior School of Agriculture "Luiz de Queiroz" - University of São Paulo (Brazil)	Metabolic pathway of terpenes in metagenome-assembled genomes from Brazilian soda lakes	
E9	Marcial Silva	Pontificia Universidad Católica de Chile (Chile)	Cyanobacteria circadian mechanism: multicellularity and environment as a modulating factor.	
E10	María Fernanda Manrrique De La Cuba	Universidad Mayor (Chile)	A novel pipeline for taxonomic and diversity analyses using QIIME 2	
E11	Gabriel Silvestre Rocha	UNIRIO (Brazil)	Combining molecular primer design and ecological niche models for the arbuscular mycorrhizal fungi *Rhizophagus clarus*	
E13	Cristian Grisales	Universidad de Antioquia (Colombia)	Metabiome: A flexible and modular pipeline for metagenomic analysis	
G2	Carlos Díaz	Universidad de los Andes (Colombia)	Reconstrucción de modelos metabólicos a partir de los genomas ensamblados del metagenoma asociado un consorcio bacteriano lignocelulolítico.	**Room 7b**
H1	Coral Pardo	Universidad Andrés Bello (Venezuela)	Seasonal and spatial variability in microbial composition from sediments across the Altiplanic Salar de Huasco	
H2	Carolina Ospina	Newcastle University (UK)	Valorisation of nitrogen-deficient wastewater treatment systems using sludge enriched with nitrogen-fixing bacteria	
H3	María V Quiroga	UNSAM-CONICET (Argentina)	High bacterial microdiversity within an Antarctic wetland complex	
H5	Patricia Valdespino	Lawrence Berkeley National Laboratory (US)	Estudiar sistemas microbianos con bioimagen química acoplada a luz de sincrotrón	
H6	Ian Pérez	Universidad de La Habana (Cuba)	Caracterización taxonómica y fisiológico-bioquímica de cepas ambientales de *Cladosporium* conservadas *ex situ*	
H7	Katerin Almendras	Universidad de Chile (Chile)	Las bacterias asociadas a líquenes *Peltigera* del sur de Chile contribuirían a la simbiosis con la solubilización de fosfato	
H8	Yosbany Pérez	Universidad de Chile (Chile)	Levaduras basidiomicetes en líquenes: ¿un nuevo componente de la simbiosis liquénica?	
H9	Karla Veas	Universidad de Chile (Chile)	Taxones bacterianos claves en líquenes *Peltigera rufescens* creciendo en dos praderas en la región de Aysén, Chile.	
I9	Jonathan Maldonado	Pontificia Universidad Católica de Chile (Chile)	Partners to survive: plant microbiome recruitment at the Atacama Desert	**Room 8b**
I10	Daniel Felipe Cruz Suárez	Universidad de la Salle (Colombia)	¿Afecta la endozoocoria la diversidad de bacterias endófitas en semillas?	
I11	Darío X. Ramírez-Villacis	Universidad San Francisco de Quito USFQ (Ecuador)	The rhizosphere microbiome of the Andean blueberry (*Vaccinium floribundum* Kunth) is modulated by soil and plant genetics	
I12	Douglas Alfradique Monteiro	Federal University of Rio de Janeiro (Brazil)	The microbiome of the halophyte *Atriplex nummularia* (old man saltbush) in northeastern Brazil	
I13	Francisco Massot	Instituto Antártico Argentino – CONICET (Argentina)	Estudios de microbioma de raíz de *Deschampsia antarctica* para el diseño de estrategias de fitorremediación de hidrocarburos en suelos Antárticos	

I14	Fernanda Jamel	University of São Paulo (Brazil)	Assessing major patterns and the core bacteriome of endophytic communities in plant species from globally different locations	**Room 8b**
I15	María João Ferreira	University of Aveiro (Portugal)	Microbiome-metabolome relations in the halophyte *Salicornia ramosissima*	
I16	Jorge Sáenz-Mata	Facultad de Ciencias Biológicas de la Universidad Juárez del Estado de Durango (México)	Caracterización de rizobacterias promotoras de crecimiento vegetal aisladas de *Solanum elaeagnifolium* desarrollándose en suelos contaminados con metales pesados.	
J11	Yoelvis Sulbaran	Universidad Andrés Bello (Venezuela)	Antagonistic effect of *Bacillus* sp. isolated from agricultural soils against phytopathogenic fungi.	**Room 9b**
J12	Claudia Jaramillo	EAFIT (Colombia)	Using Isothermal microcalorimetry to measure cadmium-tolerant activity in soil microbial communities of cacao-growing farms in Colombia	
J13	Indira Quintero	Universidad de Panamá (Panamá)	Diversidad y taxonomía de comunidades bacterianas asociadas a suelo de dos manglares en la Bahía de Panamá	
J14	Natalia Fernández	IPATEC – CONICET, Universidad Nacional del Comahue (Argentina)	Influence of plant genetic diversity on rhizosphere fungal communities associated with *Nothofagus alpina* established under a native forest and an exotic plantation	
J15	Luis Wall	University of Quilmes, Bernal, (Argentina)	Efecto de la agricultura por irrigación en las comunidades microbianas y las funciones de un suelo semiárido de la Patagonia.	
J16	Griselda López	Center of Genomic Science, UNAM (México)	Microbiome transitions from soil to the rhizosphere of common bean (*Phaseolus vulgaris*).	
J17	Erika Vanessa Reyes Rojas	Universidad de la Salle (Colombia)	Actividad antifúngica de aceites de frutos de palmas *Oenocarpus bataua*, *Cocos nucifera*, *Elaeis oleifera*, *Maurita flexuosa* y *Acrocomia aculeata* frente a *Fusarium solani*.	
J18	Luciana Pereira-Mora	Laboratorio de Ecología Microbiana Medioambiental, Departamento de Biociencias, Facultad de Química, Universidad de la República (Uruguay)	Impacto del cultivo previo al arroz irrigado sobre la comunidad de bacterias y archaeas metanogénicas vinculadas a la fermentación de ácidos orgánicos	
J24	Vanessa Otero-Jiménez	Universidad Nacional de Colombia (Colombia)	Soil microbial community is influenced by rice straw incorporation strategy, altering carbon-cycling function	**Room 10b**
J29	Natali Zamora	Pontificia Universidad Católica de Chile (Chile)	Global diversity of desert soil prokaryotic diversity	
J31	Andrés Nicolás Rodríguez Romero	Universidad Nacional de Colombia (Colombia)	Continuous land use and fallow periods generate differential effects on the rhizospheric microbiome and greenbean production (*Phaseolus vulgaris* L)	
J35	Aldeci França	Universidade Federal de Alagoas (Brazil)	Diversity of cultivable yeasts associated with mangrove forest sediments in northeastern Brazil	
J37	Stalin Sarango	Universitet Leiden (Paises bajos)	The rhizosphere microbiome of wild tomato in the Andean mountains	
K2	Bernardo Águila Salgado	Universidad Nacional Autónoma de México (México)	Cyanobacteria of microbialites of Cenote Azul and Bacalar Lagoon, Quintana Roo Mexico: A polyphasic characterization	
K3	Luis Manuel Bolaños Avellaneda	University of Exeter (UK)	Molecular Ecology of the North Atlantic Phytoplankton Spring Bloom	
K4	Félix Andueza	Universidad Central del Ecuador (Ecuador)	Antibiotic resistant bacteria isolate from volcanics lakes water in Ecuador	
K13	Estefany Villarreal	Centro de Investigación Científica y de Educación Superior de Ensenada (México)	Efecto de la disponibilidad de nutrientes sobre el bacterioplancton fotótrofo con proteorodopsinas en un sistema productivo costero	**Room 11b**
K14	Simone Cotta	CENA/USP (Brazil)	Disentangling the bacterial metabolic-interactions on Brazilian soda lakes	
K15	Angie Díaz Ruiz	Universidad de Antioquia (Colombia)	Análisis de la redundancia funcional de la comunidad bacteriana de una planta de tratamiento de la ciudad de Medellín a lo largo de un ciclo anual, usando la herramienta de predicción funcional PICRUSt2	
K16	Natalia Bernal Hernández	Universidad de Antioquia (Colombia)	Discriminación de diferentes grupos de especialistas bacterianos en una planta de tratamiento de lodos activados, mediante el uso de análisis de redes de interacción.	
K17	Cynthia Jara	Universidad Austral de Chile (Chile)	Análisis comparativo de la comunidad bacteriana asociada a dos linajes de la diatomea invasora, *Didymosphenia geminata* utilizando QIIME y DADA2.	

K18	Marcela Alejandra Bastidas Navarro	INIBIOMA-CONICET-UNCOMA (Argentina)	Bacterial community composition in shallow lakes from *Nothofagus pumilio* forest (Patagonia, Argentina)	**Room 11b**
K19	Miguel Cuevas Cruz	Ensenada Center for Scientific Research and Higher Education (México)	Efecto de la luz en el metabolismo de la bacteria con rodopsina *Stakelama pacifica* BTS27C	
K20	Paula Vico	Instituto de Investigaciones Biológicas Clemente Estable (Argentina)	Ecotipos de la cianobacteria *Raphidiopsis. raciborskii*: más allá del individuo.	
K30	Andrés Ávila	Universidad de La Frontera (Chile)	Long-term composition of 16S-based bacterial communities associated with algal bloom events in northern Chile	**Room 12b**
K31	Clara Arboleda-Baena	Pontificia Universidad Católica de Chile (Chile)	Microbial communities network structure across strong environmental gradients: How do they compare to macroorganisms?	
K32	Carolina Croci	Instituto de Investigaciones Biológicas Clemente Estable (Argentina)	Floraciones de *Microcystis* spp. en el Río de la Plata: temperatura como determinante del tamaño y la toxicidad	
K33	Héctor Levipan	Universidad de Playa Ancha (Chile)	Rol ecológico de la formación de biopelículas por el patógeno de salmónidos *Piscirickettsia salmonis*	
K34	Lucas Gallart	Pontificia Universidad Católica de Chile (Chile)	Descifrando las relaciones intra- e interdominio en biopelículas costeras	
K35	Thierry Pellegrinetti	University of São Paulo (Brazil)	Cyanobacteria mediated nitrogen transformations in tropical soda lakes	
K36	Andrea Bautista García	Universidad Autónoma de Baja California Sur (México)	Prokaryotic microbiota and biomineral microstructure in coralline algae reveal new ecological and conservation frontiers	
K37	Jeny Adina Larrea Murrell	Biology Faculty. Havana University (Cuba)	Impacto de la contaminación sobre la actividad proteolítica en las aguas de los ríos Almendares y San Juan	
K48	María Francisca Luza-Miric	Universidad de Antofagasta (Chile)	Protists sorting optimization from a wide salinity range polyextreme aquatic system, Salar de Huasco (Atacama Desert), suitable for genome sequencing.	**Room 13b**
K50	Wendy Escobedo-Hinojosa	Universidad Nacional Autónoma de México (México)	A 31P-NMR-based method for the detection of phosphonate compounds in aquatic samples	
K51	Albert Niño	Universidad Nacional de Colombia (Colombia)	Evaluación de la actividad lacasa en bacterias epifitas de macroalgas de la especie *Ulva lactuca* localizadas en Santa Marta (Caribe Colombiano)	
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L1	Alejandra Hernández-Terán	Instituto Nacional de Enfermedades Respiratorias – INER (México)	Dysbiosis and structural disruption of the respiratory microbiota in COVID-19 patients with severe and fatal outcomes	
L2	Juan Sebastián Escobar	Vidarium, Nutrition, Health and Wellness Research Center (Colombia)	The effects of *Physalis peruviana* L. consumption on the gut microbiota of healthy men	
L3	María Cadavid Vélez	Vidarium—Nutrition, Health and Wellness Research Center, Grupo Empresarial Nutresa and Departamento de Ciencias Biológicas, Universidad EAFIT (Colombia)	Comparison of the variation of gut bacterial diversity marker genes in public genomes: a case study of the class *Clostridia*	
L4	Angie Lorena Fonseca Fernández	Universidad Nacional de Colombia, Universidad de los Andes (Colombia)	Péptidos LL-37 y ATRA-1, potenciales alternativos frente a la resistencia antibiótica en *Staphylococcus aureus*	
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L7	Kimil Acosta	University of Puerto Rico - Medical Sciences Campus (US)	Association of oral and environmental fungi with periodontal disease	
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D4	Micaela Gallicet	Centro de Investigación y Desarrollo en Fermentaciones Industriales (CINDEFI) – CONICET (Argentina)	The application of natural muds and their extreme microbial communities in the remediation of heavy metals	
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Redirecting the scientific system to combat the SARS-CoV-2 pandemic

KEYNOTE LECTURES

GONZALO MORATORIO
INSTITUTO PASTEUR DE MONTEVIDEO
MONTEVIDEO,URUGUAY

Linking the gut microbiome and metabolome to understand dietary response

ROB KNIGHT
KNIGHT LAB
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CALIFORINIA, USA

Advances in technology allow us to understand the human microbiota not as a static entity but as a complex, changing ecosystem that records substantial data about our lifestyles, our environmental exposures, and the people we live with.

Here I discuss changes in the human microbiota associated with early life events such as delivery mode and antibiotics, the subsequent development of the microbiome throughout life, and even the development of the microbiome after death and its potential utility for forensics. Of particular value for toxicological studies is the ability to transfer the microbiome to germ-free mice, allowing individualized tests of function and subsequent therapies to be tested in personalized rodent models. Relating human to rodent microbiome timescales, especially for dietary studies, and relating multi-omics data in a timeseries context, remain outstanding challenges. Rapid progress is being made in these areas, and will allow far more powerful studies of the effects of drugs in mammalian hosts and our ability to stratify responders from non-responders for a wide range of therapies.

Codiversification of gut microbiota with humans

RUTH LEY

DIRECTOR OF THE
MICROBIOME SCIENCES
DEPARTMENT
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Matching phylogenies between specific gut bacterial species and their mammalian hosts have revealed that some members of the gut microbiota co-diversified with the mammalian species they inhabit, including humans and their nonhuman primate relatives.

Within human populations, the stomach bacterium Helicobacter pylori exhibits geographic patterns of strain diversity that are consistent with patterns of human migration. Human populations harbor distinct strains of other gut bacterial species, but whether these patterns result from long-term vertical transmission and cophylogeny remains to be explored. We used matching sets of human genotype and gut metagenome data to search for gut bacteria exhibiting patterns of cophylogeny between and within human host populations. Using data we generated for for ~600 subjects from Europe (Germany), Africa (Gabon) and Asia (Vietnam), in addition to available public data (>1300 metagenomes), we compared human host trees to bacterial strain trees for roughly 60 bacterial species. Results for a number of gut bacterial species are consistent with cophylogeny both between and within the human populations evaluated. These findings imply that vertical transmission between family members occurred over long time periods and that populations maintained strains over long time periods as well. Implications for evolutionary biology as well as human health are discussed.

The human microbiome in a disruptive era

MARÍA DOMÍNGUEZ

INSTITUTE FOR FOOD,
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RUTGERS UNIVERSITY.
NEW JERSEY, USA

The microbiota is transmitted vertically, within species and throughout generations. In mammals, exposure to live microbes occurs from the time of labor and in the extrauterine life. Different body sites of the baby reshape the primordial source and assemble the site-specific microbiome during development of each organ. Perturbations during this stage caused by modern antimicrobial practices have been associated with decreased human microbiota diversity, and with increased incidence of immune and metabolic disorders (asthma, T1D, allergies, obesity). We will need restoration approaches to arrest and revert the current trend in urban diseases, and we will need conservation efforts and studies of microbial functions before we can restore the lost natural balances.

Structuring the soil microbiome by the cultivation of cover crops

FERNANDO ANDREOTE

ESCUELA SUPERIOR DE
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UNIVERSIDAD DE SAO PAULO.
SÃO PAULO, BRAZIL

The soil microbiome is known to perform essential activities in the quality of the soil-plant interface. Agriculture is known to promote a selective homogenization upon the soil microbiome along with crop cultivations. The challenge is to prompt the microbiome diversity and activity without compromising agricultural productivity and profits in the area. Here we show a designed experiment to determine the changes in the soil microbiome activity and structure due to the cultivation of cover crops. We evaluated the microbiome activity by the use of bioindicators, and we also determined the soil microbiome structure through 16S rDNA sequencing. In addition, we tested these effects upon soybean development and yield in the soils from distinct treatments. We found that specific plant species and mixes caused great changes in the soil microbiome, whats directly interfered with the soybean yield. These results validated the use of cover crops to manipulate the soil microbiome, opening opportunities for a better exploration of it in agriculture.

The Art of Harnessing Dark Energy: Symbioses between Chemosynthetic Bacteria and Marine Invertebrates

NICOLE DUBILIER

SYMBIOSIS DEPARTMENT
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Symbioses between chemosynthetic bacteria and marine invertebrates were first discovered at hydrothermal vents in the deep sea but are now known to occur in a wide range of habitats including coral reef sediments, seagrass beds, cold seeps and sunken whale carcasses. In these nutritional associations, the bacterial symbionts use chemical energy sources such as hydrogen sulfide to fix CO2 into organic compounds and feed their hosts. Chemosynthetic symbioses have evolved multiple times in convergent evolution from numerous bacterial lineages, and occur in at least nine protist and animal groups such as ciliates, flatworms, mussels, clams, snails, annelids, and nematodes.

Similar to Darwin's finches, whose beaks have evolved different shapes and forms as an adaptation to different food sources, the symbionts of hosts from chemosynthetic environments have acquired a wide and flexible repertoire of assimilation pathways in adaptation to the energy and carbon sources available in their environment. Intriguingly, this flexibility appears to have been gained through horizontal gene transfer. In my talk, I will describe how our toolkit of methods ranging from in situ experiments to meta'omic' and imaging analyses of chemosynthetic symbioses have revealed that horizontal gene transfer and symbiont diversity play a key role in the ecology and evolution of these host-microbe associations.

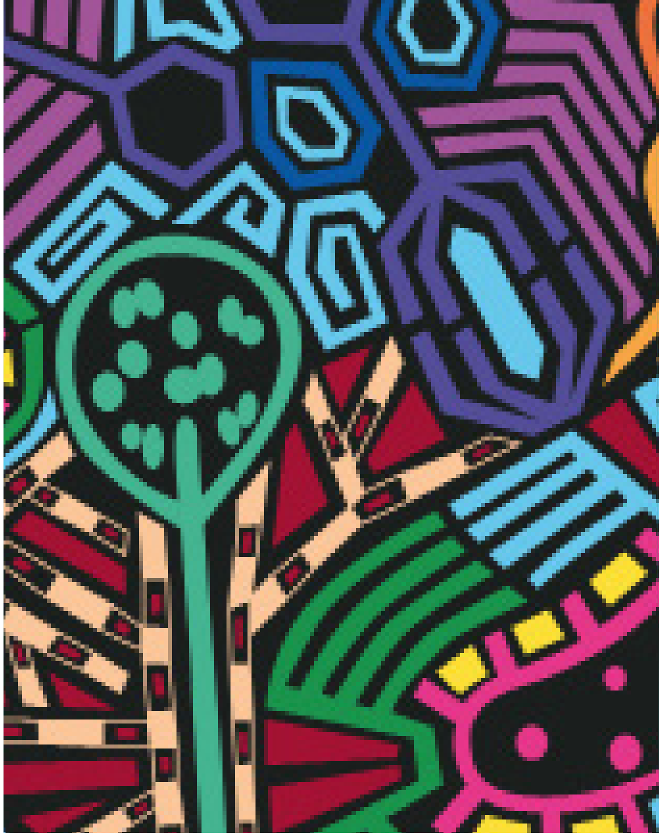
CRISTINA DORADOR

DEPARTAMENTO DE
BIOTECNOLOGÍA
UNIVERSIDAD DE ANTOFAGASTA
ANTOFAGASTA, CHILE

Microbial ecology in a changing world: public policy, interdisciplinarity and outreach

Microorganisms are the most diverse and abundant organisms on Earth. They are the original lifeform and if there is life elsewhere in the Universe, it will probably be microbial. The importance of microbes covers extends to almost all scientific fields including biology, medicine, chemical engineering, architecture, agronomy, climate change, and others. Microorganisms can live (and even thrive) under almost climatic and geographic conditions. In the Atacama Desert and Altiplano of northern Chile, numerous aquatic and terrestrial ecosystems exist where life is almost entirely microbial. Saline aquatic wetlands (salares) have a high biodiversity and their associated taxa show specific adaptations to polyextreme conditions. The salares of northern Chile, Argentina and Bolivia are also globally important reserves of lithium, a key element for batteries and electromobility. The current process for lithium extraction results in major negative impacts on ecosystems and to future water availability for local human communities. If these ecosystems are mostly microbial systems, how can microorganisms be protected? Will worldwide demand for energy transition impact diverse, abundant, but mostly invisible life? Our work for over two decades in these ecosystems has allowed us to recognize that the dynamic field of microbial ecology provides unique opportunities to highlight links and understanding that can be deeply relevant to other disciplines and human cultures. We propose an interdisciplinary pathway for the conservation of microbial life in polyextreme environments. This relies on the inclusion and combination of trans-disciplinary theoretical backgrounds to recognise and avert pending environmental microbial disasters (microdisasters). We also call for directed and powerful outreach campaigns that place microorganisms at the centre of life (microbial love) and the production of microbially-focused maps (a microbial map of Chile). This work would include and promote a recognition of the multiples roles of microbial taxa that include, but go beyond the biodiversity-associated economy, extending to the still under-recognised view of humans as complex ecosystems including the role of the human microbiome. This pathway will help to not only conserve at-risk, globally unique environments due to mineral extractivism, but also identify threats from climate change. It is also hoped that the pathway will aid economic diversification in the short- (post-Covid) and long-term (movements from a resource-extraction driven economy).

SPEAKERS



A

A- MICROBIOMES ASSOCIATED WITH ANIMAL HOSTS

A1 - Insects are Empowered by Microbes

JAVIER A. CEJA-NAVARRO

Lawrence Berkeley National Laboratory
USA

Host-microbe interactions are recognized as critical factor for the ability of numerous organisms to survive, thrive, and dominate an environmental niche. Many insect species are clear examples of the benefits that higher organisms obtain from their microbial symbionts. Throughout the time of their evolution, insects and other arthropods developed diverse associations with microorganisms that shape how they interact with each other and the environment.

In this presentation, I will share my findings from the study of the distribution of microbial function in the gut of a coffee pest that relies on its microbiome for detoxification of caffeine and a wood-feeding beetle that developed specialized microbial niches within its gut to survive on a recalcitrant diet.

Overall, my research demonstrates that just as in other ecosystems such as soil, environmental filtering is a key driver for the distribution of microbial community composition and function in the guts of insects. My studies support the hypothesis that the establishment of beneficial microbial partners within a host requires more than the acquisition of the microorganisms. The host must provide suitable habitats developed through co-evolutionary processes to sustain and promote the critical microbial metabolic processes that allow the host to survive even on extreme diets.

Understanding the biological and ecological mechanisms that have driven complex host-microbe interactions in insects may facilitate the development of strategies to improve how we manage pests and guide the design of new biotechnological processes for metabolite and energy production.

A2 - La microbiota intestinal de las abejas melíferas

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¿Qué microorganismos forman parte de la microbiota? ¿Cuál es la su función? ¿Qué factores generan desequilibrios? ¿Qué consecuencias tiene esto en la salud de los hospederos? Son algunas de las preguntas que han guiado estas investigaciones. Un modelo interesante para responderlas es la abeja melífera. Estos insectos poseen una microbiota intestinal simple y estable, dominada por 7-10 grupos bacterianos cultivables. Además, las abejas melíferas se pueden criar en el laboratorio en condiciones controladas, lo que facilita la experimentación. Por otro lado, las abejas son importantes polinizadores que favorecen la producción de alimentos y el mantenimiento de la biodiversidad. Su salud es una preocupación a nivel mundial, habiéndose reportado grandes pérdidas de colmenas de abejas melíferas en todos los continentes. Estas pérdidas están asociadas a la infección con múltiples patógenos, la intoxicación con pesticidas y a deficiencias nutricionales. En este contexto, cobra relevancia el estudio de su microbiota intestinal y el rol que cumple en el mantenimiento de la salud. En esta presentación mostraremos información sobre la composición de la microbiota intestinal de las abejas melíferas, su variación a lo largo del ciclo de vida, y su variación estacional durante el año. También discutiremos el impacto de diferentes factores de estrés vinculados a la pérdida de colmenas en esta microbiota, incluyendo la infección por el microsporidio Nosema ceranae, la exposición a pesticidas como el glifosato o imidacloprid y la deficiencia nutricional. Finalmente, discutiremos sobre las posibles implicancias de estos cambios en la salud de las abejas.

A3 - Unveiling the neglected fraction of the ruminal microbiome at the intersection of culturing and molecular approaches

RUTH DAYANA HERNANDEZ[3], LINA BOTERO RUTE[1,2], ALEJANDRO REYES[3], ALEJANDRO ACOSTA-GONZALES [2], HUGO JIMÉNEZ[1], **ALEJANDRO CARO-QUINTERO[1,4]**

[1] ***Corporación Colombiana de Investigación Agropecuaria - AGROSAVIA,*** *sede Tibaitatá.*

[2] *Grupo de Investigación en Bioprospección (GIBP), Facultad de ingeniería Universidad de la Sabana.*

[3] *Grupo de Biología Computacional y Ecología Microbiana BCEM - Max Planck Tandem Group in Computational Biology, Universidad de los Andes.*

[4] ***Grupo DARMA, Universidad Nacional de Colombia, Departamento de Biología.***
Cundinamarca, Colombia

The rumen microbial community is an intricate system of anaerobic microorganisms that can transform non-digestible complex carbohydrates and non-protein nitrogen, into volatile fatty acids, amino acids, and vitamins that are assimilable by the animal. The modulation of the ruminal microbial community is an area of intense research, as this can potentially affect cattle's productivity and health. Thousands of bacterial species are commonly found in the rumen, from which a large fraction still uncultured and uncharacterized. Understanding the relationship between microbial diversity and function is even more relevant in creole Breeds (e.g., Blanco Oreji Negro breed), which have successfully adapted to Colombian climatic and agroecological conditions. The lack of characterization of ruminal microorganisms is still a big limitation to assess the effect of treatments on the tunning of the microbial community. This talk will present the current inter-institutional efforts to improve the characterization of ruminal microbiomes and the culturing strategies to recover a larger diversity of this community. In brief, we present a sucrose-based method that allows the separation of cells based on cell size that allows the decomposition of the microbial community on a less diverse subpopulation, this increases the sensitivity for the detection of subtle population changes and has the potential to allowed more targeted isolation of genetic characterization of groups of interest. Especially, low abundance groups which responses to treatments go unnoticed under the currently used methods. Given the high numbers of research studies aiming at manipulating the ruminal microbial community, the proposed tool will allow the researchers to understand the effect of treatments not only in the more abundant taxonomic group, but also in low abundance, but not less important, taxonomic groups of bacteria in the rumen.

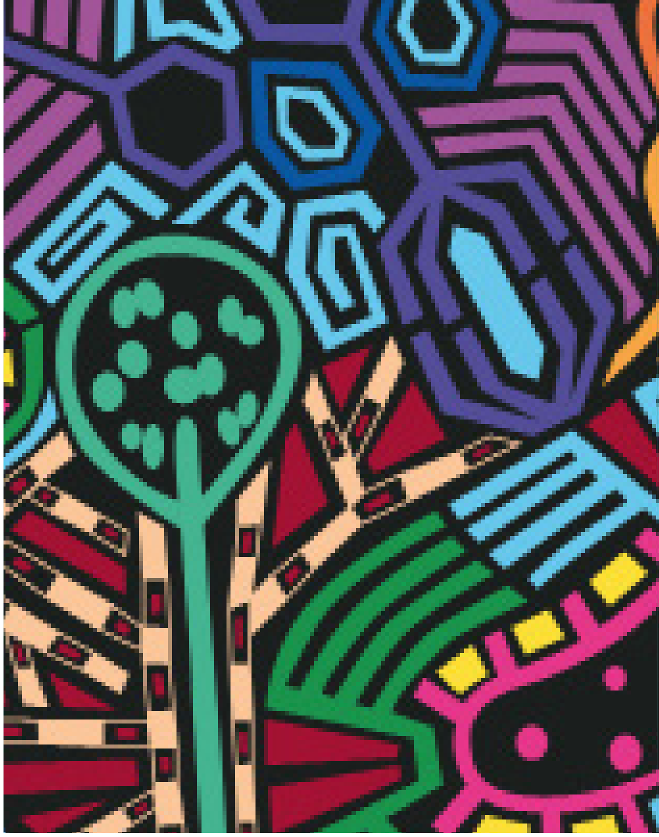
A4 - Prokaryotic, fungal, and unicellular eukaryotic core communities across three sympatric marine sponges from the southwestern atlantic coast are dominated largely by deterministic assemblage processes

CRISTIANE HARDOIM

State University of São Paulo
São Paulo, Brazil

Marine sponges are known to harbor a diverse and complex microbiota; however, a vast majority of surveys have been investigating the prokaryotic communities in the north hemisphere and Australia. In addition, the mechanisms of microbial community assembly are poorly understood in this pivotal player of the ecosystem. Thus, this survey addressed the holobiome of the sponge species in the São Paulo region (Brazil) for the first time and investigated the contribution of neutral and niche processes of prokaryotic, fungal, and unicellular eukaryotic assemblage in three sympatric species Aplysina caissara, Aplysina fulva, and Tedania ignis along with environmental samples. Remarkably, between 47 and 88% of the assigned Operational Taxonomic Units (OTUs) were specifically associated with sponge species. Moreover, around 77, 69, and 53% of the unclassified OTUs from prokaryotic, fungal, and unicellular eukaryotic communities, respectively, showed less than 97% similarity with well-known databases, suggesting that sponges from southwestern Atlantic coast are an important source of microbial novelty. Host species was the major driver shaping the sponge-associated microbial community. Deterministic processes were primarily responsible for the assembly of microbial communities in all sponge species, while neutral processes of prokaryotic and fungal community assembly were also detected in the sympatric A. caissara and T. ignis replicates, respectively. Most of the species-rich sponge-associated lineages from this region are also found in the Northern seas and many of them might play essential roles in the symbioses, such as biosynthesis of secondary metabolites that exhibit antimicrobial and antiviral activities, as well as provide protection against host predation. Overall, in this study the microbiota was assembled by interactions with the host sponge in a deterministic-based manner; closely related sponge species shared strong phylogenetic signal in their associated prokaryotic and fungal community traits and Brazilian sponges were a reservoir of novel microbial species.

SPEAKERS



B ENVIRONMENTAL EFFECTS ON MICROBIAL COMMUNITIES

B1 - Taxonomic, functional and environmental interactions in hot springs microbial mats

BEATRIZ DÍEZ[1,2,3]

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2. Center for Climate and Resilience Research (CR2), Universidad de Chile, Chile
3. Center for Genome Regulation (CGR), Universidad de Chile, Chile
Santiago, Chile

Hot springs represent ideal natural models for understanding the principles of microbial ecology and evolution. Nowadays, the use of the integrated high throughput meta'omics' approaches (primarily metagenomics) enables to uncover the identity and specific role of each biotic component of the community, and the recovery of genomes of hundreds of microbes and their interactions. These approaches were used to investigate the effect of both viruses (as major predators) and abiotic factors (e.g., temperature, water chemistry, etc.) on the composition, structure, and function of highly cooperative thermophilic microbial mat consortia. We obtained the main viral populations interacting with relevant thermophilic hosts across environmental conditions (40 to 80°C and pH 6 to 8) in 48 geographically distant hot springs from around the world (21 in Chile). We recovered up to 2000 assembled genomes from metagenome (MAGs) (>50% completeness, <10% contamination), of which 300 and 55 MAGs were affiliated by GTDB assignations to the phyla Chloroflexota and Cyanobacteria, respectively. Some of the new MAGs also represent new complete genomes of microbes and virus with low or no representation in public databases. These genomes are increasing our databases for better comparative genomic analysis in search of evolutionary relationships and new adaptations. We recover a marked presence of vOTUs (viral Operational Taxonomic Unit) belonging to the Caudovirales (mainly from the families Siphoviridae and Myoviridae, followed by Podoviridae), whose protein profile suggests the presence of known but also potentially novel AMGs involved in the biogeochemical cycles. Microbial hosts CRISPRs allowed us to infer that most viruses infect the phyla Cyanobacteria and Chloroflexota, main primary producers (such as the thermophilic cyanobacterium Fischerella spp.), suggesting a strong phage-host interaction that could be shaping these hot spring ecosystems.

B2 - Composition, diversity and functional analysis of long-term hydrocarbons-contaminated soil microbiome

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BIBIANA COPPOTELLI[1], MARÍA TERESA DEL PANNO[1]

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Soils exposed to long-term contamination with hydrocarbons may present extreme challenges to maintain diverse structural and functional microbial communities. A low metabolic diversity may imply a reduction in soil service, resistance and resilience of soil microbial communities to different stresses as well as limiting the response to bioremediation strategies.

This presentation describes the microbiome characterization of a chronically hydrocarbon-contaminated soil (IPK) sampled from a landfarming unit belonging to a petrochemical industry in La Plata city (Argentina), where the landfarming treatment had been completed about twenty years before. The contaminated soil had reached hydrocarbon concentrations below the Argentinian cleanup standards for industrial use; however, polycyclic aromatics hydrocarbons (PAH) of three and four rings were detected.

Culture approaches, 16S rRNA metabarcoding and shotgun metagenomic analysis showed a highly impacted community with low species richness and diversity. Also, a reduction in the substrate assimilation capacity and enzymatic activities, compared with a nearby soil outside the land-farming unit, was detected. These soil characteristics correlated with a low resistance to metal contamination, salinity, and acid stresses.

No significant PAH degradation was detected under natural conditions, even though the functional analysis of metagenomic sequences showed that almost all genes codifying for enzymes of naphthalene degradation upper pathway (78% of pathway completeness) and a complete set of enzymes (between 80% and 100) for phthalate, salicylate and catechol degradation were present.

Either soil homogenization and sieving or the addition of Triton X-100 at sub-critical micelle concentration, but not bio-augmentation with an allochthonous bacteria, enhanced the degradation of PAH bioavailable fraction, possibly due to the equilibrium disruption of organic carbon in pore/water particle system, increasing availability of easily assimilable organic compounds.

PAH-degrading consortia from the IPK soil were obtained, with special interest in knowing the metabolic interactions that could have contributed to the characteristics of this chronically contaminated soil.

B3 - Composition and health impact of city public transport microbiomes

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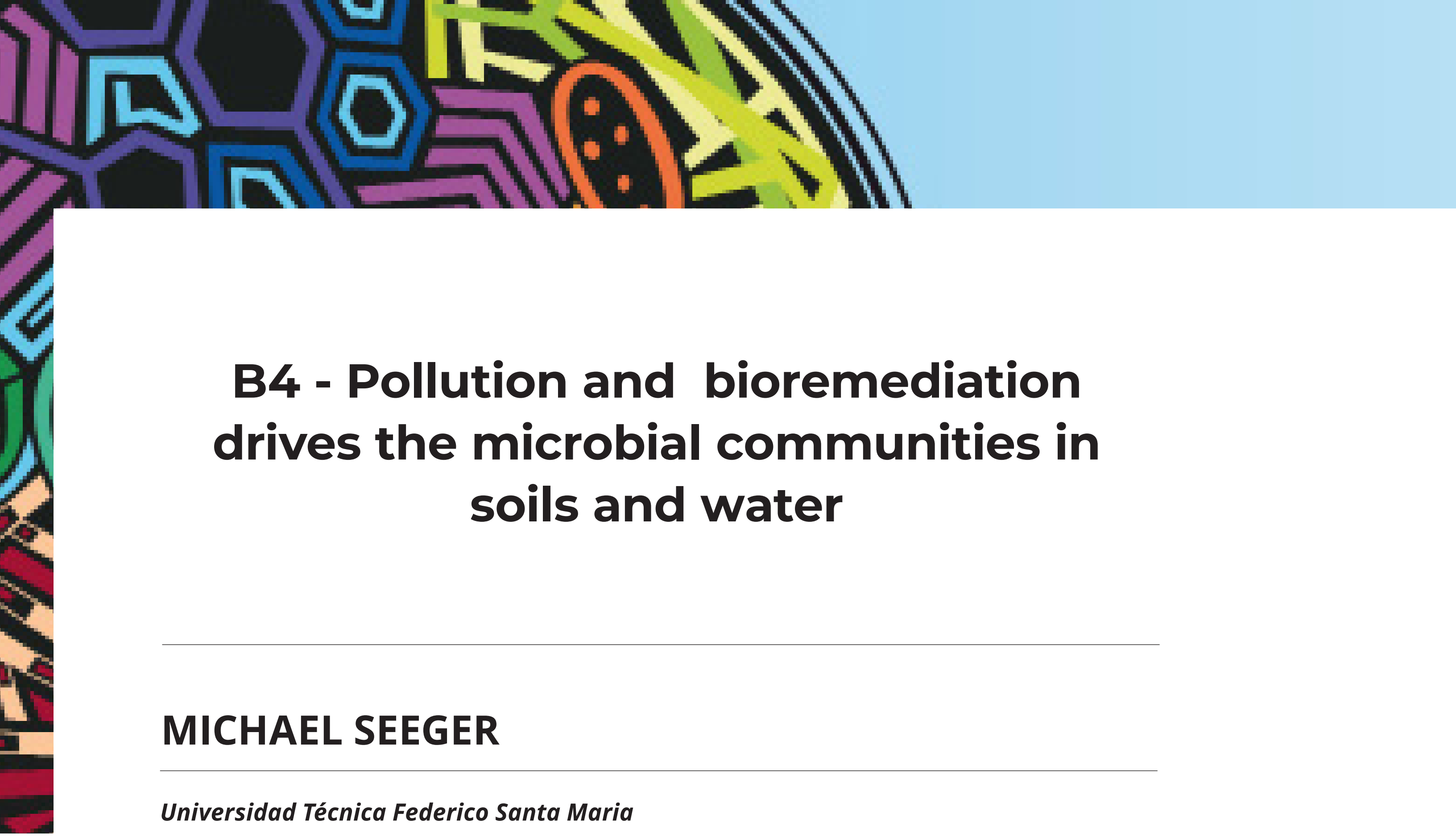
MARÍA MERCEDES ZAMBRANO

CORPORACIÓN CORPOGEN
BOGOTÁ, COLOMBIA

As part of the international consortium MetaSub, we have focused on the study of the microbiome present in the public transport system Transmilenio in Bogotá, Colombia. We sampled diverse stations and buses and sequenced these samples to identify microbial communities and their potential functions. These communities were quite diverse, differed among sites sampled and seemed to be associated with geographical location. We also isolated bacteria harboring diverse antibiotic resistance genes using selective media in the lab. The taxonomic analysis of these isolates suggests that they are probably environmental organisms, even though they belong to bacterial genera that are associated with pathogens and nosocomial infections. These data will help to understand the composition and functional potential of microbial communities present in highly frequented constructed environments and enable future studies geared towards monitoring and generating data useful for public health decisions.



B4 - Pollution and bioremediation drives the microbial communities in soils and water

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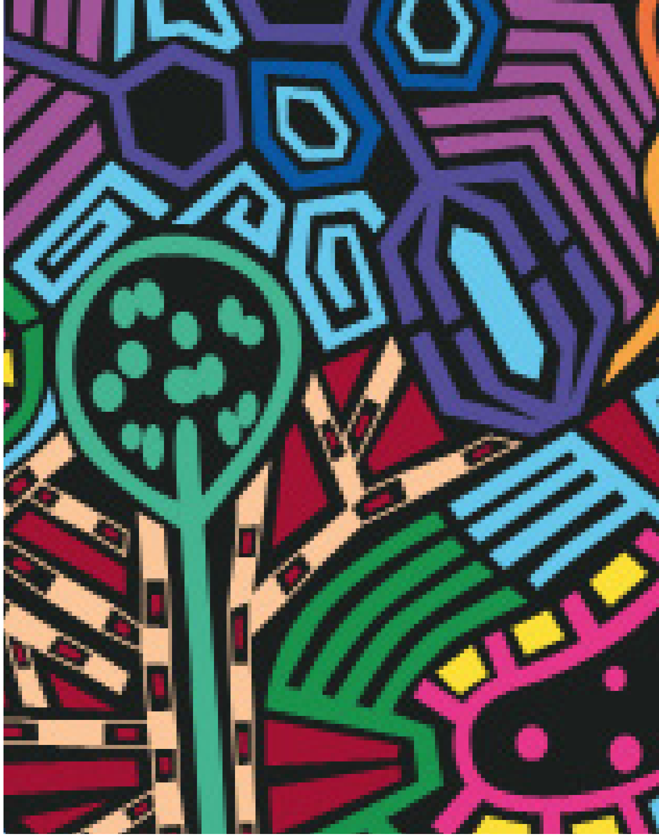
MICHAEL SEEGER

Universidad Técnica Federico Santa Maria
Valparíso, Chile

SPEAKERS



C

PHAGES AND VIRUSES

C1 - Human gut phages and their role as modifiers of microbial communities

ALEJANDRO REYES

Universidad de los Andes
Bogotá, Colombia

For the last 15 years there has been a continuing increase in the interest of researching and understanding the viral component of the gut microbiome. As we understand more about the complex dynamics and profound health consequences that the human microbiome displays, it becomes crucial to understand the role of phages in such community. From the early studies, the last decade has shown a consistent evolution in the experimental and computational tools for understanding those viral communities, however, their genetic diversity and the limited information in public databases maintain a veil on the coding and functional potential contained by those viruses. The healthy gut virome is diverse and vary greatly from one individual to another, and its diversity mimics the one of the corresponding microbiome. We know of the presence of ubiquitous viral families such as the crass-like viruses, and their abundance seem highly variable among individuals. However, the specific dynamics and capacity of the viruses to modify microbial communities remain understudied. We have shown that a single phage transplant in an artificial mice microbial community has the potential to temporarily disturb the community within a couple of days, however, such challenge coupled with an accompanied change in the microbial component of the community may have a longer lasting effect.

C2 - Bacteriophage-mediated manipulation of the gut microbiome

JOSUÉ L. CASTRO-M.

Department of Food Science
University of Copenhagen
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Gut microbiome (GM) composition and function are linked to human health and disease, and routes for manipulating the GM have become an area of intense research. The gut virome, and particularly bacteriophages (so-called “phages”), are viruses that target bacteria and new evidence shows their therapeutic effect for targeting commensal bacteria or inducing immunomodulation. During the last years, our lab has focused on studying the influence of environmental factors that shapes the virome composition, viral communities associated with disease states, and the therapeutic use of virome treatments against chronic diseases, e.g., obesity and type-2 diabetes. These findings have opened a premising road for future applications aiming to revert disease phenotypes.

C3 - Bacteriophages as a precision tool for controlling undesired microbiota partners

MARTHA VIVES

Universidad de los Andes
Bogotá, Colombia

Bacteriophages are an alternative to antibiotics due to its ability to control bacterial populations. An additional feature of bacteriophages is their specificity, which can be considered a drawback for their application but we value as a benefit, since phages can be used as precision tweezers, able to remove particular species from a complex community, extracting the problematic partner but keeping intact the structure of the general bacterial assembly. Here, we will present examples of this capacity and focus on the performance of a phage cocktail designed to control Salmonella sp. serovars in broilers and hens models. The World Health Organization considers Salmonella one of the most important zoonotic, foodborne pathogens, which is transmitted mainly through the poultry products. Control of the pathogen has been extensively enforced but still remains a problem. Therefore, control at the origin becomes necessary. The phage cocktail SalmoFree® was used at the productive scale to evaluate its reduction capacity on the Salmonella presence, as well as its safety for the animals. In broilers, the incorporation of SalmoFree® in the drinking water did not affect the animals health nor the microbiota development. Salmonella presence dropped to zero in the treated houses, and also in some of the control ones in the second iteration (cycle) of the assay. We considered this reduction in the control houses the result of the cross-contamination with phages, which was confirmed by the detection of the phages. Analysis showed that the Enterobacteriaceae abundance decreased in a direct correlation with the Salmonella detection. When comparing the bacterial community structure, no variations were detected. A few selected taxa were associated with the treatment. We considered these minor changes a side effect of the “surgical” removal of Salmonella from the complex intestinal microbiota and a fine modulation of its composition. Altogether, these results suggest that phages can work as nano-bio-tweezers. We foresee phages usage for the modulation of the desired microbiota in rhizosphere, phycosphere and the intestine of endangered species during habitat re-introduction programs.

C4 – Metagenomic CRISPR reconstruction disentangle bacteria-phage dynamics

LEANDRO D. GUERRERO

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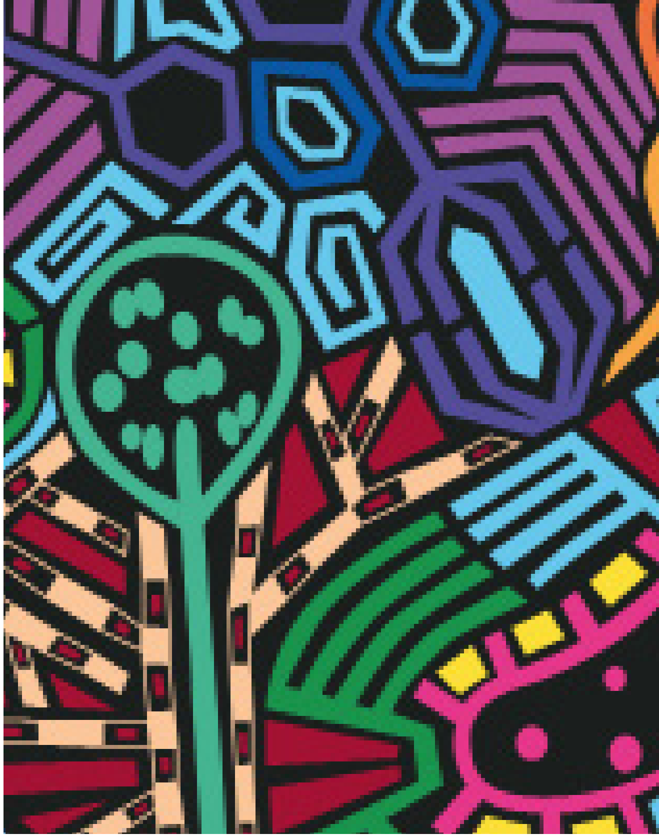
The high number of bacteriophages in microbial-dominated ecosystems has led to the hypothesis that they are key components that affect the structure and dynamics of microbial populations. However, it remains poorly understood how phages and bacteria manage to coexist, avoiding complete host and virus eradication. This is largely due to the experimental challenge of monitoring the coevolutionary dynamics of phages and their host within complex natural environments. CRISPR sequences provide an unequivocal signal of interaction and the spacers acquisition by the CRISPR-Cas machinery keep an organized record of previous phage infections in the population across time. This concept was validated in a longitudinal metagenomic study of a wastewater treatment plant, which allowed us the reconstruction of different coexisting CRISPR variants in a bacteria of the genus Gordonia and two of their infecting phage genomes. Analysis of CRISPR arrays showed that different Gordonia subpopulations have evolved from an almost clonal population through the acquisition of new spacers against the coexisting phages. Although almost all bacterial cells have one of the CRISPR variants, approximately half of the population has a variant devoid of spacers sequences against the circulating phages. On the other hand, phages have evolved introducing directional changes without preference for CRISPR targeted regions. These observations, contrary to what has been seen under laboratory conditions, which resembles an arm-race dynamics, revealed the complexity of the bacteria-phage dynamics suggesting that the study of communities in natural conditions is crucial to understand such complex interactions.

SPEAKERS



D

MICROBIAL BIOTECHNOLOGY

D1 - Biotechnological Potential of Insect Gut Microbiome

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****Instituto Nacional de Tecnología Agropecuaria (INTA),***
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La Plata, Argentina

A low-cost conversion of lignocellulose into fermentable sugars is of particular interest in second generation bioethanol production as well as in animal feed, food, textile, pulp and paper industries, among others.

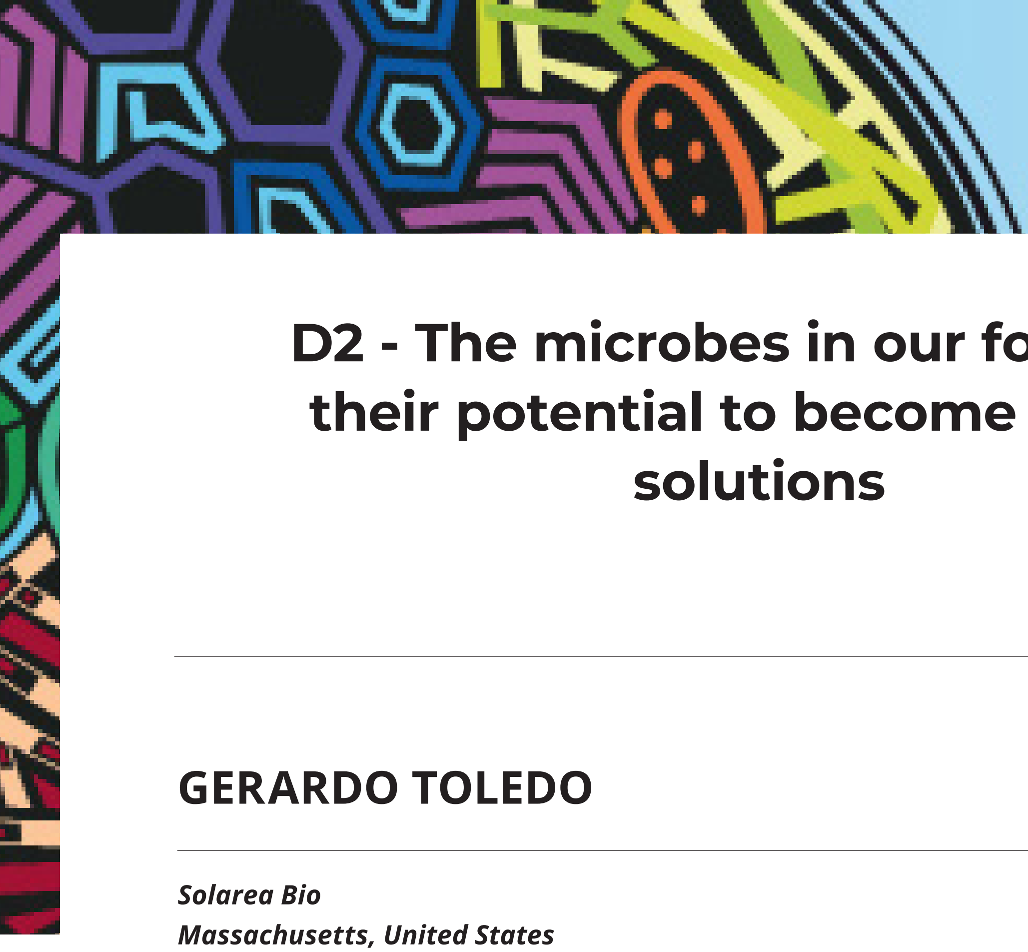
In termites, as in other insects, the efficient digestion of lignocellulose material is accomplished by the coordinated action of endogenous and endosymbiont microbial enzymes present in their digestive tract.

The goal of this work was to chacterize the microbiome of two termites Cortaritermes fulviceps and Nasutitermes aquilinus and the cotton boll weevil Anthonomus grandis (coleptera) with the aim to discover novel biocalaysts for biorefinery applications.

The whole metagenome sequencing analysis of two Argentinian higher termites allowed us to compare the bacterial communities and their metabolic diversity, and to identify bacterial genes involved in lignocellulose degradation. In order to further consider the gut microbiome as insect biorefinery, three glycosyl hydrolase named GH5CelA, GH5CelB and Xyl10E, belonging to families GH5 and GH10, were selected, cloned or synthesized and expressed in Escherichia coli. Furthermore, the selected enzymes were subjected to a structural analysis and their enzymatic activities were characterized.

The recombinant enzymes showed different enzymatic activities: GH5CelA (MW 40.94 kDa and IP = 1.1) showed specific cellobiohydrolase (42,3±2,0 IU/mg) and β-glucanase activities (0,95±0,02 IU/mg), GH5CelB (MW 39,73 kDa and IP = 6,03) had endoglucananse (0,1±0,01 IU/mg), cellobiohydrolase (29,2±0,4 IU/mg), β-glucanase (1,3±0,4 IU/mg) activities while Xyl10E (MW 49.2 kDa and IP = 6.31) showed specific xylanase activity of 231.3 IU/mg. Thus, the GH sequences identified in these termites represents a unique opportunity to isolate new genes useful in lignocellulose deconstruction.

Keywords: Gut microbiota, Lignocellulolytic Enzymes, Metagenomics



D2 - The microbes in our food and their potential to become health solutions

GERARDO TOLEDO

Solarea Bio
Massachusetts, United States

- Solarea Bio explored and discovered microorganisms present in healthy foods

- By building a discovery platform it was possible to rapidly generate and test rationally design microbial combinations including bacteria and fung

- These show multiple health benefits including protection against bone loss in postmenopausal mice models when acting synergistically in specific combinations

D3 - Effect of inhibitors over the anaerobic digestion process based on the metabolic reconstruction of the process

MARÍA FRANCISCA VILLEGAS

Universidad ICESI
Cali, Colombia

Vinasse is a by-product from the bioethanol production process and has a high content of organic matter and nutrients, which can be used for the generation of renewable energy in the form of biogas through anaerobic digestion. However, the high complexity of the interactions and metabolic dynamics of the microorganisms that participate in the process make it highly sensitive to the presence of inhibitory substances and other environmental conditions. Our work focused on evaluating the metabolic effect on anaerobic digestion of the presence of inhibitors in vinasse by means of the metabolic reconstruction of the process over time and at different vinasse concentrations. The results suggest a greater amount of transferases and oxidoreductases, mainly associated with carbohydrate metabolism, and a differential effect is evidenced in the activation and deactivation rate of various reactions in different metabolic pathways important for the generation of biogas when vinasse concentration is varied. Even so, this variation does not affect the microbial composition, identifying a high abundance of the species Defluviitoga tunisiensis and Methanoculleus marisnigri in both cases.

D4 - Genomic analysis of biodegradation pathways for furans and their relevance for bioconversion of lignocellulosic biomass

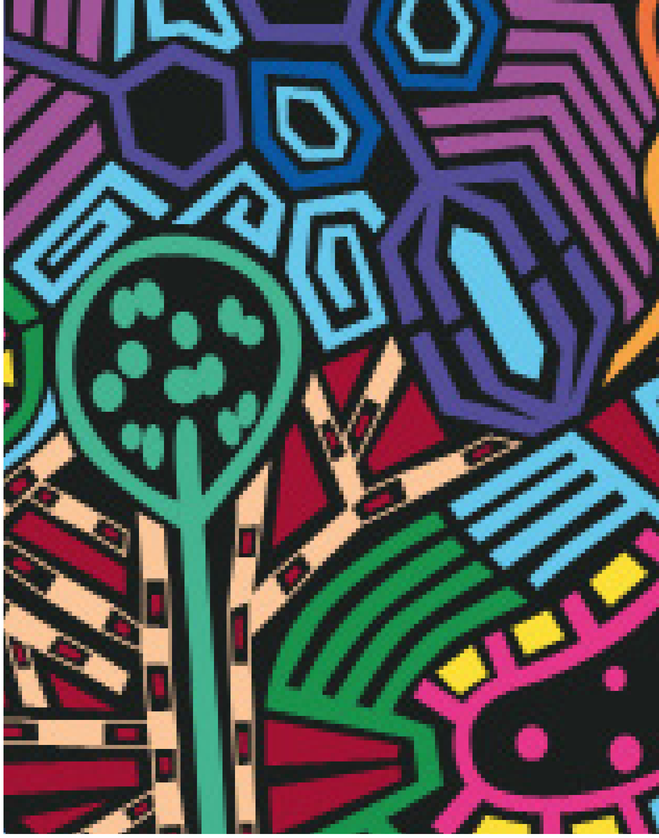
DANILO PEREZ-PANTOJA

Universidad Tecnológica Metropolitana Chile
Santiago, Chile

Furans represent a class of promising chemicals, since they constitute valuable intermediates in conversion of biomass into sustainable products intended to replace petroleum-derivatives. Conversely, generation of furfural and 5-hydroxymethylfurfural (HMF) as by-products in lignocellulosic hydrolysates is undesirable due its inhibitory effect over fermentative microorganisms. Therefore, the search for furans-metabolizing bacteria has gained increasing attention since they are valuable tools to solve these challenging issues. A few bacterial species have been described at genetic level, leading to a proposed HMF pathway encoded by a set of genes termed hmf/psf, although some enzymatic functions are still elusive. In this work we performed a genomic analysis of major subunits of furoyl-CoA dehydrogenase orthologues, revealing that the furoic acid catabolic route, key intermediate in HMF biodegradation, is widespread in proteobacterial species. Additionally, presence/absence profiles of hmf/psf genes in selected proteobacterial strains suggest parallel and/or complementary roles of enzymes with previously unclear function that could be key in HMF conversion. The furans utilization pattern of selected strains harboring different hmf/psf gene sets provided additional support for bioinformatic predictions of the relevance of some enzymes. On the other hand, at least three different types of transporter systems are clustered with hmf/psf genes, whose presence is mutually exclusive, suggesting a core and parallel role in furans transport in Proteobacteria. Finally, the presence of hmf/psf gene clusters in different microbiomes is assessed revealing their ecological significance. This study expands the number of bacteria that could be recruited in biotechnological processes for furans biodetoxification and predicts a core set of genes required to establish a functional HMF pathway in heterologous hosts for metabolic engineering endeavors.

ACKNOWLEDGMENTS: FONDECYT 1201741, ANID PIA/Anillo ACT172128, and ANID PIA/BASAL FB0002 grants of Chilean government

SPEAKERS



E

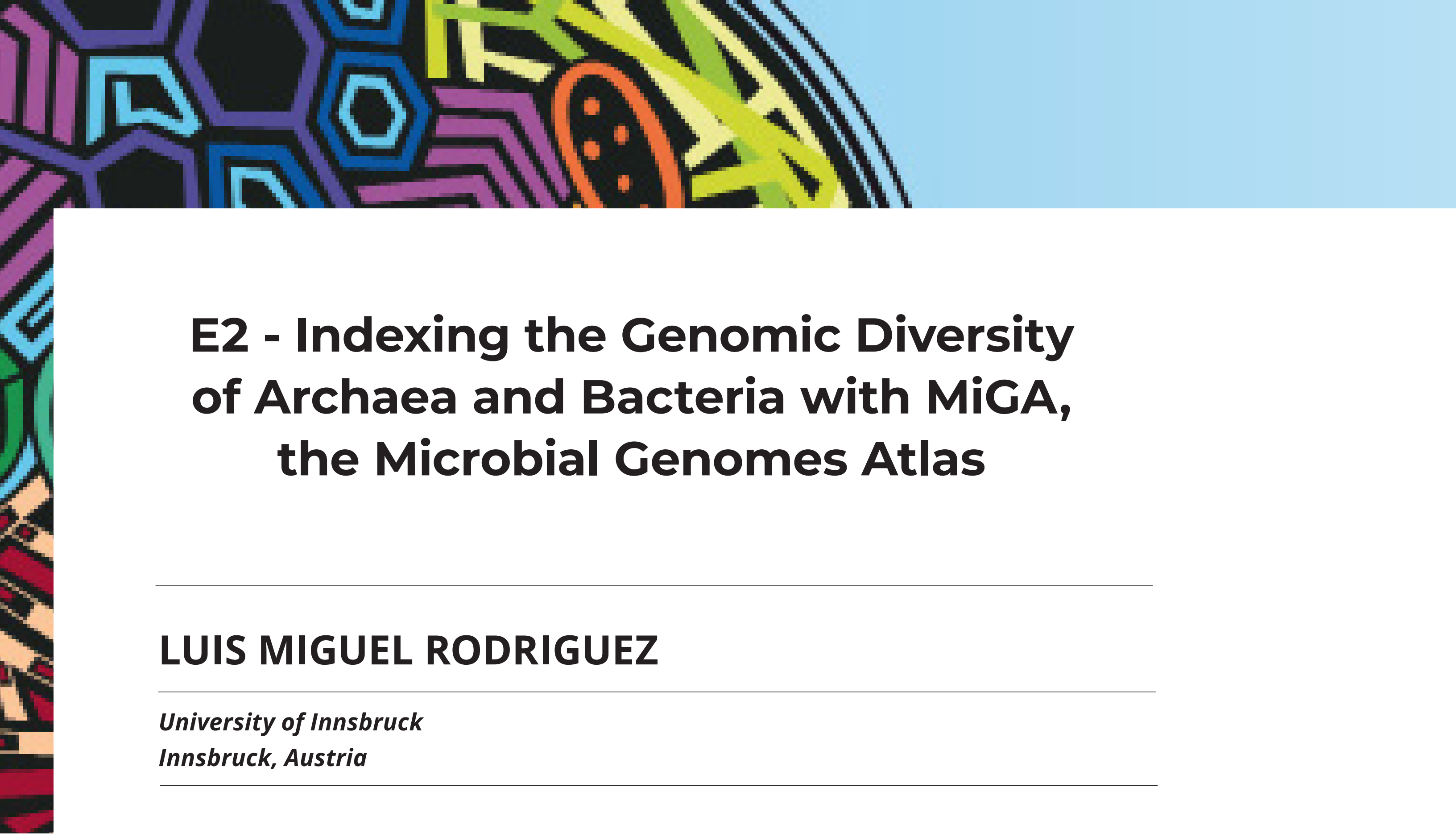
METHODS APPLIED IN MICROBIAL ECOLOGY AND COMPUTATIONAL TOOLS

E1 - Quantitative prediction of complex functions in constructed ecosystems using machine learning

ULISES NUNES DA ROCHA

The Helmholtz-Centre for Environmental Research
Leipzig, Germany

The ability to quantitatively predict ecophysiological functions of microbial communities provides an important step to engineer microbiota for specific biochemical conversions. In my presentation I will introduce different approaches that can be used to predict ecosystem functions as well minimum requirements that should be taken into account when planing experimental design and data validation. In this context, I will discuss the prediction of medium-chain carboxylate production in twocontinuous anaerobic bioreactors from 16S rRNA gene dynamics in enrichment cultures. Although the data presented will involve amplicon sequencing data, such approach may be adapted to different omics techniques. This presentation may encourage the audience to introduce predictive biology in their current future studies.



E2 - Indexing the Genomic Diversity of Archaea and Bacteria with MiGA, the Microbial Genomes Atlas

LUIS MIGUEL RODRIGUEZ

University of Innsbruck
Innsbruck, Austria

During the past decade the number of publicly available sequenced prokaryotic genomes has grown at an unprecedented rate. Yet, the information behind this trove of data remains difficult to access, and genome-based comparisons against comprehensive databases remain technically cumbersome and computationally intensive. To address these issues, we have developed MiGA, the Microbial Genomes Atlas, a genomic data analysis framework integrating best practices in genome processing and quality evaluation, fast genome-based querying of reference databases, and robust statistical tests of taxonomic classification and novelty. In order to democratize access to the MiGA framework, we have also implemented user-friendly interfaces including web-based browsing and administration for all users, a complete command-line interface for intermediate users, and a fully documented Ruby API for advanced users. In addition, we have deployed MiGA to a variety of environments that users can access freely including MiGA Online for detailed manual curation of individual entries and MiGA @ XSEDE for high-throughput genome processing. In addition, we use the various MiGA features to curate and maintain reference genome collections including all determined genomes from type material of named species (TypeMat), a dereplicated set of genomes determined by culture-independent techniques such as single cell genomics and genome-resolved metagenomics (Uncultivated), 8 environment-specific genome collections, and over 700 collections for specific taxonomic groups. To date, MiGA has processed over 50 thousand jobs from users around the globe (including 4000 registered users), the MiGA Online webserver has been used in over 100 publications, and the framework is actively being ported to additional environments including high-performance computing centers and cloud computing platforms. The MiGA codebase, its interfaces, and the online deployments are available at http://microbial-genomes.org/miga.

E3 - PIME: capturing biological differences using prevalence

VICTOR PYRLO

Federal University of Lavras
Lavras, Brasil

The data used for profiling microbial communities is usually sparse with some microbes having high abundance in a few samples and being nearly absent in others. However, current bioinformatics tools able to deal with this sparsity are lacking. PIME is provided as an R package that applies a novel approach for the analysis of microbial communities based on the prevalence of organisms across samples. It also identifies those organisms that contribute significantly to the cohort or treatment differences being tested. PIME removes the within group variation found in metataxonomic surveys (16S rRNA datasets) by capturing biological differences at high samples prevalence levels.

E4 - Genomes comparative analysis in PGPR: Identifying genetic traits involved in plantbacteria interaction under abiotic stress conditions

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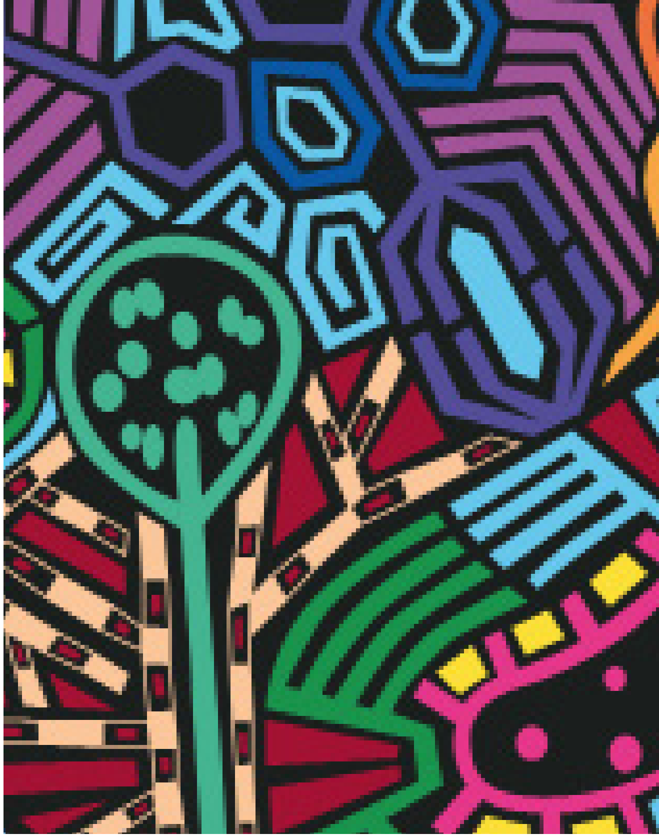
La Serena, Chile

El estrés abiótico, es una de las principales causas de la reducción del crecimiento, calidad y productividad de las plantas, por lo que diversas estrategias son estudiadas para reducir su impacto. Entre ellos, el uso microorganismos beneficiosos, particularmente de bacterias promotoras de crecimiento vegetal (PGPR), ha sido descrito, dado que poseen mecanismos que permiten mitigar el estrés abiótico en la planta hospedero, e.j. a través de la producción de osmolitos, fitohormonas, sideróforos, entre otros. Una estrategia en la caracterización de cepas corresponde a la secuenciación de sus genomas, lo que permite tener una visión global de los mecanismos moleculares/fisiológicos posiblemente involucrados en la promoción del crecimiento vegetal. Además, con esta información se pueden realizar estudios comparativos entre cepas, evaluando la adquisición o perdida de rasgos funcionales (genes) según cercanía taxonómica. Este trabajo hipotetizó que, debido a su historia evolutiva, bacterias taxonómicamente distantes, poseerían diferentes mecanismos de interacción con plantas bajo condiciones de estrés abiótico. Para ello, el objetivo de este estudio fue: Establecer, mediante el uso de genomas de bacterias PGPR de géneros distantes (Serratia, Pseudomonas y Paenochrobactrum sp), rasgos funcionales (similares o distintos) que favorezcan la inducción de respuestas de tolerancia a estrés. A partir del ensamble de genomas bacterianos y posterior estudio pangenómico y de genómica comparativa, fue posible identificar diferentes mecanismos PGPR. Nuestros resultados muestran diferencias pangenómicas y la comparación de las categorías KEGG identificadas en cada cepa demuestra que 34% de los rasgos PGPR son compartidos entre Sm_MAS25 y Psp_CC01. Los resultados sugieren que, dada la distancia taxonómica, existen mecanismos de interacción planta-microorganismos diferentes entre las cepas en estudio, donde la convergencia entre los rasgos compartidos serían un indicio de una adaptación ecológica y evolutiva en la interacción con la planta.

SPEAKERS



F

EXTREMOPHILES

F1 – Microbial diversity in deep-sea habitats of the Southwestern Atlantic

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VIVIAN H. PELLIZARI

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São Paulo, Brazil

The deep-sea at the Brazilian margin has an incredible geological heterogeneity with many unique seafloor features providing habitats that sustain rich communities. Given its abundant offshore oil and gas reservoirs, sites as Santos Basin on the SW Atlantic have been one of the well- studied deep-sea basins with respect to its seafloor biodiversity. During the last decade increasing efforts are made to discover the microbial community composition, their metabolic diversity and ecological role in the deep ocean across oceanographic features in SW Atlantic Ocean.

We will present some findings about microbial composition, metagenome-assembled genomes and community modelling for deep-sea sediments at the Brazilian margin, as well as for specific habitats, including asphalt seeps, carbonate ridges, pockmarks, seamounts and ferromanganese crusts. Machine Learning analysis applied to 16S rRNA sequences and environmental data from sediment of Santos Basin were able to determine different deep-sea related habitats. Presence and distribution of chemosynthetic communities among these habitats have been studied. Although gas seepage were not reported in Santos Basin yet, we showed that taxa previously described in carbonate mounds with seepage activity are present, but lack the key taxa involved with the anaerobic methane oxidation. Also, our studies of microbial communities of Fe-Mn Crusts, indicate that Atlantic seamounts harbor an unusual and unknown Fe-Mn deposit microbiome when compared to Pacific seamounts.

The results are certainly helping to unveil the current scenario of the microbial community structure of Southwestern Atlantic Ocean. The data can also improve our knowledge on the ecological importance of Bacteria and Archaea in these deep-sea ecosystems, filling some gaps and fostering for potential connections worldwide.

F2 – Biodiversity in the Copahue geothermal region; a study case of biogeography and community structure of acidic and thermophilic extremophiles

MARÍA SOFÍA URBIETA

Universidad Nacional de la Plata
La Plata, Argentina

The Copahue geothermal area is located on the Northwest of Neuquén province (Patagonia, Argentina). It is a naturally extreme environment dominated by the still active Copahue volcano, whose cyclic eruptive periods shape the landscape and its physicochemical characteristics. The area, of approximately 250 Km2, has two different zones: the Copahue volcano-Río Agrio system and the geothermal ponds. Río Agrio is a natural acidic river of geothermal origin that maintains low pH values for almost its entire path, despite receiving many tributary neutral water courses. The results of different biodiversity studies show that Rio Agrio is dominated by ubiquitous acidophilic, sulphur and/or iron oxidising chemolitoautotrophic species, which have been isolated from similar environments around the world; however, there are also autochthonous species, many of them yet uncultured.

On the other hand, the geothermal manifestations are a constantly changing environment, highly dependent on the volcanic activity. There are pools, ponds and hot springs in a wide range of temperature and pH. In general, the acidic ponds are also dominated by acidophilic chemolitoautotrophic species, more frequently associated with acid mine drainages than geothermal environments and by thermoacidophilic archaea, specially at higher temperatures. According to our comprehensive biostatistical analysis the microbial community structure of geothermal areas is extremely complex and could not only be determined by temperature or pH; other shaping factors such as sediment composition or even location (which inevitably includes sampling and methodological bias) need to be considered. However, there seem to be specific taxa strongly associated with certain conditions of pH and temperature widely distributed around the world.

Our results show that the biodiversity of extreme environments is a still interesting topic with much yet unknown, and particularly confirm the relevance of Copahue geothermal region as a study case and the habitat of novel microbial species of biotechnological and scientific relevance.

F3 – Recovering microbial genomes in Antarctic and subsurface ecosystems through metagenomics

AMANDA BENDÍA

Universidad de São Paulo
São Paulo, Brazil

The advance of bioinformatic tools is allowing the description of novel and not-yet cultivated microbial lineages in different ecosystems, due to the genome reconstruction approach from metagenomic data. In this context, our group has been applying metagenomics tools to recover microbial genomes from extreme ecosystems, such as an active volcano in Antarctica (with extreme temperature gradients) and caves from Brazil. We were able to reveal the metabolic potentials and survival strategies of underrepresented taxonomic groups, especially related to hyperthermophiles, thermophiles, psychrophiles and radioresistant lineages, which showed to be metabolically diverse. The majority of predicted genes in these genomes are involved with iron oxidation, methanotrophy, sulfate reduction and ammonia oxidation. Pangenomic analysis has indicated some of these genomes as novel genus and species. The recovery of genomes from metagenomes has shown to be a powerful tool on revealing novel life-styles, metabolic processes and ecological roles of microorganisms, mainly in extreme ecosystems that are largely unknown, and for which cultivation is often not viable.

F4 – Tracking arsenic metabolism in the Salar de Huasco - Altiplanic environment, via genome-resolved metagenomics

JUAN CASTRO-SEVERYN[1], CORAL PARDO-ESTÉ[2], FRANCISCO REMO-SELLEZ[1,3], EDUARDO CASTRO-NALLAR[4], CLAUDIA P. SAAVEDRA[2]

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Antofagasta – Chile

Arsenic is a toxic natural component of Earth crust and a major contaminant of aquatic ecosystems. In nature, microorganisms cope with arsenic toxicity through precipitation, chelation, sequestration, expulsion and biochemical transformation (redox processes or methylation). In extreme environments with arsenic, such as the Salar de Huasco (SH), the inhabiting microorganisms presenting these capacities abound. The genes and mechanisms responsible for these phenotypes are not yet fully clarified, and the vast majority of these communities members are little characterized, unknown and uncultured, which limits our understanding. Hence, we set to address this using genome-resolved metagenomics, this approach allows us to identify and characterize unknown microbial species from metagenomes, getting insights of their functional potential. Therefore, starting with sediment samples from five different SH sites along an arsenic gradient (9 to 321 mg/kg), we carried out shotgun metagenomic sequencing. Here, we use 96 million reads from the 5 metagenomes to reconstruct and manually curate 195 metagenome-assembled genomes (MAGs), from which 18 were high-quality ones. The taxonomy affiliation of these non-redundant MAGs resulted in 9 Proteobacteria, 7 Bacteroidetes, 1 Cyanobacteria and 1 Gemmatimonadota phylum members, only 4 of those were assigned to a known genus. Moreover, the global functional potential of reconstructed MAGs broadly showed some level of variability, a total of 267 KEGG modules were detected, presenting differential absence/presence and completion patterns. Particularly, in relation to their repertoire of arsenic associated genes, a considerable number was detected with a clear dominance of those related to arsenic expulsion (acr3, arsA, arsJ), followed by reduction (arsC) and methylation (arsM) being the most recurrent widespread mechanisms in the SH to cope with the high arsenic concentrations. This study has contributed to the knowledge of the microbial “dark matter” that inhabits this special and fragile ecosystem, harboring candidates for advancements in science and technology applications.

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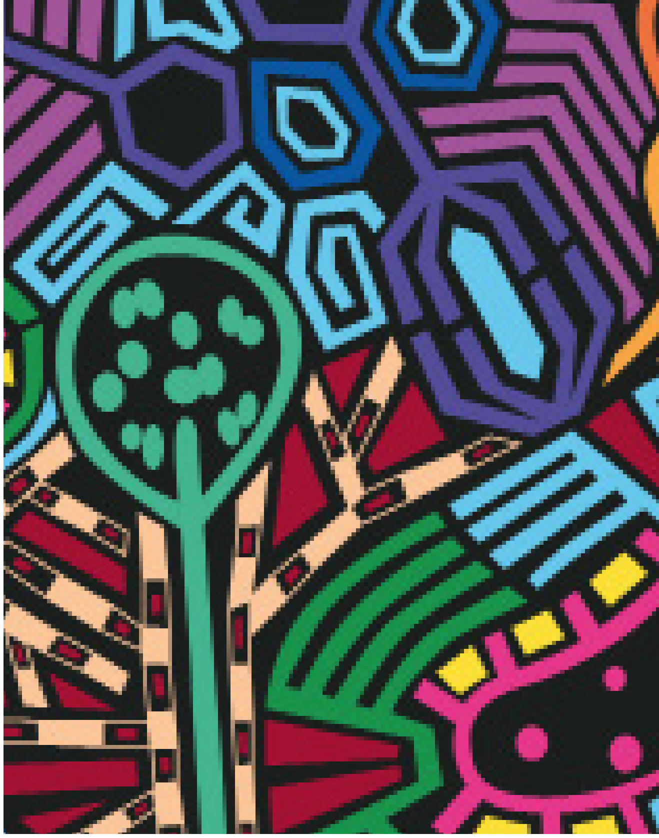
SPEAKERS



G

SYNTHETIC MICROBIAL ECOLOGY

G1 - Rules of microbial community assembly in simple environments

SYLVIE ESTRELA

Department of Ecology and Evolutionary Biology.
Yale University
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Predicting the composition and function of microbial communities in a given habitat is a major aspiration in microbiome biology. To realize this goal, it is critical to identify which features of microbial communities are reproducible and predictable, which are not, and why. We have addressed this question by studying the assembly of hundreds of communities in simple replicate habitats and connecting the experiments with modeling. We have found that microbial community assembly is generally reproducible and convergent at higher levels of taxonomic community organization and reflects an emergent metabolic self-organization between different functional groups whose ratios can be quantitatively explained with simple models. In turn, taxonomic divergence among replicate communities may arise from multi-stability in population dynamics, which can also lead to alternative, dynamically stable functional states.

G2 - Providing complex biological outputs by engineering division of labor in bacteria

JUAN NOGALES

Centro Nacional de Biotecnología
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Microbes do not live in isolation but in microbial communities. The relevance of microbial communities is increasing due to growing awareness of their influence on a huge number of environmental, health and industrial processes. Hence, being able to control and engineer the output of both natural and synthetic communities would be of great interest. However, in vivo microbial consortia development is extremely difficult and costly because it implies replicating suitable environments in the wet-lab. Computational approaches thus emerge as alternative to study and engineer microbial communities. In this talk it will be discussed the use of computational approaches toward the design of complex biological phenotypes in the context of microbial consortia. Furthermore, it would be shown the application of this technology in unconventional biotechnological applications, e.g. living architecture.

G3 - A top-down enrichment strategy to guide the design of synthetic microbial consortia

DIEGO J. JIMENEZ

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Universidad de los Andes
Bogotá, Colombia

The engineering of complex communities can be a successful path to understand the ecology of microbial systems and improve biotechnological processes. However, the vast complexity of natural microbial communities can be a challenge to in-depth understand interactions and metabolic processes. Recently, we developed a top-down enrichment strategy to select a minimal and versatile lignocellulolytic bacterial consortium using a sequential combination of dilution-to-stimulation and dilution-to-extinction approaches (Diaz-Garcia et al. 2021). We demonstrated that mainly two selectively enriched bacterial species (Pseudomonas sp. and Paenibacillus sp.) are required to drive the effective degradation of plant polymers. Moreover, this combined top-down enrichment strategy has been successfully applied to build a keratinolytic bacterial consortium (Kang et al. 2020). These selective strategies can guide the design of an effective synthetic microbial consortium that could improve some biotechnological applications and expand our ecological understanding of natural microbial systems.

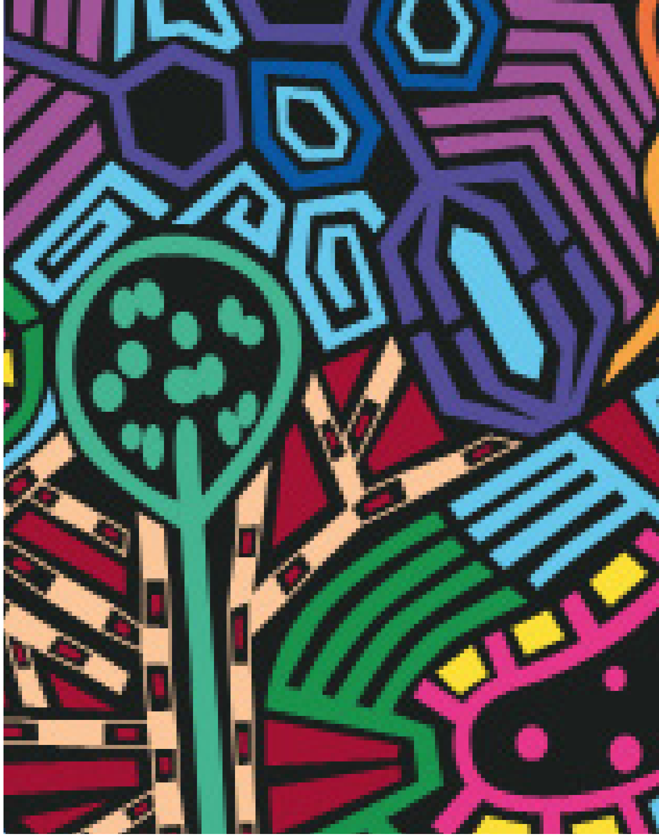
G4 – Synthetic community invasion depends on secondary metabolite production in *Bacillus subtilis*

CARLOS N. LOZANO-ANDRADE, MARIO WIBOWO, AKOS T: KOVACS

Bacterial Interactions and Evolution Group
Technical University of Denmark
Lyngby, Denmark

Isolates of the B. subtilis complex produce a plethora of biologically active molecules. Among those, lipopeptides (LPs) have been extensively studied under in vitro conditions, revealing inhibition of various other microbes, impact on motility and colonization, signaling and cellular differentiation. Despite the vast knowledge about B. subtilis secondary metabolism, there is still a gap in understanding the role of those compounds on the ecology of the producers and the resident communities in situ. To address these questions, B. subtilis wild type (WT) and mutant derivatives impaired in LPs production were introduced into a synthetic bacterial community using a soil-mimicking matrix. Population dynamics and changes in the community metabolome were assessed over two weeks. Interestingly, neither the WT nor the mutants had a major impact on the synthetic community assembly. However, assessment of B. subtilis growth dynamic revealed that the sfp and srfAC mutants declined drastically compare to the WT strain after six days. Interestingly, inoculation of B. subtilis strains capable of surfactin production as well as purified surfactin alters the chemo diversity of the community, including attenuation of several compounds exclusively produced by the synthetic community. Overall, our results highlight that non-ribosomal peptides, and more specifically surfactin, determine the invasion success of B. subtilis in a simplified bacterial community, suggesting a broad spectrum of action of this natural product.

SPEAKERS



H

MICROBIAL ECOLOGY OF MIXED COMMUNITIES

H1 – Verrucomicrobiota degrade sulfated methyl pentoses during diatom blooms

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Algae blooms annually sequester gigatons of carbon dioxide into biomass and thereby comprise a critical component of the global carbon cycle. Specialised heterotrophic microorganisms quickly remineralise much of the labile organic matter released by decaying phytoplankton. During this period phytoplankton synthesise large amounts of sulfated polysaccharides containing high amounts of fucose. Nonetheless, bacteria capable of degrading complex methyl pentoses during algae blooms remain unknown. Here we show that small, coccoid, and free-living Verrucomicrobiota cells arising with the onset of the spring blooms, account for up to ~8% of the microorganisms, and are highly specialised for the consumption of fucose and rhamnose. Glycoside hydrolases, sulfatases, and bacterial microcompartments that metabolise fucose and rhamnose were active in Verrucomicrobiota populations during a spring bloom in 2016 in Helgoland. These specialised pathways were assigned to novel and discrete candidate species of the Akkermansiaceae and Puniceicoccaceae families which we here describe as Candidatus Mariakkermansia forsetii and Candidatus Fucivorax forsetii. Our results indicate that sequestration of phytoplankton-derived sulfated deoxy sugars will critically depend on the presence and activity of specialised Verrucomicrobiota populations.

H2 - Bacterivory by mixotrophic phytoflagellates

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**** INSTITUTO TECNOLÓGICO DE CHASCOMÚS (INTECH), UNSAM-CONICET.***
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Mixotrophy in algae, defined as the combination of phagotrophy and phototrophy in a single cell, is widespread among most algal groups containing flagellate species. Phytoflagellates vary widely in their ingestion capability and response to the abiotic conditions. Here, we used literature data to review the ecological strategy and impact on bacterioplankton of the different algal groups. We extracted information from about 50 articles, including marine and freshwater systems, resulting in more than 600 measurement of grazing rates from natural communities. In addition, we summarised results of experiments performed with isolated strains. Chrysophyceae are the most “heterotrophic algae”, with three times higher grazing rates than any other algal class, and a significant impact on bacterioplankton. Dictyochophyceae (Pseudopedinella) has grazing rates comparable to Chrysophyceae, however its low abundance results in a lower impact. Ingestion rates of these phytoflagellates are correlated with bacterial abundance, a typical functional response of “primary heterotrophic” organisms. Haptophyceae are moderate grazers, while Cryptophyceae seems to be the least heterotrophic phytoflagellate. Despite its lower grazing rate, Cryptophyceae can account for a significant percentage of the total bacterivory during period of high abundance. Dinoflagellates are important bacterivorous, however because of their cell-size they usually prefer larger preys, and bacteria contribute little to their carbon budget. In situ measurements of Prasinophyceae and Raphidophyceae are scarce and precluded a clear characterization of these groups. As a general rule, the addition of nutrient have a negative effect, or no effect, on the grazing rates of all the groups. Contrarily, the effect of light on grazing rates is not straightforward and it seems to be more species-specific dependent.

H3 - A proposed framework for the consolidation of a South America mycorrhizal database

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Mycorrhizal symbiosis is an important driver of plant distribution and ecosystem functioning at global scale. However, our understanding of the nature and degree of their involvement in ecosystem processes regionally and worldwide is hindered by a lack of knowledge on global distribution patterns of mycorrhizal plants and related plant and fungal traits. Comprehensive databases need to include and analyze literature in multiple languages (such as Spanish and Portuguese), perform critical data evaluation of the source reliability, provide geographical and environmental information about the study sites, and update taxonomy. Here, we present a proposed conceptual framework to systematically review the state of the art of knowledge with respect to mycorrhizal data generated in South America; present discussion about the variables and methods detected in the literature; and provide recommendations for further improvement of our understanding of mycorrhizal traits for the consolidation of a regional database. We aim to share this proposal to encourage synthesis of a local reference database to support testing of ecological generalities that govern mycorrhizal functioning in South American ‘ecosystems.

H4 – Genome of a new Candidatus anammox bacteria assembled from the metagenome of two anammox reactors

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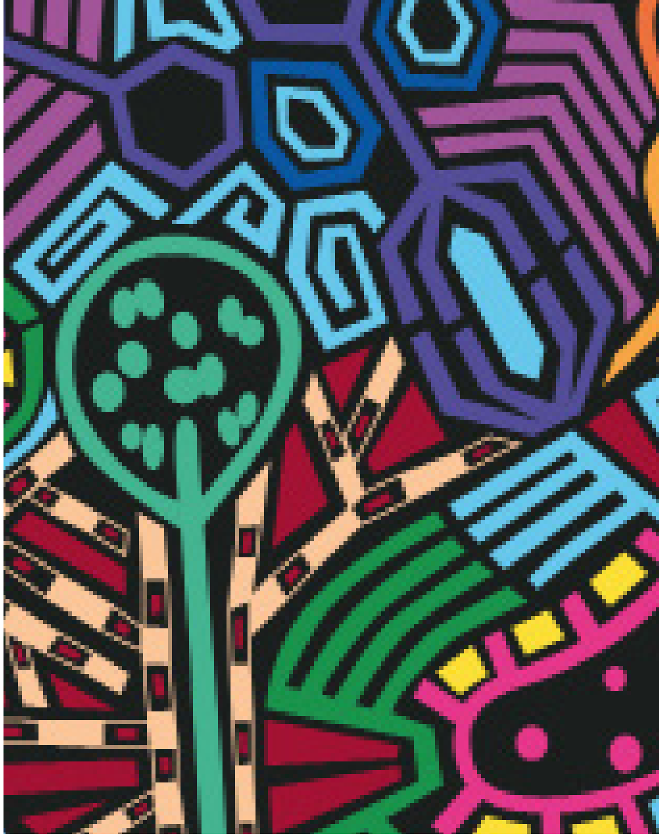
The anaerobic ammonium oxidation bacteria (anammox) process is a cost-effective technology widely applied for nitrogen removal from wastewater treatment plants (WWTP). The process is carried out by anammox bacteria, a group of microorganisms belonging to the Brocadiae class that can oxidize ammonium and reduce nitrite to form dinitrogen gas. However, due to its very slow growth rate and not be isolated in pure culture, molecular techniques are widely used to study it. This work aimed to apply genome-centric metagenomics to obtain representative genomes to study the metabolic potential and diversity of the anammox community of two granular sludge anammox reactors. The first reactor was an anammox enriched culture operated with synthetic influent for over six years. The second reactor was operated at mainstream conditions treating real wastewater from a partial nitritation process of a municipal WWTP and was inoculated with the biomass from the first reactor. Three metagenomics assembled genomes (MAGs) were obtained with over 90% completeness and less than 5% contaminated belonging to Brocadiae class, Planc-16, Planc-27 and Planc-45. The phylogenetic analysis was performed based on concatenated alignments of 120 single-copy marker genes and compared with 24 near-completed reference genomes. According to this, Planc-27 bunched with Candidatus (Ca.) Brocadia pituitae and Planc-45 with Ca. Brocadia fulgida. Planc-16 was not directly associated with any previously described species. Thus, a phylogenetic tree based on the 16S rRNA gene was constructed. Planc-16 bunched in the same clade of our recently proposed new specie, Ca. Brocadia barcinensis, dominant in the enriched anammox culture. From the potential metabolic analysis, the functional genes hydrazine synthase and hydrazine dehydrogenase were founded. This MAG lacks nitrite reductase genes (nirK and nirS). Nevertheless, the hydroxylamine oxidoreductase gene was found, which could be used as nitrite reductase. In addition, marker genes for dissimilatory nitrate reduction to ammonia were founded.

SPEAKERS



I

PLANT-ASSOCIATED MICROBIOMES

I1 - Seed Transmitted Proteobacteria form the Core Microbiome of Juvenile Angiosperm Plants

DAVID JOHNSTON-MONJE

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Bioprospecting for beneficial bacteria within plant microbiomes offers much potential to develop inoculants for sustainably improving plant productivity, mitigating stress, and controlling diseases. With the goal of finding beneficial endophytes for maize agriculture, I discovered that seeds were a rich source of endophytes, especially belonging to the genus Pantoea, Enterobacter, and Burkholderia, and that some of these had the ability to systemically move through adult plants, exit through the roots and colonize the rhizosphere. Some examples of these beneficial seed bacteria were the strongly plant growth promoting Burkholderia phytofirmans isolated from seeds from a giant Mexican landrace, root growth enhancing Enterobacter asburiae isolated from seeds of a wild variety of Nicaraguan swamp grass and the fungal biocontrol strain Burkholderia gladioli isolated from seeds of a Mexican desert popcorn. We went on to find that seeds are more important than soil in the formation of young maize endospheres, and likewise the rhizospheres of young maize plants are dominated by seed transmitted Proteobacteria, primarily Burkholderia and Enterobacter. Expanding the study to include 16 other species of angiosperm plant including Arabidopsis, Brachypodium, wheat, tomato, rice and coffee, we found evidence that the seeds, spermospheres, shoots, roots and rhizospheres of angiosperms are all dominated by taxonomically similar strains of Pantoea, Enterobacter and Pseudomonas. Shared by dicots and monocots alike, this core microbiome perhaps hints at an important and ancient relationship between seed transmitted Proteobaceria and angiosperm plants.

I2 – El efecto de la domesticación sobre el microbioma rizósferico de tomate

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LA SERENA, CHILE

El efecto de la domesticación sobre el microbioma vegetal ha sido investigado en algunos cultivos, como trigo, legumbres, maíz y cebada, encontrándose una menor diversidad taxonómica y funcional en plantas domesticadas comparado a sus ancestros silvestres. En nuestro trabajo estudiamos el efecto de la domesticación sobre el microbioma rizósferico de tomate (Solanum lycopersicum), mediante amplicon-sequencing de las regiones 16S rRNA (bacteria) e ITS (hongos), comparando 4 cultivares de tomate (ancestro silvestre, estado intermedio y 2 domesticados) y 2 suelos diferentes (natural, agrícola). Nuestros resultados indican que el tipo de suelo es muy determinante para la composición, estructura y función del microbioma rizosférico. En bacterias, la diversidad aumenta en el suelo agrícola, mientras que los hongos son mas diversos en el suelo natural. El efecto de la domesticación solo es detectable en el suelo agrícola y más evidente para bacterias. Al comparar las predicciones funcionales, las mayores diferencias se registraron entre Cal Ace (un cultivar domesticado) y el S. chilense (ancestro silvestre). En suelo natural, el metabolismo microbiano en diversos ambientes aumentó significativamente en el cultivar Cal Ace, mientras que en suelo agrícola los grupos funcionales asociados a rutas metabólicas, biosíntesis de aminoácidos, GlicolisisGluconeogénesis y sistema de fosfotransferasas (PTS) incremento en S. chilense. Finalmente, independiente del suelo y de los cultivares, se identificó un grupo de microorganismos “permanentes” en la rizosfera de tomate, cuyo perfil funcional varía entre los cultivares en respuesta al tipo de suelo. Destacamos la importancia de incluir un suelo natural (similar al de origen del ancestro silvestre), para poder registrar los cambios en el ensamble de la comunidad microbiana producto de la domesticación.

I3 - Harnessing the microbiome to control plant parasitic weeds

FRANCISCO DINI-ANDREOTE

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Microbiomes significantly expand the genomic and functional potential of plants. In doing so, beneficial plant-associated microbes largely contribute to enhanced nutrient acquisition, plant growth promotion, and tolerance to biotic and abiotic stresses. Root parasitic weeds (RPWs) constitute a major biotic stressor hindering food production and impacting food security in developing countries, with great relevance for smallholder farmers in sub-Saharan Africa. Here, I will present a conceptual synthesis devised to explore the putative mechanisms by which soil and plant-associated microbiomes can be harnessed to develop innovative strategies for RPWs control. In brief, I will detail how direct (microbial effects on RPWs) and indirect (microbial-induced changes in plant physiology and soil edaphic properties) modes of actions interfere in the association between host plants and RPWs. Then, I will set a focus on presenting a study-case that shows the effect of specific microbial volatile organic compounds (mVOCs) on the suppression of RPW seeds germination. Interestingly, such a suppressive effect was found to be maintained even when seeds were continually exposed to a germination stimulant. This nicely illustrates how specific microbial activities can act in disrupting the chemical signaling cascade between host plants and RPWs. I will close this lecture by arguing that understanding the intricate eco-evolutionary, chemical and genetic mechanisms operating at the root-soil interface constitutes an essential step towards developing new microbial-based integrated strategies to mitigate the adverse impacts of RPWs on crop production.

I4 – Simulated climate change in a semiarid shrubland decreased the phylogenetic diversity of arbuscular mycorrhizal fungal communities

MARÍA DEL MAR ALGUACIL[1*], MARIELA LIS AMBROSINO[2], IVÁN PRIETO[3], ÁLVARO LÓPEZ-GARCÍA[1], JOSÉ IGNACIO QUEREJETA[3]

1) Soil Microbiology and Symbiotic Systems Department, Estación Experimental del Zaidín, CSIC, 2) Facultad de Ciencias Exactas y Naturales, Universidad Nacional de La Pampa, Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), Ruta Nacional 35 Km 334 (6300) Santa Rosa, La Pampa (Argentina). 3) CSIC-Centro de Edafología y Biología Aplicada del Segura. Department of Soil and Water Conservation. P.O. Box 164, Campus de Espinardo 30100-Murcia (Spain).

Estación Experimental el Zaidín
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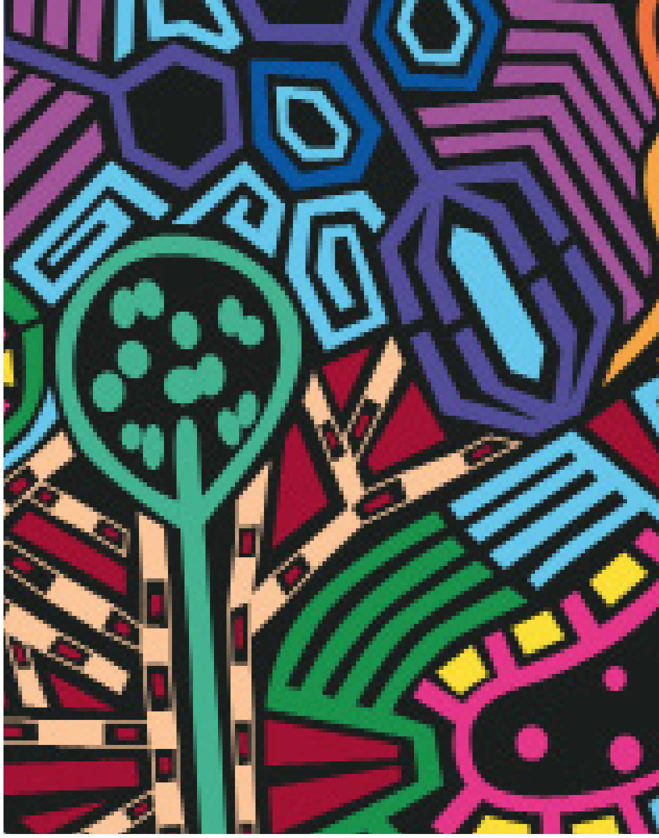
In this study, we carried out a 9-year manipulative field experiment in a semiarid shrubland in Southeastern Spain (Sorbas, Almería) dominated by several shrub species, such as Helianthemum squamatum, Helianthemum syriacum, Teucrium turredanum, Santolina viscosa, Coris hispánica and Gypsophila struthium. The AM fungal community associated with soil was characterized by DNA sequencing using Illumina technology. We simulated the warmer and drier climate conditions (~2-7°C temperature increase by using open top chambers and ~30% rainfall reduction using rainout shelters), in order to investigate the effect of increased temperature, rainfall reduction and their combination on the taxonomic and phylogenetic diversity of arbuscular mycorrhizal fungi communities in these areas. Warming factor had a significant effect on AMF community composition, favoring the presence of Glomeraceae family members mostly under the W+RR treatment. Rainfall reduction and its interaction with warming did not show a significant effect on AMF community composition. Indicator species analyses found that six VTs were indicators only for the W+RR treatment, the majority belonging to Glomeraceae family. In the phylogenetic diversity index, the W+RR treatment had the smallest and more negative value than rest of climate change treatments (-1.07 ± 0.41) and it was found to be significantly different from the generated null values ($t = -2.70$, $p < 0.05$). This means that the AM fungal communities associated with W+RR treatment exhibited a significant phylogenetic clustering. In conclusion, the combination of experimental warming and rainfall reduction significantly reduced the AMF phylogenetic/functional diversity with predominance of Glomeraceae members which were linked to decreased water content in the soil. This finding indicates that environmental filtering has selected AMF species with functional traits well-suited to cope with environmental stresses, which allowed them to survive under future climate changes in semiarid conditions.

SPEAKERS



J

SOIL MICROBIAL ECOLOGY

J1 - The rhizosphere microbiome as a tool for a sustainable agriculture

LUCAS WILLIAM MENDES

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University of Sao Paulo
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The rhizosphere is the interface between plant roots and the soil, where the interactions between thousands of microorganisms and invertebrates affect the biogeochemical cycles, plant growth, and the tolerance to biotic and abiotic stress. The rhizosphere is a hot spot of microbial diversity, being considered a complex and dynamic environment, and a better understanding of their ecology is the key to improve plant productivity and ecosystem use. The rhizosphere microbiome also plays a fundamental role in plant protection against soil-borne pathogens by inducing systemic resistance in plants and/or suppressing root colonization by soil-borne pathogens. For decades, plant breeders have exploited genetic traits to improve plant growth and development; however, they have not yet taken the rhizosphere microbiome into account. In our studies, we have assessed the microbiome of four common bean cultivars with different levels of resistance to the soil-borne pathogen Fusarium oxysporum and we demonstrated that breeding for resistance unintentionally co-selected for changes in rhizosphere microbiome composition and functions that may act in concert to restrict root infections. More specifically, the results showed that beneficial taxa such as Pseudomonas, Bacillus, and Paenibacillus, and antifungal traits such as protein secretion systems and biosynthesis of phenazines, rhamnolipids, and colicin V were enriched in the rhizosphere of the fox-resistant bean accession. Our findings suggest that breeding for Fox-resistance in common bean have co-selected for plant traits that support a higher abundance of specific beneficial bacterial families in the rhizosphere with functional traits that support a more complex rhizosphere microbiome and reinforce the first line of defense against the pathogen. Disentangling the link between root exudation and microbial community assembly in the rhizosphere is essential to engineer and integrate root microbiomes in plant breeding programs focused on improved growth and tolerance to (a)biotic stresses.

J2 - The ecology of bacterial invasions

JOANA FALCAO SALLES

University of Groningen
Groningen, The Netherlands

Biological invasions have the potential to alter the ecological and evolutionary trajectory of the Earth's ecosystems. Although less studied, microbial invasions are a constant in many fields of microbiology, including agricultural, medical, and environmental, where the entrance of a foreign microorganism into a resident community of microbes (a microbial invasion) is a common phenomenon. Despite the commonality, these fields view microbial invasions as a mere snapshot rather than a process. The latter is however crucial to foster cross-comparisons and enhance the understanding, interpretation and development of future strategies to facilitate or hamper invasions. In my talk I will look at bacterial invasions from continuum framework, in which invasion processes are divided in introduction, establishment, spread, and impact phases. Using the invasion of pathogenic E. coli strains in soils as example, I will examine the patterns and mechanisms associated with invasion resistance and create a mechanistic synthesis of how species diversity and resource availability influence invasion resistance. In the second part I will discuss the outcome of an invader's introduction on the resident community. So far, only successful invasions have been explored, and it remains unknown to what extent an unsuccessful invasion can impact resident communities. I will thus explore how unsuccessful invasions impact soil functioning and generate shifts in native bacterial communities, both in terms of community composition and niche structure. I will conclude by exploring the advantages of using this theoretical invasion framework in the context of agricultural research, such as the application of biological control agents to enhance plant resistance to biotic and abiotic stress.

J3 – Using soil probiotics to improve the efficiency of phosphorus fertilizers in the tropic

GERMAN ESTRADA

Corporación Colombiana de Investigación Agropecuaria, AGROSAVIA
Mosquera, Colombia

Phosphorus is a finite resource essential to guarantee the production of crops with high economic relevance. Typically, tropical soils have most unavailable P due to their high P fixation capacity. Therefore, the application of large amounts of soluble phosphorus fertilizer are needed in order to supply sufficient phosphorus levels to allow adequate crop yield. Thus, efforts have been made to improve the efficiency of inoculation with phosphate-solubilizing microorganisms as an alternative to this problematic. Here, we present the advances on the use of phosphate-solubilizing bacteria (PSB) to decrease the phosphorus rate fertilization and enhance the agronomic efficiency of low solubility phosphate fertilizer. Furthermore, we investigated the relation between PSB inoculation and changes in the soil microbial community structure and functionality. Our results showed that inoculation of PSB enhances the soil phosphorus availability and phosphorus efficiency use in crops as sugarcane, grasses and legumes used in livestock production. The improvement in plant growth promotion under phosphorus limitation was related to shifts in the soil bacterial community. The phenotypic and genomic characteristics of the strains influenced the phosphorus solubilization and mineralization in soil. Our research provides evidence of the biotechnological potential of PSB with several plant growth-promoting activities capable of modulate the soil bacterial community improving the plant growth and phosphate nutrition in soil with low P availability.

This abstract comes from a selection from submitted abstract. It can find in page

J4 – Spatial and temporal biogeographic distribution of soil bacterial community in cranberry soils

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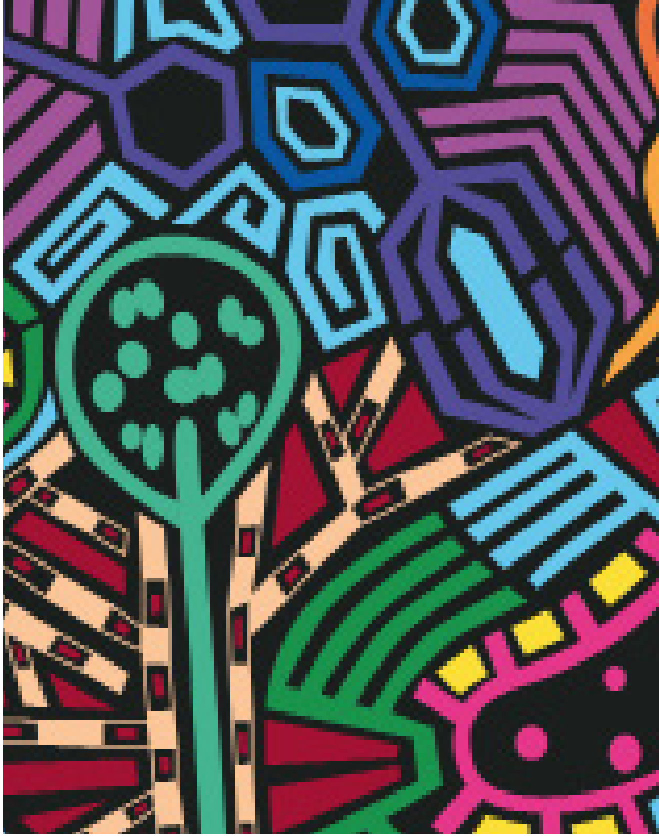
Laval, Canada

Cranberry fruits have potential human health benefits, reducing the risk of urinary tract infections and improving immune function, and their production is concentrated in North America. Canada and the USA represent 98% of cranberry production. Based on 16S sequencing (Illumina MiSeq2500 platform), a biogeographic study was performed to evaluate the temporal-spatial dynamics of bacterial community in cranberry soil across three regions under different soil managements (Conventional and Organic), and two plant stages (flowering and fruit growth). Preliminary results indicated that four phyla represent more than 80% of the soil bacterial community abundance, which are Proteobacteria (~36.6%), Actinobacteria (~19.48%), Acidobacteria (~18.03%), and Bacteroidetes (~9.15%). Organic management showed a higher abundance of Acidobacteria (20.71%) and a lower abundance of Actinobacteria (16.44%) when compared to conventional areas (15.34% and 22.51%, respectively). Our results suggest selecting soil bacteria in the fruit growth stage. Across the regions, the structure of the soil bacterial community is more similar in the fruit growth stage (ANOSIM = 0.084, p-value <0.001) than in the flowering stage (ANOSIM = 0.38, p-value <0.001). The areas under organic management showed less temporal variation in the structure of the soil bacterial community (ANOSIM =< 0.27, p-value <0.001) than conventional management (ANOSIM > 0.35, p-value <0.001). Thus, areas under organic management were more similar between the two stages than areas under conventional management. Significant enrichment of PGPR (Plant Growth-Promoting Rhizobacteria) during the fruit growth period (such as Massilia sp.) and in areas under organic management (e.g., genus Sphingomonas and Caulobacter). The results suggest a first selection filter in the soil bacterial community associated with the plant stage, with a smaller shift in the organic management areas. These findings compose an effort to increase the knowledge of the soil microbial community, which could further help increase crop production and maintain the system's sustainability.

SPEAKERS



K

MICROBIAL ECOLOGY OF AQUATIC ENVIRONMENTS

K1 - Mangrove Microbiome Initiative (MMI)

ALEXANDRE SOARES ROSADO

King Abdullah University of Science and Technology
Thuwal, Kingdom of Saudi Arabia

Mangrove ecosystems provide important ecological benefits and ecosystem services, including acting as major carbon sinks and stabilizing coastlines; but they also suffer great anthropogenic pressures. Microorganisms associated with mangrove sediments and the rhizosphere play principal roles in this ecosystem and make essential contributions to its productivity and carbon economy. Understanding this nexus and moving from descriptive studies of microbial taxonomy to hypothesis-driven field and lab studies will facilitate a mechanistic understanding of mangrove ecosystem interaction webs, and opportunities for microorganism-mediated approaches to mangrove protection and rehabilitation. Such an effort requires a multidisciplinary and collaborative approach, involving chemists, ecologists, evolutionary biologists, microbiologists, oceanographers, plant scientists, conservation biologists and government representatives, using standardized methods. We have formed the Mangrove Microbiome Initiative (MMI), an international network of researchers aimed at advancing mangrove microbiome research through collaboration, discussion, and advocacy. Read our recent Perspectives article (https://bit.ly/3o8FpK9) for our thoughts on the most urgent research priorities to advance the field.

K2 - Differences in the microbial community structure in sediments from the Yucatan underground aquifer appear to be determined by physical and chemical characteristics posed by coastal and inland environments

ALEJANDRA PRIETO DAVÓ

Universidad Nacional Autónoma de México
Ciudad de México, México

Sink holes are unique environments where the underground aquifer in the Yucatan peninsula connects to the open atmosphere. Karstic conditions in the peninsula, which encompasses the largest underground river in the world, suggest it could hold a unique microbial composition in its sediments. To explore and understand more about the microbial ecology of microorganisms in sediments from the karstic underground aquifer, a 16S rRNA gene amplicon study was performed. Our study shows significant differences between microbial communities in sediments from inland vs coastal cenotes. While inland cenote sediments have a fully freshwater column above them, coastal ones are influenced by seawater intrusion from the nearby ocean resulting in a shift from microbes known to be involved in nitrogen metabolism at the former, to those more specialized in using sulfur at the latter. Interestingly, microbial communities also changed inside the cenotes from a transect covering the open-air area through deeper caves into the system. Physical and chemical characteristics of water column and sediments from the cenote sections suggest a direct relationship with microbial community changes in the transects. This first study of microbial communities in cenote sediments poses new questions about their roles in the geochemical cycles of the karst underground aquifer in Yucatan.

K3 – Microbiome manipulation elicits metabolic and genetic restructuring and improves coral biology

RAQUEL PEIXOTO

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Thuwal, Kingdom of Saudi Arabia

Coral reefs are extremely diverse ecosystems that support the livelihoods of close to a billion people. Despite their importance, these ecosystems and their provided services have been massively threatened by the current intensity and pace of global and local change, which may outpace their ability to adapt. One of the several different human-accelerated adaptive strategies being proposed and explored to increase coral resilience is the manipulation of Beneficial Microorganisms for Corals (BMCs), the so called coral probiotics. Here, I will present our recent results indicating some of the underlying mechanisms associated with microbe-mediated coral health improvements and mortality evasion, as well as new ideas and approaches to understand and explore key symbiotic interactions between corals and their associated microbes.

K4 – Disentangling the bacterial metabolicinteractions on Brazilian soda lakes

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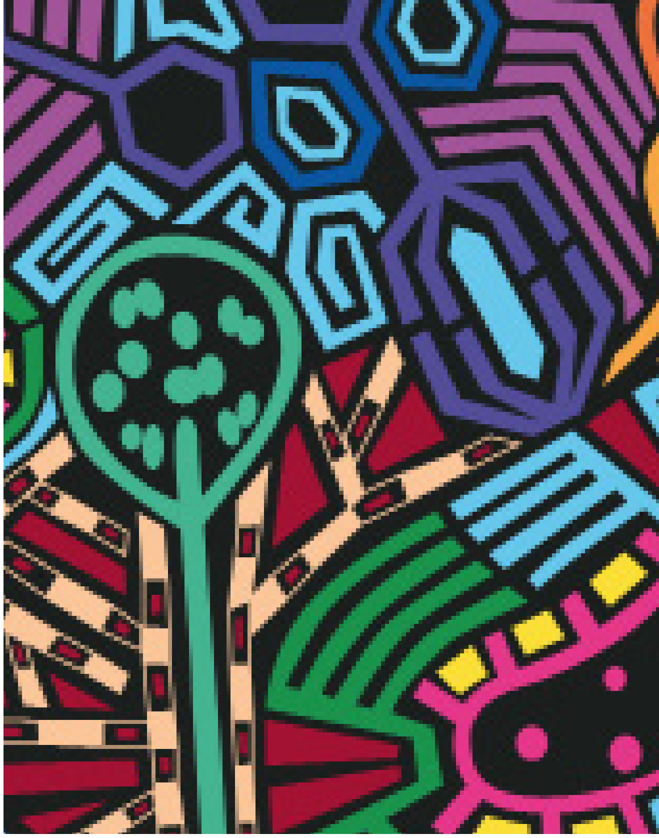
The microorganisms communicate with each other using different chemical signal molecules. These molecules are critical for synchronizing the activities as nutrient uptake, and for that directly impacting the environmental functioning. This work aims to describe the main metabolic pathway found on Brazilian soda lakes. Applying flux balance analyses (FBA) on metagenomic data, we evaluated the main metabolic pathways found on Brazilian soda lakes to predict how these organisms support the higher productivity observed in this alkaline environment. Three different watercolor soda lakes (crystalline, black and green color) were evaluated on three sampling times (dry-wet-dry periods). The relative abundance of total bacterial varied through the time, but the most prevalent phyla were Actinobacteria, Bacteriodetes, Cyanobacteria and Planctomycetes. The green color lake has this color due to the occurrence of Cyanobacteria bloom and this lake was enriched with amino acids and nitrogen compounds as urea and nitrite. The compounds predicted on evaluated lakes variety through the sampling time. Considering the CAZy (carbohydrate-active) enzymes, the green-water lake was enriched in almost all evaluated categories, except to redox enzyme categories enriched in the black-water lake. The green lake seems to show a more dynamic production of compounds, specially associated with nitrogen metabolism. This observation could be a result of Cyanobacteria activity. These results shed light on the complexity of metabolic interactions detected on Brazilian soda lakes and they still under evaluation.

SPEAKERS



L

HUMAN MICROBIOME AND HEALTH

L1 - A simpler niche? A microbial ecologist's guide to cervicovaginal microbiota in health and disease

FILIPA GODOY-VITORINO

Department of Microbiology and Medical Zoology
University of Puerto Rico
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The vagina is an interface between the host and the environment, and its protective epithelium is colonized by bacteria and other microorganisms. It serves a pivotal role as a gatekeeper to protect the upper genital tract from microbial invasion and subsequent pathology. Human microbiome research has taught us that from an ecological point of view the vagina is the simplest of the human body niches and that microbes play a role in the susceptibility in neoplasia. At the forefront of microbiome studies are extensive taxonomic surveys associating bacteria with disease phenotypes, however much less is known of the shifts in metabolites during HPV infections. We hypothesized that there would be microbiome taxonomic and functional changes associated with cervical dysplasia with HPV infections in the cervicovaginal lavages of Hispanic Patients.

We collected cervical lavages from a group of 100 women coming for gynecology and colposcopy evaluation at the UPR and San Juan City clinics (Puerto Rico). We performed typification of HPV for all samples using the LIPA25 kit, sequenced 16S rRNA genes with Illumina MiSeq and performed untargeted metabolomics with GC-MS from womeen's samples grouped as healthy, CIN 1 and CIN 3 (Pre-cancer).

In this conference I will discuss the predominant role of Lactobacillus, discuss if the vaginal niche is home to other populations that seem to facilitate HPV infections and carcinogenesis and discuss what are the metabolomic changes that could have an impact in the progression of HPV related disease.

L2 – A systems genetics approach to dissect interactions between gut microbes, metabolites and the host

FEDERICO REY

University of Wisconsin-Madison
Madison, USA

Over the last decade several systems genetics studies have shown that host genetics influences intestinal microbiome composition, and loci modulating abundance of bacterial taxa and facets of metabolism have been discovered. A central premise of these approaches is that genetic variation drives phenotypic variation, i.e., genetic locus -> phenotype. This powerful premise produces an anchor for creating causal network models that can connect microbes, metabolites, and host genes to complex phenotypes. Thus, when traits without known relation (e.g. abundance of a microbe and a particular metabolite) are highly correlated at a specific host locus, novel hypotheses emerge connecting these traits. We are exploiting the power of systems genetics and Quantitative Trait Loci (QTL) mapping to start deconvoluting interactions between gut microbes, metabolites and the host. Toward this end, we are leveraging the Diversity Outbred (DO) mouse cohort, an outbred mouse resource with high genetic diversity. We performed whole-genome shotgun DNA sequencing of fecal DNA from samples collected from ~300 DO mice, and generated metagenome-assembled genomes (MAGs), profiles of microbial functions and microbial pathways. Additionally, we performed LC-MS/MS-based profiling of plasma and cecal lipids, bile acids and small molecules, and carried out transcriptional analyses of intestinal tissue. QTL mapping of these traits is revealing numerous regions of the mouse genome that associate with the abundance of microbial features and metabolites. Notably, we have identified several QTL hotspots—genome regions associated with multiple microbial traits. Several of these hot-spots are not only associated with abundance of multiple MAGs but also with specifics type of lipids and bile acids that may be important for microbe-host interactions. During my talk I will discuss specific examples that illustrate the power of genetics to identify novel interactions between microbial and metabolite traits.

L3 - The Latinbiota Consortium: understanding composition and variation of human gut microbiota in Latin American populations

GREGORIO IRALOA

Instituto Pasteur de Montevideo
Montevideo, Uruguay

Compositional variation in the human microbiota has been vastly associated to healthy and disease conditions. Also, variations in the human microbiota are driven by socioeconomic and cultural factors that influence behavioral and dietary habits. Despite microbiome research is today among the most rampant and dynamic fields in science, most current paradigms have been constructed based on data from human populations inhabiting high-income countries from Europe and North America. Today, there is a marked bias in metagenomic data availability towards the north hemisphere that is even clearer in Europe and the US. Latin America has a combination of demographic and socioeconomic characteristics making its populations an extremely suitable target for expanding our knowledge about variation in the human microbiome and its role in health and disease. We have currently generated 255 human gut shotgun metagenomes from Latin American populations from Uruguay, Argentina, Chile, Brazil, Bolivia, Colombia, Ecuador and México and other 300 samples are being processed. Preliminary analysis revealed that 16% of found species were novel, expanding our general knowledge about bacterial diversity in the human gut. Some novel species are restricted to particular countries, indicating potential geographic patterns of variation. Consolidation of the Latinbiota consortium is expected to constitute a hallmark for understanding the role of the human gut microbiota in the Latin America and low- and middle-income countries in particular.

L4 – Gut bugs matter to viroimmunotherapy: bacterial changes associated to the efficacy of Delta-24- RGDOX against glioblastoma

NATALIE M. MELENDEZ-VAZQUEZ[1*], TERESA NGUYEN[2], SAGAR SOHONI[2], ASHLEY OSSIMETHA[2], JUAN FUEYO[2], CANDELARIA GOMEZ-MANZANO[2] AND FILIPA GODOY-VITORINO[1]

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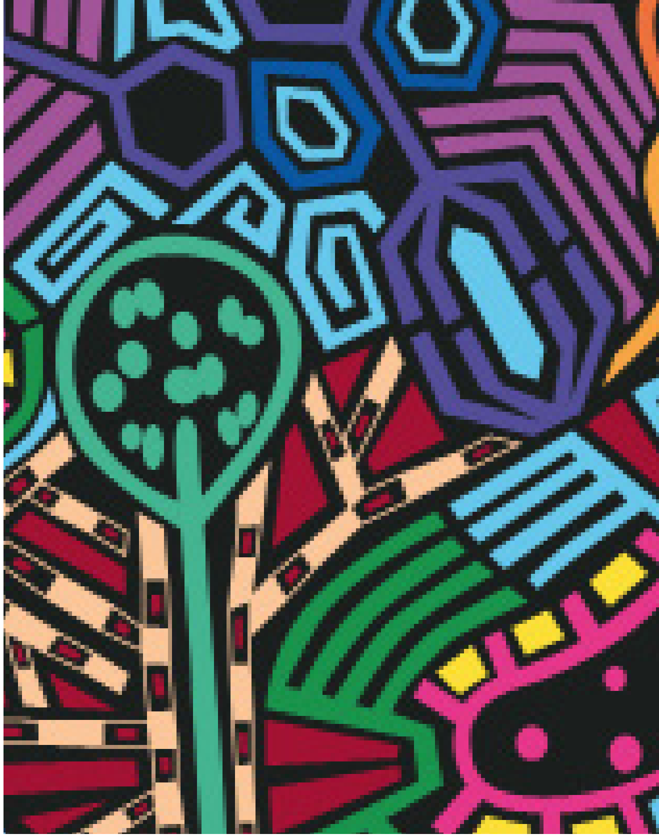
Puerto Rico,USA

Introduction: Glioblastoma is a notoriously invasive and devastating disease that requires new and more effective treatments as less than 5% of patients survive 5 years post-diagnosis. To improve clinical outcomes, the MDACC laboratory developed an oncolytic adenovirus armed with the T-cell activator OX40L, named Delta-24-RGDOX. Objective: Here, we evaluated to which extent there were gut microbiome changes in glioma bearing mice treated with viroimmunotherapy. GL261-5 glioblastoma cells were implanted in the brain of immunocompetent C57BL/6 mice and treated with control or a combination of Delta-24-RGDOX and Indoximod, an inhibitor of indoleamine 2,3-dioxygenase (IDO). Methods: Genomic DNA was isolated from fecal pellets collected from glioma-bearing mice, followed by sequencing of the 16S rRNA gene using the Illumina platform. Results/Discussion: We found significant differences in the gut microbiome community structure of viroimmunotherapy-treated animals compared to those with depleted CD4+ T cells and controls (p-value=0.001). Particularly, an increase in Actinobacteria compared to control-treated mice and those with shorter survival was observed. In fact, we found significantly higher amounts of Bifidobacterium and Lactobacillus in the viroimmunotherapy-treated mice while Parabacteroides and Akkermansia were more dominant in the control group ($p<0.05$). Also, we found significantly higher abundance of Lactobacillus and Alistipes in mice with a survival period 56-86 days, while Ruminiclostridium was more dominant in the mice with shortest survival. Conclusion: Our data suggests bacterial communities play an important role in modulating viroimmunotherapy against glioma. Importantly, increase in certain gut bacteria was associated with a better response to the therapy, likely strengthening antitumor immunity and raising efficacy of Delta-24-RGDOX; thus revealing the benefits of gut microbiome therapeutics in positively influencing the final clinical outcome of viroimmunotherapy.

POSTER SESSIONS



A

MICROBIOMES ASSOCIATED WITH ANIMAL HOSTS

A3 - One from the mother, the other from the daughter: a genomic survey of two *Vibrio* strains isolated from different life stages of the marine sponge *Plakina cyanorosea*

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Decoding the genomic data is essential in gaining new insights into host-dependent and ecophysiological adaptative traits in sponge microbial symbionts. Here, we provide a comprehensive genomic survey of two Vibrio strains, PA3G1 and PL1G11, isolated respectively from adult and larvae of Plakina cyanorosea, a Homoscleromorpha sponge from a small tidal pool in the Brazilian Southeast Coast. High-quality draft genomes were generated and fully annotated: the Vibrio sp. PA3G1 genome was 5.95 Mb in length, with a GC content of 45.5% and 5,297 coding sequences (CDSs), while Vibrio sp. PL1G11 had a genome of 5.08 Mb, a GC content of 44.58% and 4,594 CDSs. Both genomes are structured in two chromosomes, with a small 24.83-Kb plasmid likely to be present in Vibrio sp. PA3G1. Genes potentially encoding surface adhesins, cellular lysins and eukaryotic-like proteins, mostly with tetratricopeptide repeats, were identified in both genomes. The host invasiveness potential for PL1G11 appears high given the presence of complete type III and VI secretion systems, despite PA3G1 having a larger number of putatively secreted effectors. Cellulose, chitin, starch and alginate were among the complex polysaccharides potentially being targeted by the CAZomes of these Vibrio, with PA3G1 possessing a greater diversity and number of catabolic glycoside hydrolases (GHs). Regarding their mobilome, PA3G1 harbours one prophage sequence and a higher variety of insertion sequences (ISs); in contrast, three complete prophages and fewer ISs were observed for PL1G11. The strains shared similar resistome features, including chromosomally encoded beta-lactamases, multiple multidrug efflux pumps and detoxification systems for different heavy metals. Genome-based taxonomy and phylogenomic analyses allowed us to classify Vibrio sp. PA3G1 and PL1G11 as Vibrio owensii and Vibrio alginolyticus, respectively. These results indicate that both Vibrio strains are likely to have adapted to a sponge host-associated lifestyle, but cannot exclude their potential origin from environmental sources.

A4 - *Clostridium difficile* in Western Australian native animals: Prevalence and molecular epidemiology

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Clostridium difficile infection (CDI) is the most common cause of infectious diarrhea in hospitalised humans. C. difficile colonises the gastrointestinal tract, causes disease in a variety of animal species and can persist as a spore in diverse environments. Genetic overlap between C. difficile strains from human, animal and environmental sources suggests CDI has a zoonotic or foodborne aetiology. In Australia, C. difficile PCR ribotype RT014 (MLST clade 1) and several ST11 (MLST clade 5) RTs are found commonly in livestock. The high prevalence and diversity of ST11 strains in Australian production animals indicates Australia might be the ancestral home for this lineage. This project describes for the first time the ecology of C. difficile in Australian native animals, providing insights into the prevalence, molecular epidemiology and evolution of C. difficile in this unique environment and a possible role in CDI in humans and animals in Australia. Faecal samples were collected from wild/captive reptiles (n=37), mammals (n=104) and birds (n=102) in Western Australia in 2020/21. Anaerobic enrichment culture was performed, and C. difficile isolates were characterised by PCR ribotyping and toxin gene profiling. Seventy isolates of C. difficile were recovered (prevalence of C. difficile in faecal samples 28%, n=68/243); 27 unique RTs were identified, 5 were novel. The prevalence of C. difficile was similar for reptiles and mammals, 46% (n=17/37) and 43%(n=45/104), respectively, but significantly lower in birds (7.8%, n=8/102; $p<0.00001$ for both reptiles and mammals). Of the 57 isolates available for typing, RT237 (clade 5) and RT002 (clade 2) were the most prevalent, 15.8% (n=9/57) and 14% (n=8/57), respectively. The high prevalence of C. difficile in reptiles and mammals, particularly clade 5 strains, supported by previous studies of C. difficile in Australian soils, suggest that Australia might be the ancestral home of MLST clade 5.

A5 - Diverse methanogens, bacteria and tannase genes in the feces of the endangered volcano rabbit *(Romerolagus diazi)*

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The volcano rabbit is the smallest lagomorph in Mexico, it is monotypic and endemic to the Trans-Mexican Volcanic Belt. It is classified as endangered by Mexican legislation and as critically endangered by the IUCN, in the Red List. Romerolagus diazi consumes large amounts of grasses, seedlings, shrubs, and trees. Pines and oaks contain tannins that can be toxic to the organisms that consume them. The volcano rabbit microbiota may be rich in bacteria capable of degrading fiber and phenolic compounds. We obtained the fecal microbiome of three adults and one young rabbit collected in Coajomulco, Morelos, Mexico. Taxonomic assignments and gene annotation revealed the possible roles of different bacteria in the rabbit gut. We searched for sequences encoding tannase enzymes and enzymes associated with digestion of plant fibers such as cellulose and hemicellulose. The most representative phyla within the Bacteria domain were: Proteobacteria, Firmicutes and Actinobacteria for the young rabbit sample (S1) and adult rabbit sample (S2), which was the only sample not confirmed by sequencing to correspond to the volcano rabbit. Firmicutes, Actinobacteria and Cyanobacteria were found in adult rabbit samples S3 and S4. The most abundant phylum within the Archaea domain was Euryarchaeota. The most abundant genera of the Bacteria domain were Lachnoclostridium (Firmicutes) and Acinetobacter (Proteobacteria), while Methanosarcina predominated from the Archaea. We obtained 18 bacterial tannase sequences. Potential functions were identified including carbohydrate and amino acid metabolism. We found genes encoding enzymes for plant fiber degradation such as □-1-4-endoglucanases, xylanases, □-glucosidases and arabinofuranosidases. The volcano rabbit microbiome showed distinct bacterial and archaea abundances compared to other lagomorphs. The gut microbiota may contribute to the digestion of complex plant molecules. The diversity of methanogenic species could be influenced by the type of diet. In addition, we observed differences between adult and young rabbits.

A6 - Biological effects and differences on the gut microbiome of *Galleria mellonella* larvae consuming plastics

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Plastic pollution is a footprint of the Anthropocene that is evident in all types of ecosystems. The main polluting plastics are polyethylene, polypropylene and polystyrene. In the last decade, different studies have assessed the capacity of insect microbiota to degrade plastics. We evaluated the consumption of a variety of plastics by wax moth (Galleria mellonella) larvae, and its effects on the biology of the species and the diversity of their gut microorganisms. We performed diet trials with two (polyethylene, polystyrene) and four (polyethylene, polystyrene, bioriented polypropylene, silo-bag) plastics, registered their times of development, and examined their gut microbiome through 16S and ITS sequencing. The larvae consumed all types of plastics and completed their development in all treatments, however the duration of the larval stage was shortened when consuming plastics. Gut bacterial communities were different in larvae consuming beeswax and plastics. At the phylum level, the most abundant were Proteobacteria (72.2%), Firmicutes (14.9%) and Bacteroidetes (7.9%). In addition, Fusobacteria were present almost exclusively on beeswax while Fibrobacteria were dominant only on plastics. In relation to fungi, we found Ascomycota (72.1%) and Basidiomycota (27.9%), with no clear differences among treatments. Beeswax had dominant bacteria composed by taxa within the Neisseriaceae family, the genera Fusobacterium, Actinobacillus, Alloprovotella, Streptococcus and Leptotrichia; and in plastics we found more dominant Pseudomonas sp J27 and Pseudomonas citronellolis. In conclusion, plastic consumption shortens the development of G. mellonella larvae and affects their gut microbiome. This is the first evaluation of the multi-kingdom response of gut microbiota (bacteria and fungi) to plastic consumption in wax moth larvae. Further analysis of the biological impacts of plastic consumption in G. mellonella and the role of their gut microbiome is critical to evaluate the species potential for plastic biodegradation.

A7 - Specific Pathogen Free and Conventional primates differ in microbiota composition and diversity

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Rhesus macaques are a widely popular model used in biomedical research. Studies in microbiota have established a correlation between alterations in the microbiota with lifestyle and diseases. Specific Pathogen Free (SPF) animals (free of STLV-1, SRV-D, Herpes B and SIV) could have high implications when translated into human studies, due to their likely altered microbiota. Our study aims to characterize the oral and anogenital microbiota in SPF and Conventional rhesus macaques (Macaca mulatta) from the Caribbean Primate Research Center (CPRC) in Puerto Rico. Oral, anal, vaginal, penile, and penile skin samples were collected using sterile cotton swabs from two primate groups: SPF and Conventional. Forty Macaca mulatta animals from the CPRC were sampled resulting in 140 collected samples. Genomic DNA was extracted from the samples collected and 16S rDNA was amplified and sequenced through Next Gen Sequencing using Illumina MiSEQ. Microbiota was analyzed through different bioinformatic pipelines. Bacterial composition and structure was significantly different across body sites, and between SPF and Conventional animals (PERMANOVA P-value = 0.001), with oral samples being the most distinct. Alpha Diversity was significantly higher in the anal samples compared to the vagina similar to what we know from the human microbiota. In most sample sites, the SPF group was more diverse than its Conventional counterpart. Taxonomic biomarker analyses showed that Neisseria, Alloprevotella, and Gemella were characteristic of the oral cavity, Prevotella, Lactobacillus, and Streptococcus of the anal region, while the vaginal tract had dominant Fusobacterium and the penile region Porphyromonas, or Corynebacterium. Body sites showed differences both in bacterial community structure and diversity suggesting translocation of bacteria through sexual transmission. Differences in the microbiota between SPF and Conventional primates associated with the viral bioexclusion, suggests a potential impact in the outcome of trials using SPF animals and their translatability to humans.

CE Disclosures: Authors declare no conflicts of interest

A8 - Exploring the gut microbial community associated with herbivorous hosts in Costa Rica

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The symbiotic gut microbial community is one of the factors that shapes host ecology. In the case of herbivores, it enables the host to feed on plant matter consisting mainly of recalcitrant compounds such as cellulose. This study set out to explore the diversity of the gut microbial community in herbivorous host species in Costa Rica with a focus on microbial taxa capable of cellulose degradation. Host species include larvae of the xylophagous bess beetles (family Passalidae; n=15) and five herbivorous mammals; Bairds' tapir (Tapirus bairdii; n=10), feral pigs (Sus scrofa; n=9), white-tailed deer (Odocoileus virginianus; n=2), two-toed sloth (Choloepus hofmannii; n=6) and three-toed sloth (Bradypus variegatus; n=5). Fecal samples of mammalian hosts were collected in the field, while bess beetle larvae were brought to the lab, kept in sterile conditions to defecate and dissected to obtain mid- and hindgut samples. The microbiome was characterized using culture independent methods (16S rRNA) and the presence of symbionts was verified in a subset of samples using scanning electron microscopy. A total of 6742 taxa were encountered with the majority belonging to Firmicutes, Bacteroidetes and Proteobacteria. Across samples 20% of encountered taxa remained unclassified at family level, suggesting that samples harbor unknown microorganisms. Alpha diversity differed significantly between species ($p<0.001$) with highest diversity found in bess beetles and lowest diversity in three-toed sloths. Beta diversity analysis revealed clear host specific differences ($p < 0.001$) and dominant microbial taxa were differentially abundant across the hosts. The gut microbial community of the studied host species is highly diverse and includes groups of known cellulose degraders such as Lachnospiraceae and Ruminococcaceae. These findings illustrate that neotropical fauna harbors an unexplored microbial diversity with associated functionality that may one day find applications in medicine, conservation and industry.

A9 - Effects of probiotics and prebiotics on the growth and gut microbiota of *Chirostoma estor* (Pisces: Atherinopsidae) endemic of central México

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Probiotics are live microorganisms (e.g. Lactobacillus, Lactococcus, Bifidobacterium, Bacillus, Sacharomyces) which when administered in adequate amounts confer verter growth and health benefit on the host. In aquaculture, both probiotics and prebiotics have effects in improving the growth and modulation of the intestinal microbiota of fish, being prebiotics, substrates (e.g. inulin, cell wall of S. cerevisiae, -glucans, mannan-oligosaccharides) that potentially activate host microorganisms (including added probiotics). It has been determined that combined application of probiotics and prebiotics (synbiotics), the effects are greater. Our model study is the pike silverside fish from Lake Pátzcuaro Chirostoma estor, with an ecological, nutritional, economical and cultural importance in the region of the basin mexican highlands. The objective of this work is to determine the influence of probiotics (L. acidophilus), prebiotics (inulin or cell wall) and synbiotics (L. acidophilus + inulin and L. acidophilus + cell wall) on the growth of captive C. estor and their effect on their intestinal microbiota over a 12 week experiment. Morphological measurements (length and weight) were taken to determine growth. While the intestinal microbiota was determined from a metagenomic analysis of the V3 region (16S rRNA). The results indicate that synbiotics have the greatest influence on growth, compared to control diet and prebiotic and probiotic added to the diet individually. Regarding the analysis of the intestinal microbiota, at phylum level, Firmicutes (43.36%), Tenericutes (23.34%) and Proteobacteria (21.62%) were more abundant. At genus level, Streptococcus (24.65%), Mycoplasma (23.34%) and Lactobacillus (9.16%) were more prevalent. Regarding the influence of the added diets, we found that synbiotics treatments increase the presence of lactic acid bacteria, such as genus Lactobacillus, Enterococcus and Weissella in intestinal microbiota of C. estor.

A10 - The genome of *Nitrosopumilus sp.* associated with Antarctic marine sponges, unveiling their taxonomic and metabolic signatures

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The ammonia-oxidizing archaea Nitrosopumilus sp. (phylum Thaumarchaeota) is a crucial carbon and nitrogen biochemical cycle player. This archaeon is ubiquitous among diverse environments inhabiting marine waters, sediments, and living in a complex relationship with marine invertebrates. Marine sponges are the most ancient invertebrates, which play a relevant role in the structuration and nutrient cycles in marine environments. This benthonic organism supports complex and basal symbiotic interactions among Eukarya, Bacteria, and Archaea. In Antarctica, sponges are highly endemic organisms and dominant members of the benthonic community of some polar benthonic surfaces. The Antarctic sponge microbiome, as in tropical and temperate sponges, Nitrosopumilus, dominates the Archaea domain. However, knowledge of genomic adaptations of Nitrosopumilus associated with Antarctic sponges is still limited. This work was focused on characterizing genomic adaptations of the Nitrosopumilus to the symbiotic lifestyle associated with Antarctic sponges, using the Metagenomic Assembly Genome (MAGs) approach. Four Antarctic sponge microbiome were sequenced, and metagenome sequences obtained were co-assembled. Additionally, 49 genomes of Nitrosopumilus were used to perform comparative genomics. A total of 50 MAGs were received, of which one high-quality genome (>95% completeness and <5% contamination) was taxonomically assigned as Nitrosopumilus. The Average Nucleotide Identity (ANI) and Average Amino-acid identity (AAI) analysis showed that the sponge-associated Nitrosopumilus corresponds to new species of Thaumarcheaota (85% ANI and 89% AAI). The comparative analysis of genomes revealed that the associated Nitrosopumilus possesses exclusive genes related to symbiotic lifestyle, including clustered regularly interspaced short palindromic repeats system (CRISPR-Cas system type-II protein Cas9 (Cas9)), Restriction-modification system (SAM-dependent methyltransferase (SmtA)). Furthermore, the sponge-associated Nitrosopumilus displays specific genes involved in carbohydrate metabolism (6-phosphogluconolactonase) and transport of substrates (TctA family transporter), and DNA replication (DNA2 Helicase). In conclusion, the results showed that the sponge-associated Nitrosopumilus possesses adaptations to symbiotic lifestyle, carbohydrate usage, and extreme environmental conditions, supporting potentially, their lifestyle within the Antarctic sponge microbiome.

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A11 - Characterization of dinoflagellate communities in marine sponges and seawater in Fildes Bay, Antarctic Peninsula

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Dinoflagellates stand out among the symbiotic microbial eukaryotes of benthic animals. They play a role in providing photosynthates, calcification processes, and protection against UV radiation. This study represents the first characterization of dinoflagellate communities associated with Antarctic sponges by amplicon sequencing. The symbiotic relationship between dinoflagellates and marine sponges has been reported in bioeroding sponges from tropical and subtropical seas of the genus Cliona. In the Antarctic benthos, marine sponges are dominant and host-microbial communities that favor the ecosystem's dynamics. Antarctic sponges are associated with dinoflagellates. Current knowledge of dinoflagellates diversity in these sponges is limited. This work considered the dinoflagellate communities of 26 individuals of sponges and five samples of seawater collected in Fildes Bay, Antarctic Peninsula, between the years 2013-2015. Communities were characterized by analyzing the V9 hypervariable region of the 18S rRNA gene using the amplicon sequence variants (ASV) approach. Dada2 and phyloseq R packages were used for the analysis of ASV and microbial eukaryote diversity. After comparing sponge individuals and seawater samples, taxonomic profiles obtained with ProtistDB, revealed differences in microbial eukaryote communities, but recurrently, Ochrophyta and Dinoflagellata were predominant. The dinoflagellate communities showed profiles represented mainly by the Dino − Group − I − Clade − 1 and, Kareniaceae, Gymnodiniaceae families. Obtained results allow us to infer the potential functional roles of dinoflagellates in the Antarctic sponge holobiont.

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A12 - Microbial community profiles associated with the sea cucumber *Holothuria glaberrima's* regenerating gut

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The gut microbiota has been proven to play an important role in the physiological processes of the host. Among these, the dynamics of microbial communities associated to regeneration processes are receiving more attention. We previously studied the intestinal regeneration process of the sea cucumber, Holothuria glaberrima, upon evisceration. Furthermore, our research has documented the microbiota associated with the holothurian intestine, the most prevalent taxa being Proteobacteria, Bacteroidetes, and Firmicutes. Currently, we aim to characterize whether changes in microbial populations are linked to the intestinal regeneration process. For this, sea cucumbers were eviscerated and left to regrow in seawater aquaria for up to 21 days. Specimen samples were obtained at various regeneration stages, including 1- hour after evisceration, 3-days post-evisceration (dpe), 5-dpe, 10-dpe, 14-dpe and 21-dpe. Three individuals per stage had their esophagus, cloaca, mesentery, tentacles, and regenerated gut dissected and preserved separately. Non-eviscerated holothurians were maintained in the aquaria and used as controls. gDNA was extracted from a total of 186 samples followed by MiSeq library preparations. Data was processed in Qiime2 and Rplatforms using a Phred score of 10754 rarefaction level of 7,993,893 reads. Proteobacteria, Bacteroidetes, and Firmicutes were the most prevalent phyla in our preliminary microbial community profiles from non-eviscerated intestinal samples. We found significant changes in relative abundance at the phylum level in the regenerating gut, including a decrease in Proteobacteria (inflected by decreased Gamaproteobacteria and Alphaproteobacteria), and an increase in Firmicutes (mostly influenced by Bacilli and Clostridria classes abundances). Our findings support a succession in the gut bacterial ecology over the first month following evisceration and might indicate that Firmicutes is associated with intestinal regeneration. These findings, along with our prior characterization of the cellular mechanisms controlling H. glaberrima's intestinal regeneration, form the foundation for understanding the microbiota's interactions with the intestinal regenerative process.

A13 - Evaluación de estrategias alternativas de cultivo de bacterias ruminales por medio del uso de metabarcoding

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La microbiota ruminal es fundamental en los bovinos para la asimilación del material vegetal, sin embargo, la baja cultivabilidad impide conocer su función ecológica y potencial biotecnológico. Esta es una estrategia para mejorar la recuperación de microorganismos ruminales que combina la evaluación de parámetros de cultivo con el análisis de poblaciones utilizando metabarcoding. Los parámetros evaluados fueron, medios de cultivo (CAN, ER, GC, GOOD, KNT, KYO,NYO,TRB), la dilución de fluido ruminal (10-2, 10-6 y 10-12) y el tiempo de incubación (3 y 7 días). Para cada tratamiento se realizaron tres réplicas biológicas, las poblaciones bacterianas se determinaron mediante secuenciación Illumina del 16S ARNr. El análisis de las librerías muestra que los medios de cultivo no recuperan todas las poblaciones del rumen y favorecen el cambio en la abundancia relativa de los fila dominantes. En el rumen los fila Bacteroidetes y Firmicutes tienen una abundancia relativa de 75 y 15 % respectivamente, en los medios su abundancia es de 15 y 60%. Mediante el análisis de coordenadas principales (PCoA)utilizando la distancia UNIFRAC, se determinó el efecto de cada tratamiento sobre la composición poblacional. Los resultados muestran agrupación de las poblaciones por la dilución, donde 10-2 y 10-6 están más cercanas, mientras que las poblaciones de 10-12 no se agrupan entre ellas y también son más distantes a los otros tratamientos. El tiempo de incubación no mostró diferencias en las poblaciones. Para determinar cuáles medios recuperan poblaciones más similares al rumen se compararon las distancias del PCoA entre los tratamientos y el fluido ruminal. Este análisis mostró dos tendencias, medios más cercanos al rumen que recuperan los microorganismos de baja abundancia que no han sido caracterizados en su totalidad (NYO,ER), y segundo, medios más distantes, que recuperan una diversidad menor pero que son más selectivos frente a microorganismos importantes del rumen (CAN,KNT).

A14 - Impacto del herbicida glufosinato de amonio, en la microbiota intestinal e inmnunidad de las abejas melíferas

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En los últimos años se ha reportado la despoblación y pérdida de colmenas de abejas melíferas alrededor del mundo. Entre los principales factores se encuentran la presencia de múltiples plagas y patógenos, y la expansión e intensificación de cultivos agrícolas, que conlleva un aumento en el uso de pesticidas. El glifosato es el herbicida más empleado alrededor del mundo. Sin embargo, la aparición de resistencia ha impulsado su sustitución por el glufosinato de amonio, aunque existe escasa información respecto a sus efectos en insectos polinizadores. El objetivo de este estudio fue evaluar el impacto de este herbicida en la inmunidad, microbiota y supervivencia de abejas melíferas. Con este fin se utilizó un modelo de cría de abejas en laboratorio y se realizaron dos ensayos: A- Se formaron 3 grupos de abejas recién emergidas, que recibieron diferentes tratamientos, intoxicación aguda con glufosinato de amonio en jarabe (0,5 mg/ml o 0,05 mg/ml) y el tercer grupo solo recibió jarabe como control. B.- Se realizó un ensayo similar pero la intoxicación fue crónica, durante toda la vida de la abeja. Los ensayos se realizaron por triplicado. Se evaluó la expresión de genes vinculados a la inmunidad mediante qPCR y se analizó la composición de la microbiota intestinal mediante secuenciación del gen ARNr16S. Además, se estimó el consumo diario de alimento y la supervivencia de las abejas. La intoxicación con dosis subletales del glufosinato de amonio generó alteraciones en la microbiota intestinal (aumentando la diversidad □ y alterando la abundancia de especies claves), aumentó la expresión de glucosa oxidasa, proteína asociada a la inmunidad, y redujo significativamente la supervivencia de las abejas. Estos resultados muestran el efecto negativo de este pesticida en la salud de estos insectos, y contribuyen a elucidar los mecanismos vinculados a la despoblación de colmenas.

A15 - Microbiota dynamics in a unique intestinal teleost model: *Chirostoma estor*

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The Mexican pike silverside Chirostoma estor is an atherinopsid fish with an unusual digestive system as they posses a remarkably short intestine (< 0.7 total fish length) for an agastric fish. This characteristic may strongly define the dynamics of the gut microbiota, its specificity and diversity, which could help the host with rapid absorption and digestion of nutrients during the short gut transit times. We have observed that global microbiota diversity depends much of the exterior environment (i.e. wild or culture conditions), however a small microbiota core is always present. Experimental comparisons of gut include 1) fish from their wild habitat, Patzcuaro Lake, Mexico, 2) larvae in culture conditions, 3) juveniles and adults in culture conditions, 4) cultured fish fed with balanced diets supplemented with pre- and probiotics, and 5) cultured juveniles with Ag-nanoparticles (Ag-NP´s) added to the water to assess the potential effects of the latter in the digestive microbiome. Results show that despite there is a high inter-individual variation of gut bacteria at genus level, a succession pattern across the different life stages of the fish can be observed, and also a strong microbiota core. As expected, the diversity of gut microbiota decreases when fish are in culture. Additionally, the use of prebiotics and probiotics as diet supplements changes the gut microbiota diversity, increasing the abundance of certain genera. Finally, AgNP´s applied to the tank water had no significant effects on gut microbiota, further supporting their intended use as a disease control agent.

A16 - First exhaustive gut microbiota Characterization of Neotropical Bees

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Pollinators play an important role in the ecosystems and bees are one of the most important pollinators, especially bumblebees. Gut microbiota often provide beneficial services for their hosts; previous studies have shown that disturbance of social bee gut microbes can alter their health, either by decreasing their ability to digest food or by diminishing protection from parasites that cause diseases. Many species of bumblebees in the temperate zone have a relatively well characterized gut microbiota, however, there are approximately 42 species of Bombus in the neotropics and almost no information on the gut microbiota of these animals is available. Here, we analyzed the gut communities of 36 bumblebees from 4 different Bombus species and one solitary bee (Thygater aethiops) from Cundinamarca, Colombia, through 16S rRNA amplicon sequencing, and verified bee species through COI amplicon sequencing. The gut compositions varied among different species, but our data revealed two different clusters, one dominated by the core microbiome of bumblebees and the other one prevalent dominated by environmental bacteria species. Bombus rubicundus, a native Paramo bumblebee, showed the greatest diversity and abundance of bacterial core, and the one that had the least presence of environmental bacteria. On the other hand, Bombus atratus, a species with greater association with urbanizations and crops, presented more individuals with the enterotype of environmental bacteria; Thygater aethiops had a really low diversity (3 taxa) and even plant material was detected by the amplification of chloroplast 16S rRNA genes. We also found and reported for the first time two different important pathogens in Neotropical bumblebees, Nosema ceranea (Present in: Bombus atratus and B. hortulanus) and Crithidia bombi (B. atratus, B. funebris, and B. hortulanus). This study provides the first comprehensive baseline data on the gut microbial communities of some neotropical bumblebees, informing future ecological research and conservation efforts.

A17 - *Ambystoma altamirani* skin microbiome is highly influenced by host developmental stage and seasonality but not by pathogen presence

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Microbiome contribution to host health and survival it is being increasingly recognized, for instance amphibian skin microbiome contributes to host resistance against the lethal fungal pathogen Batrachochytrium dendrobatidis (Bd) which has caused dramatic population declines of at least 500 amphibian species worldwide. Even though numerous studies demonstrate the influence of several biotic and abiotic factors over diversity and function of the amphibian skin microbiome, it remains unclear how these factors influence skin symbiotic microbial communities on a temporal scale. Here we investigate the influence of seasonality, pathogen presence and host developmental stage over the skin microbiota of the endangered mountain stream siredon Ambystoma altamirani. We generated 16s rRNA gene amplicon libraries from metamorphic and non-metamorphic A. altamirnai along whit environmental samples of stream sediment and water. Sample collection spans four seasons of a whole year from July 2019 to April 2020 at four different locations in Sierra de las Cruces, Mexico. We hypothesized that A. altamirani cutaneous microbiota would a) differ from environmental bacterial communities, b) vary between metamorphosed and non-metamorphosed individuals, c) vary across seasons and, d) be influenced by Bd infection status. We found that cutaneous microbiome is mostly influenced by metamorphosis followed by seasonal temperature variation. Interestingly skin microbiota of metamorphic salamanders seems to be more stable across seasons when compared with non-metamorphic salamanders. Despite high pathogen prevalence the skin microbiota did not differ between infected and non-infected salamanders. Together these results demonstrate that A. altamirani skin microbiota is mainly affected by metamorphosis and seasonality.

A18 - Functional zebrafish microbiome as revealed by global proteomic profiling of control and infected larvae

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The animal microbiome greatly affects physiology and health of its host; however, its contribution to the response towards bacterial pathogens in fish, remains poorly understood. We have previously performed dual proteomic profiling of zebrafish larvae when infected with Pseudomonas aeruginosa PAO1 either by injection or immersion [1]. Here, we have further investigated the contribution of the fish microbiome on this infectious process by using this proteomic approach. Most fish microbiome studies have provided valuable insights into the structure and diversity of the gut microbial community but not regarding their functional composition. Metagenomic studies can solve several of these limitations, however they can only uncover DNA sequences that were present but do not provide any clues regarding their actual expression levels[2]. Consequently, the precise functions of the fish gut microbiome are still largely unknown, thereby complementary approaches are needed to elucidate its functional capacity. Here, by using a metaproteomic approach, we have determined the taxonomic and functional changes of the zebrafish larvae microbiota when infected by P. aeruginosa. First, zebrafish larvae were infected with P. aeruginosa either by injection or immersion as previously described [1]. Global proteomic profiles of infected and control larvae were performed on a Thermo Q-Exactive HF-X Orbitrap mass spectrometer. Lastly, all peptides together with their predicted function and taxa were identified by using the open-source software Unipept[3]. have found that structural and functional dynamics of microbiomes of zebrafish larvae can be revealed by using global proteomic profiling. We found that bacterial taxonomic diversity was greatly reduced in larval microbiomes infected by injection when compared to those infected by immersion. Accordingly, we have also revealed profound changes in microbiome biological processes during infection by injection in contrast with unaltered ontology changes observed by infected larvae by immersion. These contrasting microbiome profiles of infected larvae with different protocols are in agreement with our previous dual proteomic profiles that suggested that during infection by immersion, healthy larvae suffered from a lack of oxygen when exposed to P. aeruginosa [1]. Thus, we propose that metaproteomics analysis using global proteomic profiling of zebrafish larvae is a powerful tool for in vivo host-pathogen-microbiome interaction studies in fish. To our knowledge, this is the first structural and functional analysis of zebrafish larvae using metaproteomics.

A19 - Micrococcales dominate the microbiome in sloths hair and may act as a defense mechanism against bacterial pathogens

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Hair, a characteristic of mammals, presents great variations both in its proportions and functions. In some animals the hair constitutes a complex habitat where diverse collection of both macro- and micro-organisms coexist. In particular, sloths have a dense coat, where a symbiotic relationship with insects, algae, and fungi has been reported. Here, we investigated the bacterial communities that inhabit the hair of two- (Choloepus hoffmani) and three-toed (Bradypus variegatus) sloths and evaluated the presence of antibiotic-producing bacteria. A total of 28 hair samples (taken from the sloth´s back) (15 from two-toed sloth and 13 from three-toed sloth). Scanning Electron Microscopy (SEM) showed that the morphology of both species differs drastically, but were consistent in showing the presence of abundant coccoid- and rod-shaped microorganisms. Amplicon sequencing of the 16S rRNA gene revealed that the communities in both sloths are governed by members of the Actinobacteriota and Firmicutes phyla, and that they share 50% of the core-related phylotypes. Further analysis revealed that Brevibacterium, Kocuria, Staphylococcus, Rubrobacter, Nesterenkonia and Janibacter are the most abundant genera. On the other hand, 56 bacterial isolates were obtained, of which 16% showed antimicrobial activity against common pathogens. All antibiotic-producing strains isolated were classified as either Kocuria, Brevibacterium or Rothia. We propose a new symbiotic association between bacteria of the order Micrococcocales and sloths, which could play a protective role against bacterial infections.

A21 - Characterization of the intestinal microbiome of *Tapirus bairdii* from the Yucatan Peninsula, Mexico

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El tapir centroamericano (Tapirus bairdii) es el mayor mamífero de los bosques tropicales de México, existe en bajas densidades y juega un papel importante en la dinámica de los bosques tropicales a través de los procesos dispersión de semillas de numerosas especies de plantas. Existen diferentes amenazas al hábitat de los tapires (ejemplo, cambio de uso de suelo y sequías intensas). En este estudio, analizamos el microbioma fecal de T. bairdii en la región del sur de México que alberga poblaciones estables de tapires. Se recogieron un total de 47 muestras fecales, 17 en temporada de lluvias (junio a noviembre) y 30 temporada de sequía (diciembre a mayo) de 2017 a 2018. Adicionalmente, se recolectaron dos muestras de un recién nacido que murió al nacer debido a complicaciones y de un individuo enfermo (baja condición corporal), ambos en sitios cercanos al lugar de muestreo durante 2017. Describimos el microbioma mediante una estrategia de secuenciación masiva de la región hipervariable V4 del gen 16S rDNA. Los grupos más dominantes fueron Firmicutes, Bacteroidetes, Proteobacterias, Kiritimatiellaeota y Spirochaetes. Observamos una disbiosis entre las muestras de tapires comparando con la del recién nacido y del enfermo. El microbioma fecal de T. bairdii no presentó diferencias significativas en la diversidad Beta entre la estación lluviosa y la seca. Este estudio es el primer informe sobre el microbioma fecal asociado a T. bairdii. Este estudio sugiere que la estabilidad de la microbiota intestinal de T. bairdii podría estar asociada a los bosques bien conservados y a las tierras comunales circundantes. Este trabajo es una línea de base sobre el microbioma de una especie silvestre que indica el estado de salud de los ecosistemas y la información a través del microbioma representa una herramienta útil para las estrategias de gestión y protección.

A22 - Studying the bacterial diversity of the rumen at high resolution

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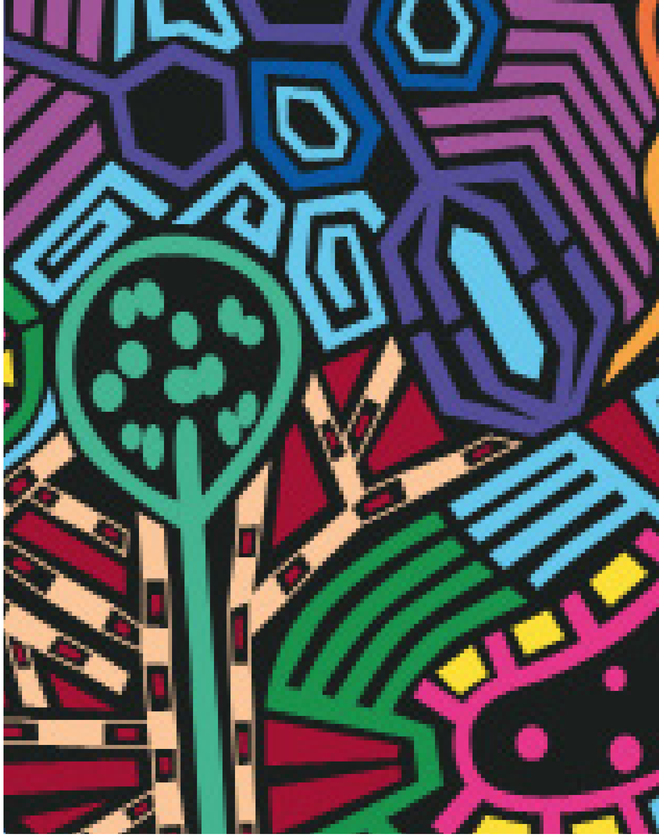
Traditional metabarcoding (16S rRNA gene amplicon) and shotgun sequencing gives different overviews of the most abundant bacteria in complex microbial communities, making difficult to characterize less abundant bacteria, which requires a significantly higher sequencing effort. We aimed to develop a methodology for sample processing that allows the recovery of a larger variety of taxonomic groups in the rumen of cattle, including those that are not dominant, beyond what the traditional methods were capable of. We used a sucrose density gradient, a simple method, that allowed the fractionation of ruminal bacterial communities by cell size and density, into different fractions (5% to 70% w/v). We evaluated the reproducibility of our methodology by comparing the ruminal microbial community of three cows of the Colombian BON breed and a bull of the Holstein breed. The16S rRNA gene amplicon libraries for each fraction of the gradient and animal were sequenced. Some taxonomic groups were enriched in certain fractions of the gradient compared to the total sample of ruminal fluid, which didn't undergo separation by a sucrose gradient. The smallest fractions of the gradient showed an enrichment in small size bacteria like some families of the Bacteriodetes phyla, the Tenericutes phyla and bacterial taxonomic group SCR1. Prevotellaceae and Lachnospiraceae were enriched in the middle fractions of the gradient, while, the families Mogibacteriaceae, Coribacteriaceae, Veillonellaceae and some families of the clostridiales order were enriched in the largest fractions. PERMANOVA analysis showed with statistical significance that there were differences in the composition of the bacteria in the different fractions of the sucrose gradient. We achieved the enrichment of taxonomic groups in sucrose gradient fractions which were not abundant in a conventional DNA extraction. In this way it is possible to deepen in the knowledge of the genome of these microorganisms and their role in the ruminal ecosystem.

POSTER SESSIONS



B

ENVIRONMENTAL EFFECTS ON MICROBIAL COMMUNITIES

B2 - The influence of the Doce river mouth on the microbiome of nearby coastal areas three years after the Fundão Dam failure, Brazil

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The Fundão Dam failure, considered the world's largest mining disaster, released more than 55 million m^3 of ore tailings into the environment. The sediment plume formed by water and tailings spread along approximately 663 km of water bodies of the Doce River basin. It reached the Atlantic Ocean sixteen days after the dam failure. However, the effects of the dam failure in the marine coastal areas years after the disaster are still unknown. This study aims to evaluate water and sediment microbial communities of nearby coastal areas three years after the Fundão Dam failure, using 16S rRNA gene amplicon sequencing. A total of 441 samples from 25 locations along the nearby coastal areas were collected in two different seasons (dry and rainy). The results showed that the Doce River mouth appears to divide the microbial community into stations south and north of the river. The plume of sediments from the Doce River appears to be impacting the marine microbiome even at the sampling stations furthest from the mouth of the river. Anaerolineaceae, Thermodesulfovibrionia, Rhodopirellula, Bathyarchaeia, and Woesearchaeia were among the most abundant bacterial and archaeal taxa in the sediment samples from the Doce River mouth. Their abundances decreased in sediment samples of more distant stations. These microorganisms were previously described in high abundance in heavy metal contaminated sediments, including the Doce River itself and mine tailings sediments. Some of these also have high numbers of heavy metals resistant genes. These results provide strong evidence that the sediment plume released by the Fundão Dam failure is impacting the marine microbiome of nearby coastal areas, even three years after the dam failure. Changes in the microbiome of marine environments can indirectly impact biogeochemical cycles, the health of benthic and planktonic animals, as well as primary production.

B3 - Metagenome-assembled genomes from glacier retreat areas in King George Island, Antarctica

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The Antarctic Peninsula has suffered an increase of 2.5°C in the last 50 years and, because of that, it is one of the areas of most risk of climate change. The environmental crisis that comes from human activities cause glacier and permafrost thawing and changes in the ecosystemic dymanics. In Antarctica, ecosystems are composed mostly by microorganisms, which tolerate extreme conditions. Nevertheless, they are highly sensitive to external disturbance. Metagenomics combined with bioinformatics tools allow us to access full genetic content of an environmental sample and study its taxonomy and metabolism. The aim of this study is to reconstruct genomes and characterize the community compostition and the metabolic potential of soil samples from two glaciers with distict time retraction: Baranowski Glacier (~30 years of retraction) and Collins Glacier (~3500 years of retraction). We reconstructed 36 metagenome-assembled genomes (MAGs) through the anvi'o pipeline, 9 high-quality (>80 completeness, <5% contamination) and 27 medium-quality (>50% completeness, <5% contamination) genomes. The high-quality genomes were selected for functional annotation with softwares Prokka, Metabolishmm, DRAM, GhostKOALA, Patric and Rast. Among our MAGs, we found genes related to the energetic metabolism of carbon (e.g. gapA, ppc, ccoN, pfkA), nitrogen (nasD, nifH, nrfA), methane (mdtA, glyA) and sulfur (sufE, sufS, cysM, cysN, cysO, dmsC). In addition, all the genomes comprised stress and DNA repair genes such as ruvA, ruvB, uvrA, uvrB, uvrC, uvrD, recA, recB, ung, dnaJ and dnaK. We found that these MAGs recruited reads mainly from the Baranowski samples and they all refer to heterotrophic organisms from the Bacteria domain, more specifically from the Cyclobacteriaceae, Saprospiraceae, Chitinophagaceae, Saccharospirillaceae, Xanthomonadaceae and Flavobacteriaceae families. These results are allowing us to characterize metabolic potentials of selected taxonomic groups to better understand the effects of glacial retreats on microbial functioning in Antarctica.

B4 - Bacterial composition and functional genes change according to mercury concentration in the Caquetá River in Colombia Amazon region

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Mercury is considered a toxic metal, whose concentrations are increasing in the Colombian amazon region because of its use in illegal small-scale gold extractions. To explore how mercury concentrations are related to taxonomic and functional diversity on Amazonian ecosystems, we sampled sediments and soils of the margins across a transect of 75 Km of the Caquetá River. We analyzed changes in bacterial community composition using Illumina MiSeq amplicon sequencing and we correlated them with mercury concentration across the transect. Our results suggest that bacterial diversity is related to mercury concentration across the sampled transect of the river and we were able to discriminate taxonomic groups that increase across the mercury gradient. Interestingly, we found that samples with higher concentration of mercury showed higher numbers of the mercury reduction (merA) gene. This work is the first attempt to correlated mercury distribution across Amazonian ecosystem in Colombia with changes in bacterial communities.

B5 - Bacterias acuáticas como indicadores de cambio ambiental en lagos de la Península Fildes (Antártida)

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Las extremas condiciones de oligotrofia que caracterizan a la mayoría de los lagos antárticos, resultan de los bajos aportes de nutrientes y de materia orgánica en sus cuencas. Por lo tanto, son sistemas muy susceptibles a los cambios ambientales y es esperable que las comunidades microbianas respondan rápidamente a los mismos. Pocos estudios existen en la Antártida en donde se haya explorado cuáles son las consecuencias de las variaciones ambientales sobre la diversidad bacteriana. Esto resulta fundamental, ya que dicho continente presenta regiones con alta actividad humana asociadas a las bases científicas y que se ha demostrado su impacto sobre el ecosistema. La Península Fildes (Isla Rey Jorge, Península Antártica) constituye una de estas regiones, además de localizarse en un área con una gran influencia del calentamiento global. En este trabajo, se analizó la diversidad bacteriana de siete lagos de la Península Fildes, relacionándola con el impacto antropogénico según su cercanía a las bases de investigación. Para esto, se tomaron muestras de agua en dos momentos: cuando los lagos estaban congelados y cuando el hielo estaba ausente. En cada lago se midieron variables ambientales (temperatura, pH y conductividad) y se colectaron muestras de agua superficial para extracción de ADN y secuenciación masiva del gen ribosomal 16s. Se encontró que la estructura de las comunidades bacterianas era diferente según los lagos tuvieran o no cobertura de hielo. Además, se observó un efecto significativo del ambiente sobre las comunidades bacterianas en los lagos no congelados, indicando que el ingreso de materia orgánica, nutrientes y contaminantes determina la estructura comunitaria. Los resultados sugieren que el cambio climático junto con la presencia humana condicionan la diversidad bacteriana y el funcionamiento ecosistémico de los lagos en la Península Fildes, algunos de los cuales ya muestran cierto grado de degradación opacando su sensibilidad ambiental.

B6 - Estudio de condicionantes urbanos y ambientales sobre la ocurrencia de patógenos microbianos en una red hidrológica de arroyos con un elevado grado de contaminación

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La presencia de patógenos en aguas superficiales es una problemática ambiental y sanitaria, siendo las enfermedades de transmisión por agua una de las principales causales de morbilidad en países en desarrollo. Complementariamente, las cuencas urbanas integran factores socio-ecológico-tecnológicos que interaccionan con la comunidad microbiana. Con el objetivo de analizar la influencia de la infraestructura urbana y el microhábitat sobre la distribución de patógenos, se establecieron 14 sitios de muestreo sobre una red de arroyos predominantemente urbana del Área Metropolitana de Buenos Aires, en los que se cuantificaron aspectos de infraestructura hidráulica y conectividad (drenaje superficial, superficie impermeabilizada, densidad caminos) y sanitaria (cloacas y agua potable, pozos sépticos) en áreas de 500m radiales, se midieron parámetros ambientales locales del cauce (hidráulicos, fisicoquímicos, cobertura de macrófitas) y se obtuvieron muestras del bacterioplancton. Se comparó la identidad de las secuencias 16S asignadas a géneros potencialmente patógenos con secuencias de referencia de especies patógenas mediante BlastN. El 10.0% de las secuencias totales se asignó a géneros potencialmente patógenos y el 6.7% a especies patógenas (identidad > 99%). La riqueza de variantes asignadas a especies patógenas correlacionó positivamente con la abundancia de E. coli y la población citométrica de bacterias con alto contenido de ácidos nucleicos (HNA) (Pearson, $p < 0.05$). Un análisis de partición de la varianza evidenció que la riqueza es explicada 30% por factores ambientales locales (velocidad de corriente, nitrógeno inorgánico disuelto y turbidez) y 21% por factores de infraestructura urbana (densidad de cloacas y pozos sépticos) espacialmente estructurados. Los resultados sugieren una influencia importante del microhábitat ecológico sobre la riqueza de patógenos, en los que fenómenos como la resuspensión de sedimentos y la persistencia ambiental favorecida por entornos ricos en nutrientes facilitarían su coocurrencia junto a bacterias metabólicamente activas (HNA), así como también del esperable aporte de las condiciones de infraestructura sanitaria.

B7 - Análisis de ocurrencia de filotipos tras la exposición a metales pesados en enriquecimientos de una muestra ambiental del Río Agrio, Argentina

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La búsqueda de indicadores biológicos que pudieran alertar tempranamente la presencia de contaminantes en ambientes acuáticos resulta interesante como herramienta de diagnóstico y monitoreo ecológico. A diferencia de los macroorganismos indicadores, los microorganismos ofrecen las ventajas de responder más rápidamente a los cambios ambientales, dada su elevada velocidad de reproducción, y de requerir un muestreo más sencillo y de menor impacto. En ese sentido, estudiar la respuesta de diferentes microorganismos ante la presencia de contaminantes permite identificar taxones candidatos para ser utilizados como indicadores. En este trabajo, se analizó la ocurrencia de distintos filotipos tras la exposición a metales pesados en cultivos en batch. Una muestra ambiental del Río Agrio, Neuquén, Argentina, fue enriquecida favorenciendo tres metabolismos: neutrófilos organótrofos, acidófilos Fe/S oxidantes, y neutrófilos anaerobios. Los cultivos fueron expuestos a altas concentraciones (hasta 400 mM) de cinco metales pesados (Cd, Co, Cu, Ni y Zn). Muestras de ADN de todos los enriquecimientos (expuestos y no expuestos) fueron secuencidas en la región V4-V5 del gen 16S ARNr por metabarcoding. Las secuencias fueron analizadas siguiendo el protocolo de variantes de secuencias de amplicón y clasificadas según la base de datos de SILVA. Se analizó la abundancia y prevalencia de los filotipos a distintos niveles taxonómicos haciendo foco en aquellos que tuvieran comportamiento diferencial en los cultivos expuestos respecto a los no expuestos a metales. Entre ellos, se resalta que el dominio Arquea se encontró en menor abundancia o ausente en los cultivos expuestos; el mismo comportamiento se observó para los filos Caldisérica y Spirochaetes y para varios géneros. En cambio, sólo se encontraron los géneros Cellulomonas y Desulforhopalus en los cultivos expuestos. Un estudio más profundo y desarrollado sobre estos filotipos está planeado para analizar sus potenciales como indicadores biológicos frente a la contaminación metálica.

B8 - Association of gram-negative bacilli harboring extended-spectrum beta lactamases with fecal contamination in waters from an urban tropical estuary

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Gram-negative bacilli producing extended-spectrum β-lactamases (ESBL) is a global health problem that can have water matrices as hotspots for its dissemination, leading to human, animal, and environmental health risks. We aimed to investigate theoccurrence and distribution of these bacteria in Guanabara Bay (GB) waters, a heavily polluted and tourist tropical estuary in Rio de Janeiro, Brazil, over 12 consecutive months, verifying its association with fecal indicators. Subsurface (1 m depth) and bottom (6-20 m depth) water samples were collected monthly from Sep/2018 to Aug/2019 at three points with pollution gradient inside GB.Potential ESBL-producers were recovered from 72 water samples in agar marine and chromogenic medium (CHROMagar) supplemented with ceftriaxone (8 µg.mL-1) and amphotericin B (1 µg.mL-1). Strains were identified by MALDI-TOF MS. Gram-negative bacilli were characterized for ESBL phenotype and genotype by disc-approximation and PCR, respectively. Fecal indicator counts (MPN.100mL-1), thermotolerant coliforms (TC) and Escherichia coli (EC), were recorded from sampling points. Over 12 months, 1,558 colony-forming units were isolated and 668 (66.9%) were identified as: Enterobacterales (89), non-Enterobacterales gram-negative bacilli (245), and other microorganisms (334). Among the gram-negative bacilli, of 124 strainstested for ESBL production, 67 (54.0%) were positive. ESBL-producersbelonged to Escherichia (29), Aeromonas (16), Acinetobacter (12), Citrobacter (7), Enterobacter (2), and Pseudomonas (1), which were isolated specially from GB34 subsurface (37). Search for ESBL-coding genes detected blaCTX-M-14 (10), blaCTX-M-1,2 (9), blaTEM (5), and blaCTX-M-8 (1). The average of fecal indicators varied of the highest in GB34 subsurface (1.4 x 105 and 1.3 x 105 of TC and EC, respectively) to minor in GB1 bottom (2.7 x 101 and 2.2 x 101). Significant correlations were observed among ESBL-producers and EC (r=0.8633, p=0.0268) and TC (r=0.8671, p=0.0253). Thus, the occurrence and distribution of ESBL-producing gram-negative bacilli in GB waters is likely related to sewage contamination.

B10 - Study of bacterial diversity for bioprospecting on Calakmul wetlands using comparative genomics and metagenomics

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The wetlands from the Calakmul Biosphere Reserve that can be temporary or permanent, are an interesting ecosystem to compare microbial populations in different conditions; those that have remained flooded for a long time and those that behave in a cyclical way depending on the rainy and dry season, being an opportunity to study the impact of climate change on microbial populations. We take samples of sediments of three cyclic wetlands (flooded and dry) and performed conventional isolation in different semi-selective media for Actinobateria, since they are known as prolific producers of secondary metabolites. We are interested in bioprospecting of bacterial to address mainly agricultural problems, to achieve this, antagonistic interactions were carried out against five phytopathogenic fungi using the isolated actinobacteria. Some of these actinobacteria were found to inhibit the growth of three phytopatogenic fungi. To explore the genetic determinants and the genomic potential of actinobacteria from the wetlands of Calakmul, the complete genomes were sequenced. Using mining of genomes and comparing with other previously reported actinobacteria genomes, we found biosynthetic gene clusters (BGC) of siderophores which have been associated with fungi inhibition as well as other new BGC that should be studied. Sequencing of 16s rRNA amplicons revealed the bacterial genetic potential in these undisturbed sites where phyla of Acidobacteria, Actinobacteria, Proteobacteria, and Bacteroidetes represent the highest percentage of 16s RNA sequences, this composition of heterotrophs is typical of tropical forest soils, given the large amount of organic matter they present and the consequent acidity of the soil. The Crenarchaeota and Euryarchaeota are the most represented groups of archaea in the three sites. However, in flooded sites, phyla such as Chloroflexi are observed, a photoautotroph involved in carbon fixation and Methylomirabiota involved in anaerobic methane oxidation with nitrite reduction in anoxic environments. This study was exploratory to show the microbial diversity of wetlands and will help to propose microbial indicators that could be useful to detect degradation in wetlands at an early-stage.

B11 - Diversidade de *Aureobasidium* spp. em bromélias de umaregião semiárida no Nordeste do Brasil

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O gênero Aureobasidium (Ordem: Dothideales, Família: Dothioraceae) é conhecido por sua produção de melanina, seu potencial biotecnológico e por combater fitopatógenos. São comumente associados ao filoplano de plantas. A partir de 21 amostras de folhas de bromélias coletadas na Caatinga do estado de Alagoas, nordeste brasileiro, avaliou-se a diversidade deste gênero. Os pontos de amostragem foram (i) Serra da Caiçara, município de Maravilha, e (ii) Reserva Tocaia, município de Santana do Ipanema. As folhas foram lavadas com solução de Tween 20 0,5% e o produto foi semeado em Ágar YM suplementado com 0,04% de cloranfenicol (pH 4,0). A identificação molecular dos isolados foi realizada por meio do sequenciamento da região D1/D2 26S rRNA. Em seis coletas, foram obtidos 28 isolados distribuídos em 4 espécies: A. melanogenum, A. namibiae, A. pullulans e A. thailandense. As maiores ocorrências foram de A. melanogenum e A. thailandense. Entretanto, houve diferença entre os locais de amostragem. Em (i) A. melanogenum teve ocorrência de 83% e em (ii) 11%, enquanto que A. thailandense apresentou em (i) 34% e em (ii) 100%. O ponto (i) é predominantemente arbustivo, com altitude máxima superior a 800m e submetido à irradiação solar intensa, o que pode ser um fator de seleção para A. melanogenum que produz melanina em abundância, conferindo resistência ao estresse oxidativo. No ponto (ii) constata-se a presença de uma vegetação mais arbórea. A espécie A. thailandense produz exopolissacarídeos, e possui um grande potencial assimilativo de fontes de carbono e matéria orgânica advindas do ambiente, podendo explicar sua frequência de ocorrência. A abundância de Aureobasidium pode ser facilitada por suas características que conferem melhor adaptação ao ambiente, possibilitando a presença de espécies do gênero em ecossistemas semiáridos. Assim, além de alta diversidade, esse tipo de ecossistema pode ser uma fonte promissora de recursos biotecnológicos.

B12 - Recambio del ensamblaje de myxomycetes a lo largo de un gradiente altitudinal y de humedad en Costa Rica

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Los myxomycetes son protozoos fagotróficos, que han sido reportados en gran diversidad de biomas del mundo. Sin embargo, el estudio de estos microorganismos es relativamente escaso en el Neotrópico. Estudios previos han mostrado que la formación de sus estructuras reproductivas depende de factores ambientales como la humedad y la temperatura; estos últimos suelen presentar grandes fluctuaciones en las regiones tropicales, al estar estrechamente ligados a los cambios altitudinales. Pero se desconoce el efecto que pueda tener la variación de estos factores ambientales sobre los ensamblajes de myxomycetes en escalas espaciales pequeñas, como las que ocurren a lo largo de gradientes altitudinales, en contraste, con variaciones de factores a gran escala asociadas a la latitud, que han sido más estudiadas para los myxomycetes. Por lo tanto, en este estudio se analizaron los cambios, a lo largo de dos años consecutivos, en el ensamblaje de myxomycetes en tres tipos de bosques dentro la provincia de Guanacaste en Costa Rica, que representan un gradiente altitudinal y climático. Utilizando análisis de componentes, se encontró una clara diferencia en los ensamblajes de myxomycetes a lo largo del gradiente analizado, con una mayor riqueza de especies en los ambientes más secos. Adicionalmente, el patrón indicó una distribución temporal que diferencia las muestras de un año a otro. Usando una escala de abundancia, separamos las especies en categorías de rareza y, observamos patrones contrastantes: mientras las categorías más abundantes presentaron cambios claros en abundancia a lo largo del gradiente estudiado, las más raras presentaron pérdida y emergencia de diferentes especies. Los datos demuestran el recambio de especies a lo largo del gradiente altitudinal en el Neotrópico, asociado con las fluctuaciones en temperatura y humedad. Nuestro estudio ofrece una base para la evaluación de las presiones ecológicas generadas sobre la biodiversidad, por ejemplo, con el cambio climático.

B13 - Microbial dynamics in an engineered sulfate reducing environment during the bioprecipitation of copper and zinc

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Microbial dynamics is an important topic to assess during metals bioprecipitation mediated by sulfate-reducing bacteria (SRB) to treat acid rock drainage (ARD). The presence of sulfate as an electron acceptor promotes competition between SRB and methanogenic archaea, and influences the diversity and structure of the microbial communities. The purpose of this study was to evaluate the changes in the microbial composition in a sulfate-reducing bioreactor provided with a limestone pre-column for 375 days. The system was fed with synthetic ARD using acetate as electron donor, and Cu(II) and Zn(II), each one in concentration of 15 mg L-1. Operational parameters were periodically monitored, pH was raised to 7.5 and high removal efficiencies of metals were obtained with values of 96.8-99.8% and 99.9% for Cu (II) and Zn (II), respectively. 16S rRNA genes were sequenced in six bioreactor-sludge samples. Alpha and beta diversities decreased over time with the bioreactor operation. The methanogen Methanosarcina spp, was the most abundant amplicon sequence variant (ASV); however, sulfidogenesis was the process dominant and methanogenesis was not observed. SRBs abundance remained stable. ASVs belonging to Desulfobacteraceae, Desulfocurvus, Desulfobulbaceae and Desulfovibrio became more abundant, while Desulfuromonadales, Desulfotomaculum and Desulfobacca decreased. Syntrophic bacteria Geobacter and Syntrophobacter were enriched along the bioreactor operation time. At beginning, ASVs with relative abundance < 2% represented 65% of the microbial community and 21% at the end of the study period, with the remaining fraction corresponding to eight dominant taxa. Thus, the results show that the microbial community gradually lost diversity; however, the metals bioprecipitation process was not affected. These findings prove new insights to understand the metabolism and the functionality of microbial populations involved in sulfate reducing process.

B14 - Diversidad de arqueas metanogénicas en sedimentos lacustres antárticos y efecto de la temperatura sobre la actividad potencial

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El cambio climático tiene el potencial de aumentar las emisiones de metano en regiones polares por el derretimiento de los hielos superficiales, dado que quedan al descubierto vastas superficies cuya materia orgánica puede ser convertida a metano. Esto a su vez induciría un mayor cambio climático, provocando una retroalimentación positiva. Dado que se pronostica un aumento de temperatura en las zonas polares para los próximos cien años, es de gran interés obtener información del comportamiento de las arqueas metanogénicas con la temperatura, ya que se podría esperar una mayor emisión de metano ocasionado tanto por el deshielo como por la mayor actividad. En este trabajo se analizó la diversidad de Archaea y se evaluó el efecto de la temperatura (5–20°C) sobre la velocidad de producción de metano a partir de acetato e H2/CO2 en sedimentos de lagos de agua dulce (Isla Rey Jorge, Shetland del Sur, Antártida). Mediante ensayos en microcosmos se determinó que a 20°C hay una máxima producción de metano (0,74–91 µmoles de CH4·d-1·g-1). Se observó también que en la mayoría de los lagos de 5–15°C la vía predominante es la acetoclástica pero a 20°C la mayor producción de metano se obtuvo a partir de H2/CO2. Se cuantificó la población de arqueas metanogénicas a través del gen mcrA mediante qPCR y se obtuvieron valores de hasta 2.8x104 copias/ng ADN. El análisis de la diversidad microbiana por secuenciación masiva (Illumina MiSeq) del gen 16S ARNr, mostró que estos sedimentos están dominados por arqueas metanogénicas, siendo Methanosaeta el género más abundante, seguido por los Methanosarcina, Methanoregula y Methanosphaerula. En conclusión, estos lagos podrían ser un reservorio potencial de emisión de metano, donde la temperatura tiene un efecto crucial. Estos hallazgos aportan al conocimiento de los procesos de producción de metano en la Antártida en un clima cambiante.

B15 - Effect of Hydrogeochemistry on Microbial Communities in Hot Springs from Geothermal Areas

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Microbial life can thrive under extreme conditions in terrestrial hot springs. Many efforts have been made to understand the effect of environmental factors on the microbial communities inhabiting these ecosystems. Water temperature and pH have been shown to have a strong control on microbial communities from specific geothermal areas. Despite the fact that the physicochemical properties of water result from subsurface hydrogeochemical processes, the effect of subsurface geochemical events on microbial life has been ignored. Therefore, this research attempts to elucidate the influence and correlation of thermal hydrochemistry with microbial communities inhabiting hydrothermal ecosystems worldwide. New sequencing of 16S rRNA amplicons from 11 hot springs from the El Tatio geothermal field (Chile) were analyzed along with 154 other hot springs 16S amplicons from 3 previous studies including 13 geothermal fields from Taupo Volcanic Zone (New Zealand), Eastern Tibetan Plateau (China) and Yellowstone National Park (United States of America). PERMANOVA results demonstrate that microbial community structure strongly depends on the geothermal field. Despite that, distance decay analysis shows phylogenetic similarities of the microbial communities from different areas. In terms of hydrochemistry, the best fit for the community structure is given by pH, Mg, and SO4 concentrations. This suggests that there are microbial communities whose ecological niche is mainly determined by these parameters and makes them different from the rest. Hydrothermal processes as mixing with volcanic fluids, boiling and steam separation could be associated with this niche. Furthermore, HCO3, Si concentrations and temperature also shows a significative effect on the microbial community composition. Overall, the results suggest that there are more factors than temperature and pH that modulate the microbial communities in these extreme environments, which raise questions about the diverse metabolisms they use to take advantage of locally specific geochemistry.

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B16 - Comparative genomics in the Genus *Brevibacterium*

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Introduction: Brevibacterium strains have been isolated from several habitats, mostly from milk products, but also from soil, clinical, and marine environments. From this study, the strain Brevibacterium sp. H-BE7 was isolated from marine sediments from a fjord in Nothern Patagonia, Chile. This strain possesses the ability to grow in culture medium with up to 10% w/v of NaCl, has high lipase activity, and presents antibacterial activity against S. enterica and L. monocytogenes. Evaluate the novelty of strain H-BE7 and niche-specific features from marine-derived Brevibacterium. Strain H-BE7´s genome was sequenced using Illumina and Nanopore. To compare strain H-BE7 to other Brevibacterium, 117 genomes were downloaded and a phylogenomic tree was constructed, later a pangenome analysis was evaluated using anvi'o pipeline. Taking into consideration niche and clade specificity, the presence of lipases was evaluated. Finally, the Biosynthetic Gene Clusters (BGCs) of each strain were compared using similarity networks. After genome quality assessment, 75 strains were considered for further analysis. The phylogenomic tree showed that all strains could be placed into four major clades. The pangenomic study revealed the presence of the core genome of Brevibacterium was approximately 5% of all the gene clusters, and singletons a 30%. Despite a bigger number of gene functions are enriched by clade specificity, some niche-specific functions could be observed. The presence of lipases displayed clade-specific features, where all lipases were present in only two phylogenomic clades. From BGCs networks, BGCs were grouped into Gene Cluster Families (GCFs). Some GCFs were clade-specific, and none niche-specific. Additionally, few families grouped with BGCs with known products. This study shows that every Brevibacterium presents unique features and uncharacterized BGCs. The biotechnological potential is enhanced when attention is drawn to strains from different environments, and Brevibacterium sp. H-BE7 displays the capacity for antibiotic discovery and food engineering.

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B17 - Estudio de la actividad degradadora anaeróbica de hidrocarburos en sedimentos de agua dulce con hidrocarburos

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En ambientes acuáticos contaminados, la degradación microbiológica de hidrocarburos ocurre simultáneamente mediante metabolismo aeróbico y anaeróbico. La ruta anaeróbica de degradación más estudiada inicia con la acción de la bencil succinato sintasa (bssA), enzima que adiciona un fumarato al hidrocarburo aromático y mediante pasos sucesivos se convierte en benzoilCoA. Este intermediario principal del catabolismo entra a □-oxidación por la acción final de la 6-oxociclohex-1-ene-1-carbonilCoA hidrolasa (bamA). Con el objetivo de evaluar la expresión de los genes biomarcadores bssA y bamA en sedimentos de agua dulce impactados con hidrocarburos, se extrajo ADN a 36 muestras de diferentes profundidades, se secuenció la región V4 del gen 16S rRNA por Illumina-Miseq. A través del software PICRUSt pudo predecirse in silico la presencia del gen bamA en todos los horizontes y, en algunos de ellos el gen bssA. La presencia y abundancia de estos genes predichos, fue evaluada y cuantificada por qPCR, encontrando diferencias significativas entre el número de copias de los genes bamA/ng ADN y bssA/ng de ADN en las muestras superficiales con respecto a las profundas ($p<0.05$). Los resultados de la cuantificación de los genes biomarcadores y del gen 16S rRNA, la asignación taxonómica, las variables fisicoquímicas y los recuentos microbiológicos determinados a las muestras se utilizaron en un análisis multivariante. Éste sugirió que los sedimentos superficiales están enriquecidos, en relación con los no superficiales, con bacterias anaeróbicas y sulfato reductoras, con predominio de las clases Deltaproteobacteria y Anaerolineae. Consecuentemente, se extrajo ARN de las muestras superficiales y se evaluó la presencia de transcriptos de bamA y bssA por RT-qPCR, encontrando expresión de ambos genes en la mayoría de estas muestras. La cuantificación de los genes y transcriptos de estos biomarcadores resultan una clara evidencia de la participación de las rutas de degradación anaeróbica de hidrocarburos en la recuperación natural del sitio.

B18 - Effect of Hurricane María on Fungal Communities in Water-Exposed Homes in San Juan, Puerto Rico

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The extensive flooding caused by Hurricane María in Puerto Rico (PR) caused an increase in humidity levels and exposed organic materials, both conditions which favor indoor fungal proliferation. This represents a public health concern since environmental fungal contamination is associated with exacerbation of asthma, allergic rhinitis and respiratory distress. We aimed to characterize airborne fungal populations present in homes classified by different degrees of water exposure using culture-based methods. The MicroBio MB2 Air Sampler was used to collect air samples from 50 homes located in a neighborhood in San Juan, PR, 12 and 22 months after Hurricane María. Occupant's self-report data was used to classify the homes as flooded, water-damaged, or dry. Fungal taxa abundance, composition and diversity was analyzed via adaptation of molecular analytical tools in the MicrobiomeAnalyst. We found significant differences in beta diversity in fungal composition by self-reported degree of water exposure during the first sampling period ($p\text{-value} < 0.001$), however, there were no significant differences in alpha diversity. Higher abundance of Aspergillus was associated with the indoor environment of flooded homes compared to the outdoor control during the first sampling period (FDR-adjusted $p\text{-value} = 0.05$). During the second sampling period, both indoor and outdoor environments were characterized by non-sporulating fungi, most likely Basidiomycetes, regardless of the degree of water-damage in the sampled homes. Our data highlights the dynamic changes in indoor fungal populations after Hurricane Maria, characterized by different types of fungi between dry and flooded homes. However, two years after the event the indoor fungal population mirrored that of the outdoors. These findings are helpful for the development of environmental mitigation strategies that could impact the elaboration of guidelines for post-flood recovery efforts in tropical environments that will positively impact the respiratory health in hurricane impacted areas.

B19 - Ecological and evolutionary correlation of *amo* genes

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Nitrification is a ubiquitous process that is indispensable for nitrogen cycling. The canonical pathway includes two phases: ammonia oxidation to nitrite and nitrite oxidation to nitrate, although ammonia oxidation is critical for the whole oxidative mechanism. The first step is carried out by an ammonia monooxygenase coded in amo genes. Between amo genes, amoA is commonly used as a molecular marker for identification, quantification, and phylogenetic surveys. In the current work, ammonia oxidizers were identified from the SILVA database and then selected those with reference genomes for this study. A total of 41 genomes were selected, including archaeal and bacterial (including comammox) species. Besides, a database was developed with their corresponding environmental and cellular info. The amoA, amoB, and amoC genes were extracted from genomes and aligned independently for phylogenetic inferences. A Neighbor-Joining tree was generated using observed differences with amoA sequences, to correlate the primary structure of AMO with environmental factors in a broad sense. We identified five clusters (two for Archaea and three for Bacteria), however, only two correlated totally with the habitat and another one partially. Optimum growing temperature presented a positive correlation with most clusters, meanwhile, pH and motility do not correlate with them. Other parameters like energy production pathway, carbon source, urea growing, or the presence of nirK genes also correlated with some clusters. Afterward, it was built a Maximum Likelihood tree using the sequences from the complete amoABC cluster. The integration of all amo genes generates a more comprehensive phylogenetical approach that was complemented with cellular data (such as genomic organization), improving the previous correlation with environmental factors. From eight new clusters, seven were well-defined evolutionary and ecologically, and just one still unclear. This new holistic analysis of amo genes contributes to clarify the biology of ammonia oxidizers from an ecological and evolutionary approach.

B20 - Comunidades bacterianas en aerosoles ambientales en granjas de pollos Broiler

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Los pollos de engorde están sometidos a aerosoles que han sido escasamente estudiados. Nuestro objetivo fue caracterizar la ecología bacteriana en suspensión (aerosoles) en dos galpones tipo túnel y un bioterio (ambiente control), considerando muestreos al inicio, mitad y final (tiempo 1, 2 y 3) del ciclo productivo. Utilizando un aero-colector de impacto, se realizó recuento de bacterias viables totales y coliformes (UFC/m3) y se secuenció el gen 16SrDNA completo (PacBio-Sequel) a partir de aire impactado sobre papel filtro.

Los resultados mostraron disminución del recuento de coliformes en galpones a lo largo del estudio. Librerías de 16S indicaron un predominio de Firmicutes, particularmente de la clase Bacilli, en todas las condiciones. Se observó un porcentaje importante de OPUs (Operational Taxonomic Units) sin filiación taxonómica a nivel familia, género y especie, que corresponderían a nuevas taxones. Se observó una gran diversidad en todas la muestras, con predominio de Streptococcus alactolyticus y Escherichia coli/Shigella en bioterio en todos los tiempos. En galpones, Erysipelatoclostridium spiroforme predominó en el tiempo 1 y Brachybacterium paraconglomeratum en tiempos 2 y 3. Análisis de beta diversidad evidencian diferencias asociadas al tipo de confinamiento y etapa del ciclo productivo. Destaca un incremento en el número de coliformes cultivables y un mayor número de lecturas 16S obtenidas en uno de los dos galpones analizados a tiempo 2, posiblemente asociado al manejo “volteo de cama”, sin observarse cambios en la estructura microbiana.

Estos resultados indican una comunidad microbiana predecible, asociada principalmente a Firmicutes, donde el manejo “volteo de cama”, que de forma mecánica airea el sustrato de viruta sobre el cual viven las aves, generaría un cambio en la cantidad absoluta de aerosoles muestreados. Estudios de este tipo cobran importancia a la hora de analizar el impacto del ambiente sobre la salud de las aves de producción.

B21 - A multidimensional approach in modulating mammal exclosure to determine plant-microbial interactions and greenhouse gas emissions in the Atlantic Forest

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Recent studies from the Atlantic Forest in Brazil, one of the world's most endangered tropical forests, have demonstrated that this hyper-diverse ecosystem has also undergone a historical process of loss and reductions of fauna (i.e., defaunation) and trophic downgrading. To determine how defaunation of medium and large mammal herbivores influences above- and below-ground forest soil processes, we used a 10-year replicated paired control-exclusion experiment where a large mammal frugivore, the white-lipped peccary, is naturally present. Inside 12 pairs of control-exclusion plots, we measured soil emissions of greenhouse gases and collected soil to assess diversity of the microbial community involved in the nutrient cycling (N, P, and C) in these native forest soils. We also identified and counted all seedlings >1 m in height within each plot. We observed that microbial diversity varied depending on the abundance and richness of seedlings which differed significantly between control and exclusion plots. The exclosure plots (2.2 µg N-N2O m-2 h-1) seem to be a larger source of N2O fluxes while the control (with fauna) plots (0.3 µg N-N2O m-2 h-1) are not. Also, N2O fluxes at exclosure plots were mainly supported by denitrification in association with higher soil N-NO3. This study highlights the importance of frugivores in regulating plant diversity and concurrently the microbial diversity and their roles in soil nutrient dynamics, one key point for understanding and avoiding further forest degradation.

Support: FAPESP, CNPq

B23 - Biomasa microbiana y respiración basal en turba de humedales de alta montaña en la cuenca alta del Río Claro, macizo volcánico Ruiz-Tolima, Colombia

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Una proporción importante de los ecosistemas de alta montaña en Colombia incluye sistemas de turberas, un tipo de humedal que provee servicios de regulación del ciclo hidrológico, protección de la biodiversidad y regulación del ciclo del carbono. Estos ambientes han sido tradicionalmente considerados reservorios de grandes cantidades de carbono debido a los procesos de deposición y estabilización de materia orgánica, pero con las nuevas condiciones que está generando el cambio climático se cree que podrían convertirse en fuentes de emisión de gases de efecto invernadero. Las variables que definen el estado de emisión o captura de carbono en un ecosistema son principalmente microbianas, impulsadas por factores hidroclimatológicos del medio y fisicoquímicos del sustrato. El presente estudio es un acercamiento a las variables de actividad microbiana de manera indirecta como un primer paso para estimar el estado y el potencial de emisión de gases de efecto invernadero en tres turberas de alta montaña, ubicadas en la zona de nacimiento del río Claro, en el macizo volcánico Ruiz-Tolima, Colombia. Se determinan las características fisicoquímicas e hidroclimatológicas que definen cada sitio y se aplican ensayos de actividad microbiana: biomasa microbiana por el método de espectrofotometría en solución por fumigación con fenol-cloroformo como medida de la biomasa de todos los microorganismos vivos en un sustrato; y respiración basal por titulación de hidróxido de sodio expuesto a los productos gaseosos de la incubación del sustrato, como medida del potencial catabólico de los microorganismos heterotróficos en el sustrato. Los resultados parecen indicar una baja disponibilidad de materia orgánica, una baja actividad metabólica y una reducción en la eficiencia metabólica a mayor altitud, indicando un bajo potencial de emisión al momento del estudio para 2 de los 3 sitios muestreados.

B25 - *In silico* analysis for identification of microbial profiles linked to potential Chromium (VI) remediation

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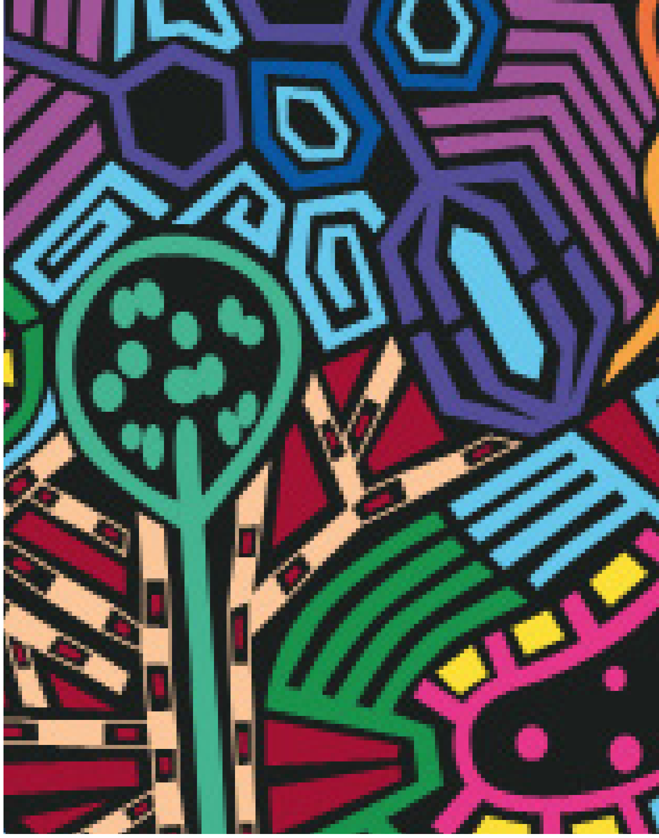
Chromium (VI) generates a negative impact on the environment and human health due to its mutagenic and recalcitrant nature. In Colombia, tanneries are the main source of discharge of this pollutant into rivers. The integration of tools such as bioinformatics and machine learning can contribute to the bioremediation of chromium (VI) in water and soils. The objective of this work was to identify functional and taxonomic profiles of microbial communities in rivers contaminated with chromium (VI). We collected metagenomic data from microbial communities in rivers contaminated with chromium (VI) and of chromium-remediating microorganisms using the NCBI and MGRast. The microbial profiles at functional and taxonomic levels were identified using applications available in Kbase. From 50 datasets, 71.2% were 16S rRNA amplicon sequences, 17.3% metagenomes, 7.7% clone libraries, 1.9% 18S rRNA amplicon sequences, and 1.5% proteins sequences. Based on differential abundance analysis, we identified Bacillus sp., Halomonas sp. and Comamonas sp. as the dominant microbial groups in environments polluted with chromium (VI). This bacterium has been linked to the ability to bioremediate heavy metals and hydrocarbons. We also found that most of the sequences from the databases analysed are classified into the phylum Proteobacteria, Firmicutes, Bacteroidetes. Functional profiles suggest diverse enzymes as possible mechanism of microbial adaptation to rivers contaminated with chromium (VI). The most representative features in the functional profiles include sequences annotated as reductases, oxidoreductases and sequences from genes associated to degradation of polyphenols. This work was the first step to design an algorithm for the identification of microbial communities that could be used in bioremediation applications. Results from the algorithm could give an insight in to the mechanism for high tolerance to heavy metals at a microbial community level.

POSTER SESSIONS



C

PHAGES AND VIRUSES

C1 - The efficacy and evolution of phage therapy in model cystic fibrosis lung environment

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The rise of antimicrobial resistance in recent years has led to urgent need for novel therapeutic approaches. Phage therapy, the use of bacterial viruses (phages) as antimicrobials, has the potential to replace or complement current antibiotic treatments. Nonetheless, knowledge on phage-bacteria interactions in the clinical context is limited, and most of the studies on this area have been conducted using simplified lab media. Particularly, it is still unclear how rapidly resistance to phages arise in such environments. Here, an experimental evolution approach was used to study the effects of lytic phage 14/1 on Pseudomonas aeruginosa PAO1 population density and evolutionary dynamics using a synthetic cystic fibrosis medium (SCFM). Bacterial density dynamics and fitness assays revealed that although phages were able to reduce bacterial density in the media mimicking the CF lung environment, phage resistance rapidly evolved during the experiment. Phenotypically, resistance was associated with clear aggregation of bacterial cells in the media and non-mucoid colony morphology. It was also found that phages were able to coevolve, displaying arms race dynamics as the infectivity of phages and bacterial resistance escalated over time. These results provide valuable insights on the potential limitations of phage therapy and the evolutionary interactions of P. aeruginosa and phage 14/1 in a nutritional environment resembling the CF lung. However, as bacteria rapidly evolve resistance to phages, a bacteriophage-based approach by itself is unlikely to offer a solution to antimicrobial resistance. Therefore, further research on ways to enhance phage therapy to overcome resistance evolution is imperative.

C2 - Search for phages and prophages in the rhizosphere of common bean *(Phaseolus vulgaris)*

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The plant rhizosphere provides an ecological niche for the growth of an ample diversity of microbes. In this work, we look for phage genomes in metagenomic samples of the rhizosphere of the common bean (Phaseolus vulgaris). We analyze eleven metagenomic samples obtained from the rhizosphere of common bean in agriculture conditions. Using the sequence readings, we did metagenome assemblies with Meta-Spades and MEGAHIT. Assembled contigs with Meta-Spades were, in general, higher in length than with MEGAHIT. Contigs higher than 1 kb were used to perform phage and prophage search using VirSorter and Vibrant. While Vibrant recover large contigs with the highest scores to contain complete phages, VirSorter showed more fragmentation in the predictions. According to Vibrant, there was quite a few phages (about 6,497) fragments unassembled and a total of 153 complete circular phages. A fraction of 31 lytic and 31 lysogenic high and medium quality phages were present in at least two samples. In agreement with the abundance of Pseudomonas, Pantoea and Rhizobium in the samples, we found phage genomes associated with them. Phages related to other bacterial species were also present in the samples. Overall, the phage and prophage diversity illustrate the ample dynamic nature of the rhizosphere microbiome.

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C3 - New lineage of single stranded DNA virus that infects the symbiotic bacteria *Rhizobium*

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Recently, we isolated phages with small single stranded DNA genomes that infect the symbiotic bacteria Rhizobium. Although, the host-range and the complete genome of some of them were determined, the taxonomy and phylogenetic relationships to the Microviridae family remain to be known. A total of 66 Microviridae phages were isolated from agricultural soils from Mexico and Argentina. The genomes of 29 of them were sequenced with Illumina procedures, and the rest was only identified by PCR. 24 of these microviruses have a length about 6.4 kb and seven genes, while two microviruses (one Mexican and one Argentinean isolates) have an even smaller genome of 4.7-4.8 kb. Two of the Microviridae are related to the Amoyvirinae subfamily, according with the major capsid protein (MCP) phylogeny; most microviruses did not show significant similarity with known subfamilies in the MCP. Instead, by using psi-BLAST, we found that the MCP of these microviruses have homologues residing in the genomes of several rhizobial species. Therefore, it is likely that they are a new lineage within Microviridae. The results confirm previous metagenomic studies on the ample prevalence of microvirus in diverse environments. Furthermore, the isolated microviruses provide the opportunity to study them experimentally.

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C4 - Globally ubiquitous viruses in oil reservoirs refute burial and isolation theory

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Prokaryotic viruses account for most of the biodiversity within ecosystems and crucially affect the host microbe. In petroleum reservoirs, the virome is poorly understood compared to the existing knowledge about bacterial and archaeal phyla within these ecosystems. Here, we analyzed the virome of 10 publicly available metagenomes that had been originally retrieved from oil reservoirs and oil contaminated sites across the globe. We were able to extract hundreds of viral sequences by combining several established tools for viral detection. Multivariate statistics on the clustered viromic data showed that metagenomes of oil reservoirs are distinguishable by their viral sequences. Multiple viruses, however, were present in samples from geologically distinct sites, e.g., in samples from US (Alaska, Texas), Russia, and China. This is an unexpected finding not only because of the great distance between sites, but also because of the different geological settings. Since viruses are the fastest evolving biological entities on our planet, we conclude that genetic material has recently been exchanged between oil ecosystems irrespective of potential ecological/geological barriers. Consequently, oil reservoirs can no longer be considered biologically isolated ecosystems but can rather be seen as continuum of biodiversity across the globe.

C5 - Genomic relationships between phages and prophages of the symbiotic bacteria *Rhizobium*

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The diversity of phages associated with Rhizobium is scarcely known. This work reports the genomic analysis of the diversity of phages isolated from agricultural soils and its comparison with predicted prophages in Rhizobium. Twenty-five phage genome sequences were done with the Illumina system, and 83 phage and 612 genome sequences were downloaded from GenBank. Bioinformatic predictions by Vibrant program identified 270 genomic regions with the highest probabilities to harbor prophages. However, mitomycin treatment of possible lysogenic strains failed to show prophage induction. Genomic comparisons by protein sharing networks (by vContacT v2) reveal viral clusters that include only virulent phages, temperate phages, and only prophages. Still, several viruses were singletons without any genomic relationship with known phages. Prophages within clusters show signals of deletions but not deleterious single-site mutations. Most viral clusters were found in clades when they were mapped onto phage large terminase subunit (TerL) phylogenetic tree, while few others show recombination signals. The results uncover a low portion of the hidden phage diversity that interact with Rhizobium. The viral clusters may represent taxonomic units corresponding to new genera or species.

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C6 - The use of bacteriophages to control *Salmonella* in poultry operations

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Bacteriophages have been used to treat bacterial infections since their discovery in the early 20th century. Nowadays, due to the increase in bacterial antimicrobial resistance, interest in these viruses as antibacterial agents has increased. The use of antimicrobials in food-animals plays an important role in the current antimicrobial resistance crisis and the use of phages to control Salmonella in poultry could be a safe alternative due to their species, serotype, or strain specificity of host bacteria. Our aim was to determine the application conditions of bacteriophage cocktails to reduce the presence of Salmonella in poultry operations. We isolated bacteriophage cocktails that infect Salmonella from wastewater and tested their lytic activity in vitro against 39 Salmonella isolates obtained from chicken caeca and retail chicken cuts; the most lytic cocktail was administered to the chickens orally with drinking water and sprayed in their houses; additionally, two individual constituent phages of the cocktail were purified and characterized by their activity and host bacteria range, and their genomic analysis will be carried out. In the in vitro essays, our cocktails showed lytic activity against 82% of the isolates, most of them belonging to Infantis serovar (67%). We found seven resistant isolates belonging to serovars Infantis, Amsterdam, Brandenburg, and Typhimurium. After the phage administration to poultry and application on the bedding, Salmonella was not detected in chicken caeca for 6 days. These findings become relevant considering that, in Ecuador, as in other Latin American countries and worldwide, multidrug-resistant Salmonella isolates have been reported from chickens and derived foods. We conclude that the phages isolated from the poultry environment can kill Salmonella strains from chickens, and we recommend permanent monitoring of their effectiveness, due to the bacterial characteristic of acquiring resistance against these viruses.

C7 - La anaerobiosis como factor influyente en la interacción fago-hospedero

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La fagoterapia es el uso de fagos para controlar poblaciones bacterianas, por esta razón es una opción al uso alternativo de antibióticos dada la problemática de la resistencia a antimicrobianos. El éxito de la fagoterapia depende entre otros factores del estado metabólico del hospedero. En bacterias anaerobias facultativas la presencia o ausencia de oxígeno representa un factor influyente en su metabolismo que puede tener implicaciones en la interacción fago-hospedero. De acuerdo con lo anterior se evaluó cuál es el efecto de la anaerobiosis en la bacteria y qué consecuencias tiene en la infección y ciclo de replicación del fago, tomando como modelo a Salmonella s25pp y el fago □San23. Se realizaron ensayos in vitro de curvas de infección y one-step, y de la evaluación del desarrollo de la resistencia bacteriana comparando las condiciones de ausencia y presencia de oxígeno. A su vez con técnicas como secuenciación, RT-qPCR y Westernblot se analizó a nivel génico y proteico el efecto de la anaerobiosis en genes como ftsZ, btuB y sus respectivas proteínas. Los resultados muestran que la anaerobiosis afecta la fisiología celular y de igual manera se disminuye la eficiencia de la infección y se afecta negativamente el ciclo de replicación viral. También se observó que la ausencia de oxígeno no favorece la aparición de variantes resistentes al fago y se determinó que la resistencia no es consecuencia de mutaciones en el receptor BtuB usado por el fago. Respecto al porqué se disminuye la eficiencia de infección se hipotetizó que se debía a cambios en la expresión del receptor, no obstante, a nivel transcripcional no se observan diferencias significativas entre las condiciones de oxígeno. Se concluye que el oxígeno es un parámetro importante en la interacción fago-bacteria y en términos de fagoterapia ofrece los fundamentos necesarios para considerarlo como una variable del tratamiento.

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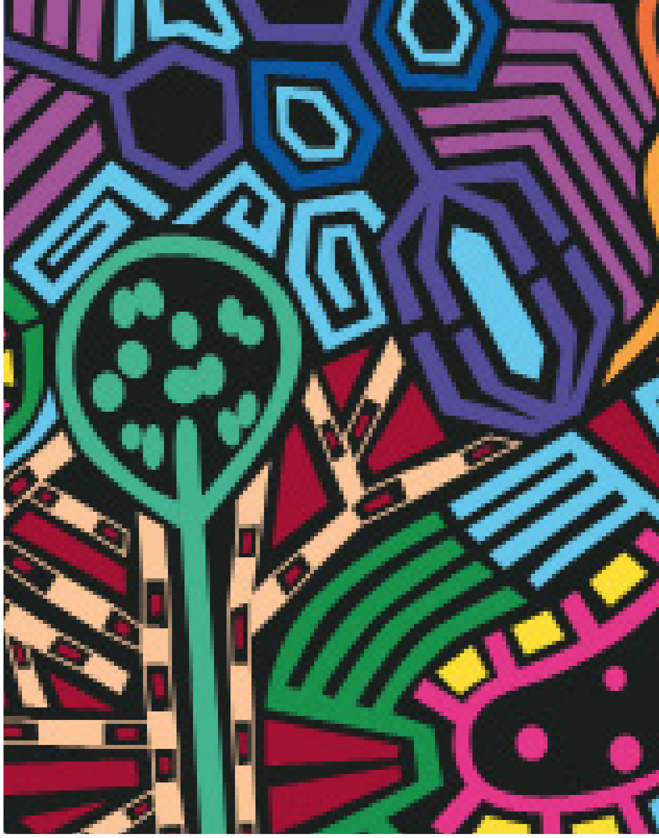

D MICROBIAL BIOTECHNOLOGY

D1 - Convergent evolution of *Streptomyces* protease inhibitory activities via divergent peptide condensation mechanisms

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Small peptide aldehydes (SPAs) with protease inhibitory activity are natural products typically synthesized by non-ribosomal peptide synthetases (NRPS). SPAs are widely used in biotechnology, as therapeutic agents, they are physiologically relevant and regulate development of the natural hosts. Here, we identified an NRPS-like biosynthetic gene cluster (BGC) in Streptomyces lividans 66 that lacked a condensation (C) domain but included a tRNA-Utilizing Enzyme (tRUE) belonging to the leucyl/phenylalanyl (L/F) transferase family. This system was predicted to direct the synthesis of a novel SPA called livipeptin. Following evolutive genome mining approaches we confirmed the presence of tRUEs within diverse Streptomyces genomes, including fusions with a C-minus NRPS-like protein. Leupeptin, whose BGC in Streptomyces roseus ATCC 31245 was also identified and characterized herein, establishing an unequivocal gene-metabolite relationship. Interestingly, leupeptin and livipeptin were shown to be synthesized by unrelated pathways, demonstrating convergent evolution within Streptomyces and with other taxonomically unrelated leupeptin-producing proteobacteria. We anticipate that the discovery of this tRUE associated to a natural product (NP) biosynthesis, will pave the way for exploiting this unprecedented biosynthetic logic to uncover novel NP, and will assist in the development of auxiliary synthetic biology tools to inhibit proteolysis. Similar implications are envisaged for leupeptin once its BGC is mechanistically characterized in more detail.

D2 - Bioactivity of coloured extracts from *Streptomyces* with potential cosmetic application

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Personal care has become an essential part of our daily routine. Therefore, nowadays, consumers are looking for quality, safety, and innovation in the cosmetic products that they buy. One of the most controversial components in the production of cosmetics are pigments and dyes. As previous studies have shown, this can trigger degenerative diseases and hormonal disruptions in people's health. Additionally, they could have a negative impact on the environment. Our aim is to evaluate colored extracts from microbial sources that can convert into cosmetic ingredients with antimicrobial, antioxidant, and non-cytotoxic properties. The antimicrobial activity was performed by the disc diffusion technique. Cell viability was analyzed in a 96-well plate with different cell lines such as HDFa and HeLa, and radical scavenging activities were evaluated by DPPH assessment. The colored extracts were obtained by fermentation in a liquid medium (ISP2) under suitable conditions and extracted with ethyl acetate, yielding raw colored extract fractions. The unrefined material obtained from Streptomyces strains 145 and 290 showed inhibition against B. subtilis, E. faecium, S. aureus, S. epidermidis. The percentage of free radical uptake was 22.1% and 5.21% for strains 145 and 290, respectively. Cell viability (CV), at the maximum concentration evaluated (1000 ug/mL), showed cytotoxic activity for both strains 145 and 290, decreasing the CV by 56.48%. The unrefined material showed moderate antimicrobial, cytotoxic, and low antioxidant activity at a 10 mg/mL concentration, becoming a powerful cosmeceutical ingredient in the cosmetic field.

D3- Biosorción de cadmio y cinc por dos especies del género *Bacillus* provenientes de la región volcánica Caviahue-Copahue, Argentina

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El tratamiento de efluentes con alta carga metálica concierne a muchas industrias que durante sus procesos pueden liberar metales pesados al medioambiente. Si bien existen tratamientos físicos y químicos, algunas biotecnologías para inmovilizar iones metálicos han demostrado ser eficientes y sustentables. Entre ellas se destaca la biosorción de metales utilizando biomasas y/o biomateriales. Los exopolisacáridos (EPS) son una amplia variedad de biopolímeros producidos por algunos microorganismos que funcionan como una barrera de protección estimulada ante el estrés. Dada su alta capacidad adsorbente, suelen ser relevantes en los procesos de sorción utilizando biomasas. En este trabajo se evaluó la capacidad de biosorción de cadmio y de cinc por biomasas de dos especies microbianas aisladas de la región volcánica y geotermal de Caviahue-Copahue, Neuquén, Argentina. Una muestra ambiental del Río Agrio fue enriquecida en medio LB y expuesta a altas concentraciones de Cd y Zn. Se realizaron aislamientos a partir de los consorcios tolerantes seleccionándose dos aislados que fueron identificados como pertenecientes al género Bacillus por secuenciación del gen 16S ARNr. Se realizaron ensayos de biosorción de Cd y de Zn en agua (pH=6, 25°C, 120 rpm) con las biomasas inactivas obteniéndose adsorciones moderadas tras una hora (40% y 20%, respectivamente). La elevada producción de EPS observada sugirió un rol central en el proceso. Se realizaron, entonces, estudios cinéticos y termodinámicos de sorción utilizando directamente los EPS. Las isotermas de adsorción ajustaron con el modelo de Langmuir obteniendo valores de adsorción máxima de 78 mg Zn/g y 349 mg Cd/g lo que comprueba que la captura metálica fue producida esencialmente por los EPS. Estos resultados muestran la potencialidad de las biomasas de estos aislados para ser utilizados en la biorremediación de efluentes contaminados con Zn y Cd y, posiblemente, con otros metales, lo cual se investigará próximamente.

D4 - The application of natural muds and their extreme microbial communities in the remediation of heavy metals

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The Caviahue-Copahue geothermal system (Northwest of Neuquén province, Argentina) presents several hydrothermal manifestations in the forms of hot springs, pools and ponds where thermal muds are accumulated. These peloids are a mixture of sulfur and clay-minerals, organic matter and fluids that contain dissolved gases like hydrogen sulfide. Besides, they are inhabited by complex microbial communities, formed by known and novel species, including sulfate reducing microorganisms (SRM). The sulfate-reducing activity in addition to the natural clay-minerals adsorption capacity, give such muds a central role in the biogeochemical processes of the area and suggests they could be used for the retention of heavy metals and metalloids as an alternative for the reduction of the metal load in contaminated effluents. To prove this hypothesis, muds from four sites with different characteristics were collected: Baño-9 (33°C, pH 5.87), Las Máquinas-I (70°C, pH 3.23), Las Máquinas-II (76°C, pH 5.95) and Las Máquinas-III (35.9°C, pH 1.53). The experiments were carried out in sealed 10 mL vials in anaerobic conditions, to favor the development of SRM, with 2 grams of each mud and 8 mL of sterile metal solution (Cd or Cr at two different pH conditions: 2.4 and 5.9) to reach the concentration of 10 ppm. The vials were stored for 14 days at 15°C, 30°C and 60°C. Each combination of factors was performed five times for statistics purposes. Samples taken at the beginning and end of the experiment were analyzed for residual metal concentration using atomic absorption spectrophotometry. The results show an important retention of metal ions proving that the Copahue geothermal muds could be an alternative in the remediation of contaminated effluents. Future studies are expected to establish the role of the microbial communities of the different muds as well as to characterize them both genetically and physiologically.

D5 - Bioproduction and bioactivity of *Streptomyces* pigments isolated the Guaviare and Arauca rivers (Colombia)

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One source of natural pigments are bacteria and some of the most common microbial pigments are carotenoids, flavonoids, azafilonas, anthraquinones, among others. In the present investigation, 20 Actinobacteria from the ceparium of the Bioprospecting Research Group of Sabana University were subjected to morphological characterization and molecular identification by sequencing of the 16S rRNA. Ethanolic extracts of the different strains were prepared and the antioxidant activity was determined using the method of DPPH (5 mg/mL), the antibacterial activity by the disk diffusion method (900 - 50 µg) and cytotoxicity (500 – 5 µg/mL) by the MTT method against cell lines: HDFA, HeLa and MCF-7. It was determined that the greatest number of pigments are produced in the ISP2 medium; molecular identification determined that 16 of the 20 strains belong to the genus Streptomyces and within the produced pigments are colored black, brown, yellow, and burgundy. Extracts of strains 290 and 4C171 in ISP 4 present activity against Bacillus subtilis, Staphylococcus aureus resistant to methicillin (MRSA) and Staphylococcus epidermidis. On the other hand, the extracts of the isolated 144 in ISP 4, 1B18B in ISP 9 and 356 in ISP 2 presented a percentage of antioxidant capacity greater than 50% with average values of 70.47, 67.96 and 59.48%, respectively. Extracts 1B247 in ISP2 and 290 in ISP4 present IC50 values of 152.6 µg/mL and 81.83 µg/ mL against HDFa, respectively; and extract 1B18A in ISP2 has an IC50 of 43.98 µg/mL in front of MCF-7. Other extracts did not cause any cytotoxic effect at concentrations under 500 µg/mL. These bacterial pigments obtained from Streptomyces isolated the Guaviare and Arauca rivers (Colombia) with different bioactivities (antibacterial, antioxidant and cytotoxic) can be employed in the cosmetic and pharmaceutical industry.

D6 - Biosurfactant and bioemulsifier activities from marine sponge-associated bacteria collected in Rio de Janeiro, Brazil

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Sponges (Porifera) are important filters animals from the environment aquatic and can harbor microorganisms able to produce substances with a broad biotechnological application. Sponge-associated bacteria constitute a source of these bioactive molecules, as biosurfactants. These amphiphilic molecules can decrease the surface and interfacial tensions and become useful to many applications, including solubilizers and emulsifiers. Thus, bacteria isolated from sponges collected in the Brazilian coast were selected for this work. In a previous study, Vibrio (5) and Bacillus (7) isolates showed antimicrobial activity. Therefore, the present study aims to evaluate the biosurfactants and/or bioemulsifiers production from these Vibrio spp. and Bacillus spp. isolates. Initial analyzes were performed with the measure of the emulsification index after 24 h (IE24) and drop collapse tests. All five Vibrio strains were positive in the emulsification tests.They showed IE24 from 17.2% to 44.8% in mineral oil and from 12.0% to 24.6% in n hexadecane. Among the Bacillus strains, four showed IE24 from 5.0% to 48.3% in mineral oil and from 25.0% to 59. 8% in n-hexadecane. The strain identified as Bacillus cereus 64BHI1:101 presented 48.3% in mineral oil and 59.8% emulsions in n hexadecane, results close to the surfactant control used (SDS 10%; IE24 65.5%). In addition, the emulsifications were stable after 35 days. From drop collapse results, only Bacillus subtilis 84-5 and Bacillus thuringiensis 64BHI1:1012 showed positive activity. The cell-free supernatants from these two isolates were able to collapse the mineral oil drop. These results indicate that both Vibrio spp. and Bacillus spp. are potential producers of substances that can be useful in the food and/or cosmetic industries. They could also be applied in the bioremediation of environments contaminated with oil.

D7 - Cartagena mangroves: reservoir of bacteria with biotechnological potential

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Mangroves are widely distributed worldwide in tropical and subtropical regions. The biochemical characteristics and environmental conditions of these ecosystems make them considered hot spots of microbial diversity and represent a source of metabolites with metabolic potential. In Cartagena (Colombia), mangroves cover an area of 824 ha and represent one of the predominant ecosystems. Although the biological and economic value of these mangroves is evident, it is essential to know in depth their biodiversity to achieve their sustainable use. Therefore, the objective of this study was to characterize cultivable bacteria associated with mangroves in Cartagena and identify their metabolic potential. The methodology used consisted of: (i) isolation of bacteria from mangroves located in Cartagena, (ii) phenotypic and molecular characterization of isolated bacteria, and (iii) evaluation of the metabolic potential (hydrolytic enzyme activity, resistance to heavy metals, perchlorate reduction capacity and antimicrobial activity). In this study, we isolated 30 heterotrophic, aerobic, and halotolerant bacteria related to the genus Bacillus. The evaluation of the metabolic potential revealed that most of the isolates produced amylases (89%), followed by proteases (74%) and lipases (8%). Likewise, it was detected that 63% of the isolated strains are resistant to Pb and 16% to Ni. In addition, some of the isolated strains presented perchlorate reduction percentages of up to 25%. Additionally, 5 strains presented antimicrobial activity against the evaluated pathogenic bacteria and one strain (UTB 07) presented antagonistic activity against Rhizoctonia solani. This study showed that the mangroves of Cartagena are a source for the isolation of bacteria with biotechnological potential due to their capacity to produce hydrolytic enzymes, resistance to heavy metals, reduction of perchlorate and antimicrobial activity.

D8 - Potencial de leveduras marinhas do Nordeste do Brasil na produção de biosurfactantes

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Biosurfactantes são moléculas anfipáticas com propriedades tensoativas, de grande variedade estrutural e funcional, sintetizadas por uma ampla gama de micro-organismos. Esses compostos biológicos possuem várias vantagens sobre os surfactantes comerciais existentes, pois são ecologicamente mais seguros, menos tóxicos e biodegradáveis. Apesar de existirem mais de 2000 estruturas reportadas na literatura, as leveduras marinhas são pouco estudadas e representam uma fonte potencial desses tensoativos. Por essa razão, o objetivo do trabalho foi avaliar a produção de biosurfactantes por leveduras marinhas e selecionar as melhores produtoras para caracterização dos compostos. Foram selecionados 20 isolados de leveduras provenientes da Micoteca do Laboratório de Diversidade Molecular da Universidade Federal de Alagoas. Os isolados foram cultivados em meio YPD líquido por 168 h a 25 °C. Após, foi realizado o teste do índice de emulsão (IE) com querosene para avaliar quais isolados produziam biosurfactantes. Os melhores produtores foram testados novamente com outras fontes de hidrocarbonetos a fim de validar a produção de biosurfactantes. O sobrenadante dos isolados selecionados foi submetido a 100 °C durante 30 min e repetido o teste do índice de emulsão a fim de avaliar a resistência do biosurfactante a temperaturas elevadas. Dentre as leveduras testadas, 3 isolados apresentaram atividade emulsificante: LMS19 com IE de 44%, LMS24B com IE de 52% e LMS29B com IE de 54%. Os isolados foram testados com tolueno como fonte de hidrocarboneto apresentando os IEs de 66%, 70% e 66%, respectivamente. Quando testados com N-hexano, apresentaram os seguintes IEs: LMS19 de 61%, LMS24B de 63% e LMS29B de 62%. Quando os sobrenadantes foram submetidos a 100°C, os isolados apresentaram os seguintes IEs: 25%, 38% e 28%, respectivamente. Os biosurfactantes das leveduras marinhas selecionadas estão em processo de caracterização, mas já demonstram serem promissores para aplicação biotecnológica, incluindo a biorremediação de hidrocarbonetos.

D9 - Biological contribution of composting and phytotechnologies to manage solid wastes of petroleum industry after chemical oxidation

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The generation of oily sludges with a high hydrocarbon content is an unavoidable problem for the petrochemical industry. These wastes are a complex mix of hydrocarbons, heavy metals, solid particles and water. The hydrocarbon fraction is classified as: aliphatic, aromatic, resins and asphaltenes, the latter two being those with the highest molecular weight and recalcitrance. Although chemical oxidation has been shown to be effective for removing complex hydrocarbons, its impact on the native microbiota can be unfavorable. One single remediation technology can hardly provide an effective treatment for petrochemical sludges.

In line with this problem, a sequential strategy was designed combining: chemical oxidation (alkaline activated persulfate), composting (goat manure and oat straw) and phytotechnologies (ryegrass) to treat the oily sludge originated in oil-water API separators of an oil refinery. Throughout the full process, a number of physical (pH, E°), chemical (total hydrocarbons, organic carbon, E4/E6 ratio), microbiological (hydrocarbon degrading bacteria, copy number of hydrocarbon degrading genes, enzymatic activities) and biological (plant growth) parameters were monitored. Persulfate was not longer detected after 19 days of oxidative treatment, and a 31% removal rate of total hydrocarbons was evidenced. Besides, after one year of composting, the oxidized compost did not show a higher hydrocarbon removal rate than the unoxidized compost. Nonetheless, a mature and stable product of improved microbial quality in terms of gene copy number and enzyme activity was generated, capable of sustaining ryegrass growth. Finally, after four months of plant growth, the oxidized-composted-planted microcosms showed a tendency to decrease total hydrocarbons and presented an active microbiota with characteristics comparable to the non-oxidized-composted control. These results show that combining chemical and biological strategies can transform a petrochemical waste into a material with added value, capable of sustaining plant growth.

D10 - Antimicrobial activity of mangrove-associated fungi from the Pacific coast of Costa Rica

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Mangrove-associated fungi are broadly dispersed and are widely known for their ability to synthesize highly biologically active metabolites, such as antimicrobial metabolites. These molecules could represent novel antibiotics that can be used to fight antimicrobial resistance, one of the biggest threats and main challenges to global health. The diversity and antimicrobial activity from Costa Rican mangrove-associated fungi are under-explored. Therefore, this study aimed to evaluate the ability of marine fungi isolated from mangrove swamp sediments from the Pacific coast of Costa Rica to inhibit bacterial growth. We evaluated the antibacterial activity of 21 strains of marine fungi against Staphylococcus aureus, Pseudomonas aeruginosa, Enterobacter hormaechei, Enterococcus faecium, Acinetobacter baumannii, and Klebsiella pneumoniae. A 7-day pre-stimulation was conducted by a co-culture of fungi and bacteria to stimulate antimicrobial metabolites production. The antimicrobial activity was performed by inoculating bacterial strains 0.5 centimeters from the fungi in Mueller Hinton medium with and without 2% sodium chloride. Nine isolates of marine fungi shown antimicrobial activity against at least one bacteria strain, especially when the medium without sodium chloride was used. Currently, we will perform fractionation and chemical identification of the potential molecules with antimicrobial activity. These results suggest an antimicrobial activity from fungal strains isolated from the Costa Rican Pacific mangrove, which could be a promising source of potentially novel antimicrobial compounds.

D11 - Toxicidad y acumulación de arsénico en cultivos de *Rivularia halophila*, cianobacteria aislada de la Laguna Negra (Catamarca- Argentina)

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El arsénico (As) es un elemento tóxico que se encuentra ampliamente distribuido en la Tierra. A pesar de su toxicidad, algunas especies de cianobacterias pueden crecer en altas concentraciones de As, dado que poseen genes de resistencia y/o detoxificación. Aprovechando dicha capacidad, es posible utilizar estas especies para retener o transformar el arsénico y así disminuir su concentración en el ambiente. Rivularia halophila (R. halophila) es una cianobacteria aislada de matas microbianas de Laguna Negra. El objetivo de este estudio es evaluar la capacidad de resistencia de R. halophila frente al As. Para llevar a cabo este objetivo, se evaluó el crecimiento, el contenido de clorofila-a y la acumulación de As en la biomasa, luego de exponer a R. halophila durante 15 días a diferentes concentraciones de As (III y V). Los resultados indican que R. halophila es resistente a As, en particular para As(V). El crecimiento y el contenido de clorofila-a se vieron afectados frente a concentraciones superiores a 2000 mg·L-1 de As(V) y 10 mg·L-1 de As(III). La dosis letal media (LD50) de As (V y III) fue 8500 mg·L-1 y 70 mg·L-1 respectivamente. Asimismo, la acumulación del metaloide en la biomasa aumentó al incrementarse la concentración de As(III), mientras que para As(V) no se observaron diferencias significativas en su acumulación, observándose un patrón no lineal a medida que subía la concentración de As. El valor máximo de As acumulado en biomasa fue 480 mg·kg-1 para As(V) y 9500 mg·kg-1 para As(III). Los resultados obtenidos hasta el momento nos indican que R. halophila no solo es una cianobacteria tolerante a altas concentraciones de As, sino que también tiene la capacidad de acumular cantidades significativas de este metaloide dentro de su biomasa, lo que la convierte en un excelente modelo para el estudio de la remoción de As.

D12 – Degradación del colorante Rojo de Fenol por extractos ezimaticos del hongo *Trichoderma sp*, empleando lignina como fuente de carbono

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Debido a las problemáticas causadas por los contaminantes orgánicos persistentes, hay gran interés en mecanismos para degradar estos compuestos, puesto que son carcinogénicos y mutagénicos. En ese contexto, el estudio quiso evaluar la capacidad de extractos enzimáticos del hongo Trichoderma sp en degradar el colorante rojo de fenol, para su posible aplicación en biorremediación. El hongo se cultivó en medio líquido (100mL) con sales minerales y lignina como fuente de carbono (1%v/v), la cual fue extraída de bagazo de caña. Se realizaron tres cultivos: 1) lignina como única fuente de carbono; 2) lignina con dextrosa (0,5% m/v) y 3) lignina con dextrosa (0,25% m/v), con adición de dextrosa (0,25% m/v) al segundo día. Los experimentos fueron por duplicado e incubados a 25oC. Luego de 8 días se centrifugó y 1mL del sobrenadante se adicionó en el buffer de reacción enzimática para degradar el colorante (0,01 %m/v); se incubó a 30oC y se hizo lectura del rojo de fenol por espectrofotómetro durante 2 horas. Los resultados mostraron que los cultivos con dextrosa presentaron mayor formación de hifas, siendo evidente un aumento al tener más dextrosa al comienzo del ensayo. No obstante, en los resultados del análisis enzimático se observó que la mayor degradación del colorante (69%) la tuvo el sobrenadante del cultivo únicamente con lignina en el medio, seguido del cultivo con el pulso de dextrosa (63%); el sobrenadante del cultivo con dextrosa al 0,5% tuvo una baja remoción (4%). Es interesante evidenciar el crecimiento del hongo en un sustrato complejo como la lignina, más interesante aún es ver que efectivamente sus extractos enzimáticos pueden degradar sustancias fenólicas. Esto permite inferir que Trichoderma sp. es capaz de producir enzimas ligninolíticas, como la manganeso peroxidasa, y que podría ser empleado en la recuperación de ecosistemas contaminados por hidrocarburos aromáticos y sustancias fenólicas.

D13 - Metabolic regulation of gluconeogenesis and glycolysis in the marine archaeon *Methanosarcina acetivorans*

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The methane-producing archaea (methanogens) are unable to take carbohydrates as external carbon sources, instead they use compounds with one or two carbons to grow, like acetate and methanol; hence, gluconeogenesis becomes an essential pathway for the generation of biosynthetic intermediates and polysaccharide storage. Those are required for cell duplication and mainly synthetized when an external carbon source is available. We analyzed the gene expression, the activities and modulation by metabolites of key enzymes involved in gluconeogenesis from methanol and glycolysis by glycogen degradation in Methanosarcina acetivorans, a methanogen isolated from costal sediments of California. We also determined the intracellular contents of metabolites and ions, and metabolic fluxes. We found a concerted regulation (at different levels) between gluconeogenesis and glycolysis that allows better carbon assimilation, limits carbon flux, and maintains cell homeostasis. Modulation of enzyme activity by physiological concentrations of metabolites and ions is the main mechanism of regulation of glycolysis and gluconeogenesis. This metabolic regulation is important when other levels of regulation are not present (for example: compartmentalization, cooperativity, allosterism or effect of hormones), and even in proteins that show post-translational modifications, like the Ser/Thr phosphorylation on ADP-dependent phosphofructokinase 1 and fructose-1,6-bisphosphatase. Energy production by glycolysis and efficient carbon assimilation by gluconeogenesis are not only necessary for providing precursors for the synthesis of macromolecules, these cell processes are also involved in the ability of microorganisms to resist different types of stresses, such as exposure to oxygen and heavy metals, where the de novo synthesis of a biofilm is required, as well as a protective barrier and nutrient reservoir. This comprehensive knowledge could be used to increase biomass and metabolite production in biotechnological processes and understand the ecophysiology role of these microorganisms in environments and host-associated microbiomes.

D14 - *Pseudomonas* spp. aislados de aguas contaminadas con plomo, productor de sideróforos y screening de la actividad enzimática microbiana

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La búsqueda de compuestos bioactivos extraídos de fuentes naturales (plantas o microrganismos), se ha convertido en una estrategia para minimizar los efectos negativos que puede tener el uso de compuestos sintéticos sobre la salud humana, animal o ambiental. Pseudomonas spp constituye uno de los géneros bacterianos reportados con amplia producción de estos compuestos bioactivos, entre los cuales se destacan: cianuro de hidrógeno, indol, fenacina, pioverdina, piocianina, entre otros; algunos de ellos denominados sideróforos, y considerados como controladores biológicos, con efecto promotor de crecimiento vegetal, y en algunas ocasiones con efecto antagónico. Por otro lado, la actividad enzimática microbiana presenta un valor agregado en microorganismos que se estudian con potencial antagónico, como factor que interviene en la efectividad del proceso. Este trabajo pretende estudiar el gènero de Pseudomonas spp. aislado de aguas contaminadas con plomo, con el fin de identificar su potencial bioactivo a partir de la producción de sideróforos y de la actividad enzimática de los microorganismos. Se obtuvieron seis aislados de aguas contaminadas con plomo aledañas al Rio Medellín, asociados al género Pseudomonas con una identidad confirmada mediante secuenciación del gen ADNr 16S (similaridad >95%). Posteriormente, se usaron pruebas colorimétricas y medios de cultivo, para identificar la presencia de sideróforos (prueba de Arnow, prueba de Neilands, crecimiento en medio King B). Cuatro cepas resultaron positivas para la producción de sideroforos, sin embargo, solo tres cepas de Pseudomonas aeruginosa mostraron capacidad de producir pioverdinas en ausencia y presencia de plomo, en medio King B. Por otro lado, se valoró la actividad enzimática usando diferentes sustratos (caseína, almidón, carboximetilcelulosa, tween 20/80), para resaltar el potencial enzimático del género de Pseudomonas. De manera exploratoria, se identificó la actividad enzimática proteolítica y lipolìtica con potencial biocontrolador. El género Pseudomonas spp., aislado de aguas contaminadas con plomo es productor de compuestos bioactivos, con alto potencial de ser biocontrolador y/o bioindicador.

D15 - DCPIP (Colorimetric method), determination of the ability of *Bacillus licheniformis* to biodegrade diesel S10 and AFFF - *Aqueous Film-Forming Foam*

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Accidents with oil and oil products can occur at different stages of production. The difficulty of fighting fires involving petroleum-derived hydrocarbons led to the use AFFF (Aqueous Film-Forming Foam) and, in some cases, it is impossible to prevent them from reaching the environment. Bioremediation processes have high efficiency and low cost, making them an important biological tool in the treatment of contaminated areas. The objective was to evaluate the biodegradation of Diesel S10 and fire control foam - AFFF, by Bacillus licheniformis, isolated from the Santos-SP estuary, using DCPIP (2,6- dichlorophenol-indophenol) colorimetry. The technique is based on the color change of this compound when reduced; so when the DCPIP indicator is oxidized its color is blue and when reduced it is colorless. The change takes place through the electron exchange reaction, indicating the microorganism's ability to biodegrade compounds. The composition of the colorimetric tests was BH culture medium (Bushnell-Hass); DCPIP; Fire Control Foam – LGE Kidde Sintex AFFF; Diesel S10 and Bacillus licheniformis. The tests were performed with the necessary controls and in triplicates. Qualitative results considered the change in the color of the medium over the incubation time (48 hours). It was possible to observe that after the incubation period, the assays with the presence of the strain showed discoloration, while the control assays did not show color change, maintaining the blue color of the DCPIP. Studies show that environmental strains are more adaptable to degrade the contaminants they have had contact with, accelerating the bioremediation process. Methods such as colorimetric - DCPIP, provide data on biodegradation that are fundamental for strategic decision making in choosing the most appropriate bioremediation, in addition to providing references on the biodegradability of substances, as well as characterization and profile of microorganisms.

D16 - *Aspergillus* sp. y *Mucor* sp. como potenciales hongos degradadores de hidrocarburos

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Los productos derivados del petróleo son usados masivamente a nivel mundial. Si bien son muchas sus aplicaciones, también son muchos los residuos que generan, ocasionando una amplia contaminación ambiental que se ve intensificada por la baja degradación natural que tienen; junto al alto costo que implican las alternativas de degradación convencionales. El objetivo de este trabajo fue comparar la capacidad degradadora de hidrocarburos por parte de morfoespecies fúngicas aisladas de muestras de crudo adsorbidas en fibras vegetales en las que se evidenció crecimiento espontáneo de hongos. Para esto, se sembraron los hongos crecidos en las muestras y porciones de fibras vegetales limpias, los hongos crecidos se aislaron, purificaron e identificaron morfológicamente. Se seleccionaron al azar seis ejemplares a los cuales se les realizó ensayos preliminares de degradación de crudo y curvas de crecimiento usando como única fuente de carbono petróleo crudo; los hongos con mejores resultados fueron probados con materiales hidrocarbonados de difícil degradación e identificados molecularmente. De los seis aislamientos examinados en crudo, las cepas con mejores resultados fueron dos clasificadas en el género Aspergillus sp., con una ganancia en masa de 0,150 g y 0,089 g, y una perteneciente a Mucor sp., con 0,046 g, cada una en matrices con 15% de crudo. Posteriormente, estos aislamientos fueron probados para degradar poliestireno expandido, nailon, espuma de poliuretano y llanta; el mejor resultado se evidenció en las muestras de nailon con un crecimiento en masa de las tres cepas probadas de aproximadamente 0,350 g. Investigaciones previas han señalado las rutas enzimáticas como la principal vía de degradación de los compuestos utilizados donde las peroxidasas parecen cumplir un papel principal. Los ensayos mostraron la capacidad de las cepas probadas para utilizar el crudo como única fuente de carbono, y el uso de los compuestos hidrocarbonados recalcitrantes como sustrato para su aprovechamiento.

D17 - Interacción entre el extracto de *Azadirachta indica* y el hongo *Metarhizium anisopliae* para el control biológico de *Anopheles albimanus* un vector de la malaria

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El biocontrol a comparación de los insecticidas químicos es una alternativa para reducir el tamaño poblacional de un organismo de una forma amigable con el medio ambiente; las diferentes interacciones y mezclas entre compuestos plaguicidas pueden reducir la generación de resistencia de los mosquitos hacia los insecticidas más usados en el mundo. En este estudio se determinó el efecto del aceite de nim (Azadirachta indica) en combinaciones con el hongo Metarhizium anisopliae frente a larvas de Anopheles albimanus; para lo cual se realizaron 3 pruebas frente al vector las cuales fueron la virulencia del hongo M. anisopliae de manera independiente, la toxicidad del extracto de A. indica de manera independiente y por último la interacción del hongo y el extracto de A. indica frente al vector An. albimanus; se realizaron 3 repeticiones y 3 réplicas en cada experimento. La concentración letal 50 frente a las larvas de An. albimanus al cabo de 5 días para el hongo M. anisopliae fue de 3.26x105 conidios ml-1 y del extracto Azadirachta indica fue 16 ppm; la concentración más alta del extracto de A. indica que no afecta la germinación, ni el crecimiento del hongo M. anisopliae fue de 1 ppm y por lo tanto fue la seleccionada para los ensayos binarios. las mezclas de A. indica y M. anisopliae causaron un efecto sinérgico además ocasionaron una mortalidad del 100% de las larvas al cabo de 5 días. Lo anterior, indica que tanto el hongo, como el aceite de nim son una buena alternativa para controlar larvas de A. albimanus y se pueden considerar buenos candidatos para futuros programas de control biológico de uno de los vectores de la malaria esto con el fin de reducir la incidencia de esta enfermedad a futuro.

D18 - Screening of *Actinobacteria* isolated from lichens for antimicrobial, cellulolytic and proteolytic activity

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Actinobacteria phylum contains numerous genera with biotechnological potential. Furthermore, Actinobacteria from tropical ecosystems such as páramos in Colombia can be a novel source of genomic and functional diversity. This work screened 37 isolates associated with lichens from high mountain páramo ecosystems with the aim of understanding the underlying diversity and functional potential for antimicrobial, cellulolytic and proteolytic activity. Constitutive and induced antimicrobial activity were carried out using two assays, direct confrontation in solid medium and cell supernatants in 96-well microtiter plates, against the test microorganisms Escherichia coli and Saccharomyces cerevisiae. The proteolytic and cellulolytic activity were tested in petri dishes by hydrolysis of cellulose / filter paper and casein, respectively. The strains showed ample difference in their activities, from 5% to 90% inhibition of growth, and variability depending on the growth medium. The supernatant from strains PNC2-3 and B1-2 inhibited constitutively up to 85 % the growth of Escherichia coli and the pathogens Staphylococcus aureus, Klebsiella pneumoniae and Pseudomonas aeruginosa. Strains PNB1-3, PNA1-2, H2-1 and A1-4 displayed induced antibacterial activity, when coincubated in the presence of different microbial supernatants, of up to 100% growth inhibition. Another 4 strains showed hydrolytic halo of cellulose. And strains PNC2-0, PNC3-1, PNF6-4 and 926A produced hydrolytic halo in casein medium. As a conclusion, 14 strains from 37 wild microorganisms showed a biotechnological potential. Overall, this work provides an overview of the genomic and functional potential of Actinobacteria from underexplored tropical ecosystems at high mountains and sets the groundwork for additional exploration that includes genomic sequencing.

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D19 - Efecto de cepas nativas del norte de Chile sobre los mecanismos implicados en la tolerancia a estrés salino e hídrico en plantas de lechuga

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Actualmente, el cambio climático es un problema global que afecta directamente al medio ambiente. En plantas, la falta de agua y la acumulación de sal en los suelos afectan negativamente su desarrollo causando senescencia, abscisión de hojas, restricción de la elongación celular y crecimiento; además la floración y maduración de frutos también se ven afectadas negativamente. Una estrategia para mejorar el crecimiento vegetal bajo condiciones de estrés ambiental es utilizar rizobacterias promotoras del crecimiento vegetal en plantas (PGPR). Se evaluaron cepas nativas aisladas de suelos de la Región de Coquimbo y del Desierto de Atacama respecto a su interacción in vitro con la planta modelo Arabidopsis thaliana. Además, se cuantificó el porcentaje de germinación bajo condición salina en hortalizas como lechuga (Lactuca sativa L). En base a estos resultados se seleccionaron tres cepas para evaluar el efecto de la interacción planta-microorganismo en la tolerancia a estrés salino e hídrico en plantas de lechuga a nivel de macetas. Se demostró que las cepas seleccionadas mejoraron el desarrollo morfológico y la integridad fisiológica (permeabilidad de la membrana) de la planta bajo condiciones de estrés salino y, fisiológicamente se observó un aumento en los niveles del osmoprotector prolina bajo condiciones de estrés hídrico. Los datos de los ensayos en maceta tanto para estrés salino como para estrés hídrico fueron integrados en un solo análisis y se determinó una mejora en el largo y peso fresco/seco en raíz y hoja de las plantas inoculadas con las cepas en estudio. Estos hallazgos podrían brindar nuevos conocimientos sobre la interacción planta-bacteria bajo condiciones de estrés y potenciar la agricultura en zonas áridas y semiáridas, así como promover estrategias agrícolas sustentables y adaptadas a las proyecciones de cambio climático global en el norte de Chile.

D20 - Dinámica y persistencia de indicadores de contaminación fecal microbianos y virales en lodos y biosólidos de plantas de tratamiento de aguas residuales

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La gestión de los lodos de plantas de tratamiento de aguas residuales (PTAR) se ha convertido en un tema de creciente importancia a nivel mundial buscando alternativas que conduzcan a su estabilización y reciclaje seguro para el medio ambiente. En Uruguay, el principal destino de estos lodos es la disposición en vertederos o rellenos sanitarios municipales. Sin embargo, de cumplir con los requerimientos sanitarios exigidos podrían ser utilizados como mejoradores de suelo, valorizando este residuo. La resistencia a los tratamientos de estabilización de ciertos patógenos puede ser variada, lo que genera discusión a nivel mundial respecto a qué indicadores emplear para el monitoreo ambiental de estos biosólidos. Para superar estas limitaciones, se han propuesto diversos indicadores bacterianos y virales que podrían representar mejor estos organismos. En este trabajo se estudió la dinámica de Enterococcus y Enterovirus en aguas residuales y lodos de distintas etapas del tratamiento en PTAR de Uruguay durante 5 meses utilizando métodos clásicos y qPCR. A lo largo del periodo evaluado, los Enterovirus fueron detectados puntualmente en afluente (103 copias genómicas/g ST) y en lodos deshidratados (102 copias genómicas/g ST). Sin embargo, la abundancia de enterococos cultivables se mantuvo estable en afluente (107/g ST) y se reduce en dos órdenes luego del tratamiento (efluente previo UV y lodos deshidratados), no detectándose en los biosólidos generados. Asimismo, se evaluó la persistencia y sobrecrecimiento de Enterococcus faecalis y Salmonella typhimurium mediante ensayo de inoculación (108células/g) de biosólidos y almacenamiento durante 130 días a 28°C. Si bien la abundancia de ambas especies decayó a lo largo del ensayo su dinámica fue diferente, mientras que Salmonella disminuye durante todo el período, los Enterococcus no son detectables por cultivo a partir del día 40. Estos estudios contribuyen al conocimiento del comportamiento y dinámica de indicadores de contaminación fecal en PTAR.

D21 - Formulation of an alternative medium for the growth of the cellulolytic fungus *Trichoderma* spp

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Trichoderma spp. is important in sustainable agriculture. However, the studies about its cellulolytic activity may be limited in labs with few resources and low funding. This work formulated a medium that uses easily accessible inputs for the growth of cellulolytic microorganisms The alternative medium replaced Whatman-filter-paper by Bond-paper, NO3 salt by NPK or urea fertilizers, and MgSO4, NaCl and FeSO4 salts by sea salt. The work was carried out in Agrosavia´s labs during May and June 2019. Native Trichoderma sp. Th007, Th035, M44 and M45 isolates were used and their radial growth was measured on petri dishes under stereoscope loupe. Trichoderma koningiopsis Th003 was used as positive control and Escherichia coli TOP10 as negative control. The test was carried out in triplicate on two independent replicates. Additionally, the ITS region from the isolates was sequenced for molecular identification. The results were positive for the substitution of reagents. All Trichoderma grew on NPK-Bond. However, its growth rate was half the growth on KNO3-Bond, KNO3-Whatman or PDA. The isolates M44 and M45 only grew in Urea-Bond agar. But, the growth rate was one fifth of the rate on NPK-Bond. All isolates showed higher growth rate in Bond-paper agar than in Whatman-paper. The strains Th007, M44 and M45 showed the best growth rates in all agar,respectively. Making them candidates for biomass degradation and cellulase production. Growth on the different media showed distinctive patterns to each isolated. Interestingly, all isolates grew on paperless agar or other carbon source, indicating low carbon requirements for growth. As a conclusion, low funding laboratories can use NPK fertilizer, Bond paper, and sea salt to study the growth of Trichoderma and other cellulolytic microorganisms. Future work requires understanding the role of carbon source in the growth of Trichoderma spp.

D23 - Monitoring soil microbiota and soil enzyme activities in a chronosequence of Atlantic Forest restoration

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The Atlantic Forest is one of the most species-rich tropical forests and one of the most important biodiversity hotspots in the world. However, this biome is also the second most threatened on the planet and the most devastated natural domain in Brazil; therefore, its restoration and subsequent conservation strategies are essential to prevent further losses. As soil quality is crucial for restoration and conservation, bioindicators of soil functioning with respect to biogeochemical cycles, such as extracellular enzymes, are highly relevant. Extracellular enzymes in the soil – mainly due to hydrolysis reactions – can mineralize organic compounds, making them available for plants and microorganisms. In the present study, we evaluated the soil enzymatic activity using enzyme-specific substrates and the abundance of the archaeal community by quantitative PCR (16S rRNA gene of Archaea). We took measurements in a chronosequence (time series) of restored forests in São Paulo State, Brazil. The stages were pasture (starting point), active forest restoration of 7 and 14 years, and pristine Atlantic Forest (the natural reference). We found that -glycosidase, acidic and basic phosphatase, and arylsulfatase activities were higher in soils from the pristine forest and 14-year restoration (mean = 67.4, 591.5, 143.2, and 81.6 µg PNP g-1 hour-1, respectively) than in soils under 7-year restoration and pasture (mean = 40.2, 348.8, 73.6, and 56.9 µg PNP g-1 hour-1, respectively). The number of copies of the archaeal 16S rRNA gene (ng/DNA) followed the same pattern, being higher in the pristine forest (7.38E+03), followed by the 14-year restoration (2.50E+03), pasture (1.03) E+03), and 7-year restoration (2.19E+03). The results revealed that between 7 and 14 years of restoration the soil biotic conditions start to resemble to pristine system. To check if this pattern occurs within other major microbial groups, the assessment of bacteria and fungi abundances is in progress.

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D24 - Desarrollo de consorcios microbianos para la biorremediación de suelos y aguas contaminadas con hidrocarburos provenientes del combustible fósil

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En Uruguay, el sector de transporte utiliza principalmente combustibles fósiles de países productores de petróleo. Por esta razón, se importa petróleo crudo que es refinado para obtener combustibles. El proceso de producción, transporte y almacenamiento de combustible genera pérdidas que amenazan el medio ambiente, debido a que los derivados del petróleo tienen componentes recalcitrantes de gran toxicidad para el ambiente y la salud.

Actualmente, se utilizan métodos fisicoquímicos para la descontaminación de suelos y aguas subterráneas, pero no logran la total remoción de los contaminantes. La biorremediación con microorganismos degradadores de hidrocarburos es una estrategia novedosa en Uruguay y puede contribuir a la descontaminación. Este trabajo, se enfoca en desarrollar consorcios microbianos eficientes en la degradación de hidrocarburos provenientes de la gasolina. En una primera etapa, se puso a punto una técnica de extracción orgánica para la determinación de naftaleno y TPHs (total petrol hydrocarbons) por GC-MS. En una segunda etapa, se prepararon consorcios utilizando como inóculo inicial agua de una playa cercana a una refinería, y se evaluaron distintos porcentajes (0,5% y 1%, v/v). Se obtuvieron dos consorcios con crecimiento estable alimentados con 0,5% v/v de nafta como única fuente de carbono. Adicionalmente, se realizaron extracciones de ADN para analizar por secuenciación masiva las comunidades microbianas presentes. En uno de los consorcios el género Pseudomonas tiene una abundancia de 99,8%, mientras que en el otro es de 14,3%. En este último consorcio, dentro de los microorganismos más abundantes se encuentra el género Brevundimonas (56,2 %) y el género Sporocarcina (12,8%). En definitiva, las comunidades presentes en los consorcios son diferentes, tanto en su identidad como en su abundancia relativa. Actualmente, se está evaluando la cinética de consumo de naftaleno y TPHs en ambos consorcios por GC-MS según el protocolo establecido.

D25 - Salt–induced stress tolerance during wheat seed germination is improved when *Variovorax* sp. strain P1R9 is applied as part of bacterial consortia

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Endophytic bacteria from extremophile plants are being isolated and bio–prospected to be used as part of bio-stimulant formulations to prevent the damages attributed to abiotic stress on agricultural plants. In this study, we isolated bacterial strains from the endospheres of endemic plants grown in Atacama Desert and Patagonia of Chile. Over 300 bacterial strains were isolated and screened by plant growth-promoting (PGP) traits, such as insoluble phosphate utilization, production of tryptophan-dependent auxins, ACC deaminase activity and salt tolerance. Five strains (Variovorax sp. strain P1R9, Corticicoccus sp. strain P1R11, Bacillus sp. strain P1R13, Bacillus sp. strain P1R34 and Curtobacterium sp. strain P2H47) showing the higher relative activities of PGP traits were selected for single and consortia inoculation assays. The germination index (GI) proposed by Tiquia et al. (Environ. Poll. 93:249-256 [1996]), based on relative % of germination and relative % of root growth, was adopted to evaluate the effect of salt–induced stress on seeds of wheat as plant model. Interestingly, those consortia formulated with Variovorax sp. strain P1R9 showed values of GI index > 80% denoting absence of salt–induced stress while those consortia without Variovorax sp. strain P1R9 or single inoculation showed IG index values of 50~80% and <50% denoting intermediate or high salt–induced stress, respectively. Similar result was also observed with consortia formulated with bacterial strains previously reported as PGP bacteria (Klebsiella sp. 8LJA and Klebsiella sp. 27IJA). Our results suggest that Variovorax sp. strain P1R9 can be considered as part of formulated PGP bacteria consortia to efficiently prevent salt-induced stress during germination and growth of wheat seedlings. However, higher studies are required to elucidate the interactions and mechanisms (synergisms or mutualisms) where Variovorax sp. strain P1R9 is involved when is used as part of PGP bacterial consortium.

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D26- Bioinformatic analysis of oxidative stress genes and salt stress genes in hydrocarbon degrading strains *Rhodococcus* sp. ICBD2 and *Acinetobacter radioresistens* DD78

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Bioremediation of oil-contaminated soils represents a major environmental challenge. Climate change has intensified the salinity of diverse soils. Therefore, the search of microorganisms that can bioremediate oil-contaminated saline soils is of increasing importance. The aims of this study are the genetic and functional characterization of native halotolerant hydrocarbon-degrading bacteria. Rhodococcus sp. ICBD2 and Acinetobacter radioresistens DD78 were isolated from contaminated saline soils in Valparaíso Region, Chile. The genome of Rhodococcus sp. ICBD2 was sequenced using illumina and Nanopore platforms, assembled using hybridSPAdes and annotated using DFast. The genome of Rhodococcus sp. ICBD2 is composed of one circular chromosome of 6,351,314 bp, and a linear contig of 387, 366 bp with 62.3% C+G. The sequencing and annotation of A. radioresistens DD78 was performed in a previous study. Through bioinformatic analysis of the genome of A. radioresistens DD78, we identified genes involved in the oxidative stress response, such as oxyR, fur, ahpC, katA, sodB, sodC and fdx genes. Also, we identified genes encoding for osmoprotectant proteins, such as the enzyme of glycine betaine synthesis (betB), and the osmo-dependent choline transporter. We identified genes of Rhodococcus sp. ICBD2 involved in the oxidative stress response such as sod, kat, oxyR, and soxR genes, and the osmoprotector genes encoding ectoine dioxygenase, L-ectoine synthase and Oxygen-dependent choline dehydrogenase. Functional assays revealed that both strains were able to grow in TSA and BHB media in the presence of 0 - 4% NaCl. These results suggest that both strains are capable of surviving in saline soils.

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D27 - Protective role of choline in *Acinetobacter radioresistens* DD78 during hydrocarbons degradation under saline conditions

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Salinity, pH variations and other environmental parameters may limit the bioremediation process. Diverse hydrocarbon degrading bacteria decrease their growth and degradation capability under saline conditions. Acinetobacter species exhibit a wide range of physiological adaptations, which allow them to proliferate in multiple ecosystems, including hostile environments. Acinetobacter strains are commonly applied for the clean-up of soils polluted with hydrocarbons or heavy metals under non-saline conditions. A. radioresistens DD78 is a strain isolated from the Aconcagua River estuary in the Valparaíso region, a site with a history of contamination. Genomic analyses identify key enzymes in the degradation of medium chain aliphatic hydrocarbons, biosynthesis pathway of osmoprotectans (e.g., betICBA, glycine-betaine), and other molecular components associated with the response to salt stress (ion channels and transporters). Functional assays indicate that DD78 strain is capable to grow on aliphatic hydrocarbons as a carbon source, and to tolerate saline conditions of up to 680 mM NaCl. Under saline conditions (300 mM NaCl), DD78 growth on hydrocarbons is strongly reduced. Cell cultures supplemented with choline (0.5 mM) were carried out to promote the production of the osmoprotective glycine-betaine and its protective role against salt stress during hydrocarbon degradation. The growth was evaluated by measuring turbidity and counting CFU during 72 h. The knowledge of the adaptive processes of the DD78 strain during saline stress contributes to the improvement of the bioremediation processes in hydrocarbon-polluted saline soils of coastal sites that are affected by oil spills.

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D28 - Discovering *Eunicea fusca*-derived actinobacterial isolates with a potential photoprotective capability

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Uncontrolled exposure to solar ultraviolet radiation has harmful effects on human health. Photoaging, immunosuppression and the development of some types of skin cancer are among the main UV-induced diseases. Therefore, the use of sunscreens is among the primary measures to counteract photodamage. However, most commercial sunscreens have adverse effects on human health or the environment giving rise to the need to search for new compounds with photoprotective capacity to serve as options for developing safer and eco-friendly sunscreens. Actually, marine invertebrates and their associated microbiota have been described as a prolific reservoir of bioactive compounds. Therefore, this work aimed to isolate actinobacterial strains from the octocoral E. fusca and identify strains producing photoprotective agents. The marine invertebrate was sampling in the Santa Marta Bay, and actinobacterial strains were isolated using GYM and Zobell media. Methanolic extracts were prepared from submerged fermentation of the isolates and its antioxidant capacity and UV-absorbing profile were evaluated to estimate the photoprotective potential. In addition, the cytotoxicity effect was assessed on human dermal fibroblast cells. We obtained 19 isolates, which antioxidant capacities ranged from 12.62% to 53.86% in the DPPH assays and ranged from 47.56% to 97.45% in the ABTS assays. The isolate showing the highest antioxidant capacity was selected and identified by 16S rDNA sequencing. The BLAST analysis showed >99% identity with Gordonia species. Regarding UV protection, the methanolic extract displayed an in vitro sun protection factor (SPFi) of 6.00 ± 0.24 (oxybenzone SPFi = 12.95 ± 0.27). Additionally, this extract reached a better UV-A protection profile than oxybenzone (i.e., extract UVA/UVB ratio = 1.2, oxybenzone UVA/UVB ratio = 0.9 and a higher critical wavelength). These results show a Gordonia sp. as an interesting source of photoprotective compounds that can be useful in the formulation of sunscreens.

D29 - Diversity of polyhydroxyalkanoate synthases in bacteria of the order *Burkholderiales*

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Polyhydroxyalkanoate (PHA) synthases catalyze the final step for the synthesis of PHAs. Four classes of PHA synthases (PhaC) have been described according to aminoacidic sequence phylogeny, substrate specificity and subunit composition. Diverse species of the order Burkholderiales are relevant for PHA production and other biotechnological applications. The distribution of these enzymes within the Burkholderiales order have not been addressed. The aim is to characterize PhaCs encoded in the genomes of bacteria of the order Burkholderiales. A survey through BlastP and Delta-blast algorithms was carried out using 68 genomes selected according to their phylogeny. Aminoacidic sequences, phylogeny and gene synteny of PhaCs were assessed. From all analyzed genomes, 87% possessed at least 1 phaC gene and 74% harbor 2-6 gene copies with the Paraburkholderia, Caballeronia and Cupriavidus genera representing the highest gene redundancy. Three phylogenetic groups were found grouped with previously known class I (60 sequences), II (7 sequences) and III (1 sequence) PhaCs. Specific strains within these groups polymerize short and medium chain length substrates. Interestingly, 37 protein sequences formed two clades separated from the known PhaC classes with identities of 32-45% with Class I PhaC. These enzymes possess a conserved PHA synthase domain (42-70% id) according to Delta blast results. The Cys319-Asp480-His508 catalytic triad along with the lipase-like box in PhaCs from model strains were conserved among all analyzed sequences. Most of the phaC genes grouped with class I and II are arranged in organizations like the canonical phaCABR and phaCZ gene clusters. However, outlier groups are encoded next to genes of acetate, phosphate and polyphosphate metabolism. This study shows the diversity of PhaCs within the Burkholderiales order and their genomic relations with genes of the metabolism of carbon and phosphate and rRNA modification.

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D30 - Characterization of copper tolerance in native strains of *Trichoderma* from the Valparaíso Region, Central Chile

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Trichoderma spp. are filamentous fungi widely used in agriculture for biological control of phytopathogens and as plant growth promoters. Some Trichoderma strains are also resistant to specific heavy metals. The objectives of this study are the molecular identification and the characterization of the copper tolerance of native Trichoderma strains isolated from agricultural soils in Valparaiso Region, Central Chile. The strains Ta22, Ta34 and Ta60 were identified by analyses of the ITS sequence as Trichoderma asperellum. The strains were cultivated in PDA medium in presence of different concentrations of copper ions (0.8, 1 and 1.2 g L-1 CuSO4 × 5H2O). Tolerance and radial growth rates were determined, and the growth was modeled. Strain Ta22 showed the lowest inhibition (12.5%) by copper 1.2 g L-1. Strains Ta34 and Ta60 showed higher inhibition (27.9% and 46.9%). The radial growth rate (RGR) was determined by using a linear model. For the control without copper, RGR values of 0.030 (Ta22), 0.030 (Ta34) and 0.029 (Ta60) mm/h were calculated. At the maximum concentration of copper evaluated (1.2 g/L), RGR values of 0.014 (Ta22), 0.021 (Ta34) and 0.026 (Ta60) mm/h were observed. Different non-linear models such as Gompertz, Logistic, Richards were evaluated to describe the growth of the fungus. The statistical validation and selection of the models was carried out by applying the Akaike Information Criterion (AIC), Bayesian Information Criterion (BIC), adjusted R2, □2 (Chi-square), Least squares of residuals. The coefficients that describe the different models were obtained, related to the growth parameters of the fungus for the different conditions. The Gompertz model adjusted well the cell growth data, through which the maximum specific growth rates 0.027 h-1 (Ta22), 0.028 (Ta34) and 0.026 (Ta60) were determined for the control conditions.

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D31 - Genome analysis of two manganese-oxidizing bacteria suggests manganese oxidation required for cylindrospermopsin transformation is mediated by enzymatic processes

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Cylindrospermopsin is a highly persistent alkaloid cyanobacterial secondary metabolite toxic to humans and other living organisms. Strain OF001 and A210 are manganese-oxidizing bacteria able to transform cylindrospermopsin during the oxidation of Mn2+. So far, the enzymes involved in manganese oxidation in strains OF001 and A210 are unknown. Therefore, we analyze the draft genomes of the two cylindrospermopsin-transforming manganese-oxidizing bacteria, Pseudomonas sp. OF001 and Rubrivivax sp. A210, to in silico identify the enzymes potentially involved in the oxidation of Mn2+. We also investigated specific metabolic features related to pollutant degradation and explored the metabolic potential of both manganese-oxidizing bacteria concerning the role they may play in biotechnological applications and/or in the environment. The genomes of Pseudomonas sp. OF001 and Rubrivivax sp. A210 encode sequences with high similarity to already described multicopper oxidases and haem peroxidases which may catalyze manganese oxidation required for cylindrospermopsin transformation. Strain OF001 and A210 have genes that might confer them the ability to remove aromatic compounds via the catechol meta- and ortho-cleavage pathway, respectively. Furthermore, both strains have a broad metabolic potential which may allow them to grow over a wide range of O2 concentrations, fix nitrogen, and form biofilm. The analysis of the general metabolism of the two manganese-oxidizing bacteria strains, including the enzymes potentially involved in manganese oxidation, may contribute to a better understanding of the niches of cylindrospermopsin-removing manganese-oxidizing bacteria in natural habitats and their implementation in biotechnological applications to treat water.

D32 - Evaluation of polyvinyl chloride biotransformation by freshwater-derived *Streptomyces* strains

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Polyvinyl chloride (PVC) is widely used for many industrial applications such as construction, clothing, etc., due to its chemical/physical, and environmental resistance. These characteristics make PVC the third most consumed plastic worldwide and, consequently, an increasing waste accumulation problem. In the current research, 62 Actinobacteria strains from the Bioprospecting Research Group were evaluated for PVC resin biotransformation (i.e., powdered samples with 150 µm particle size). Hence, an initial screening on ISP-2 broth was done, and an evaluation on Mineral Salt Medium (MSM) with PVC resin as the sole carbon source (2 g/L) was then carried out. Weight loss percentage was measured for each strain after incubation time completion (i.e., 18 days) on both culture media. Strains with more than 50% weight loss on ISP-2 were identified by the 16S gene sequencing. Thermogravimetric analysis was subsequently performed for the PVC incubated with three strains with higher weight loss on MSM. GC-MS analysis was also performed for the organic extract of culture media supernatant of these three strains. Once incubation time was reached, 14 strains showed a PVC weight loss percentage higher than 50% on ISP-2 broth, which were evaluated in MSM obtaining PVC weight loss percentages between 21 and 61%. These 14 strains were identified as Streptomyces strains. Strains coded as 208, 250, and 290 showed higher weight loss percentage values, i.e., 57.6%, 60.2%, and 61.5% respectively. The thermal stability of PVC after bacterial exposure, using these three strains, was evaluated and a modification against the representative degradation stages of non-incubated PVC was observed, indicating possibly a change on polymer's backbone. Additionally, GC-MS analysis showed the presence of aromatic compounds on inoculated culture media. The results of gravimetric, thermal, and GC-MS analysis observed in this work evidence an interesting potential of freshwater-derived Streptomyces strains as candidates for the PVC biotransformation strategy.

D33 - Isolation and characterization of glyphosate-degrading bacteria (GDB) isolated from Uruguayan soils

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Glyphosate (N-phosphonomethyl-glycine) is an herbicide used for in crop weed control, developed by .Monsanto company in 1974 known as Roundup ®. It is the leading herbicide for the control of annual and perennial weeds, chemical fallow and weeding in urban areas. It represents in average more than 50% of the imported herbicides in Uruguay in the last years, accompanying the introduction of genetic modified crops. Being a polar compound, it can be transported to aquatic systems, and despite its relatively short half-life compared to other pesticides, when it is combined with soil particles or sediment, its persistence may extend. As a consequence of its extensive use, the concern on its environmental toxicity have arisen. Bioremediation strategies can use the ability of microorganisms to convert harmful toxic substances into less toxic forms. When possible, to confine runoff waters, microorganisms could be used as remediation agents for glyphosate, immobilizing them in inert matrices that allow their later removal. Seven different microbial strains were isolated from glyphosate-contaminated sites in Uruguay. All of them were able to grow in a medium containing glyphosate as the sole phosphorus source at 6 mM. They were identified based on 16s rRNA and biochemical tests as Stenotrophomonas sp. and Acinetobacter sp, Ochrobactrum spp., Pseudomonas sp. Four strains from the last two genus were able to grow when glyphosate was introduced as a sole carbon source at 1.8 mM and may be using AMPA pathway. Acinetobacter sp. demonstrated to use glyphosate as the only P source at comparable growing rates. Therefore, the co-metabolic pathway, which is the use of glyphosate as P source while relying in other nutrients as C source seems to be the most reasonable pathway to degrade glyphosate while achieving the highest growth rates.

D34 - Integration of bioinformatic tools in a automatized workflow for the search of novel biosynthetic gene clusters

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Novel antimicrobial compounds are a major need. The appearance of multi-resistant bacterial pathogens is a reality that hospitals worldwide must face daily. In addition, after the golden age of antibiotics we are facing the high re-discovery rates of the same compounds, leading us into a dangerous position that even the World Health Organization catalogued as a global crisis. To contribute to this problem, our research group have collected marine samples from the Chilean coastline for the search of actinobacterial strains with antibiotic activity. These strains present a wide phylogenetic distribution, showing an example of the extensive biodiversity of the Chilean marine environment. To unlock the true biosynthetic potential of these bacteria, the complete genome of 25 Streptomyces strains were sequenced and used for mining their Biosynthetic Gene Clusters, which are groups of genes that together synthesize specialized metabolites. Genomes presented an average of 8,0 Mbp in length, 72 % of G+C content and approximately 20 BGCs per strain, involved in the synthesis of several specialized metabolites according to predictions using the softwares antiSMASH and PRISM. Here we present a bioinformatic automatization workflow written on python 3.7 than can be used for the search of novel biosynthetic clusters, that goes from the download of genomes from Refseq database, analysis of quality and filtering of assemblies through CheckM, and visualization of similarity networks through BiG-SCAPE. This workflow allows us to efficiently analyze, compare and characterize our collection's biosynthetic clusters versus both its closest phylogenetic strains and the complete MIBiG database.

D35 - Cloning, expression and evaluation of a GH10 alkali xylanase from termite gut microbiomes

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In recent years, interest has increased in the development of robust biocatalysts both for the hydrolysis of lignocellulosic biomass and for the synthesis of value-added bioproducts. Termites are among the most efficient lignocellulose decomposers on earth, with hydrolysis efficiencies of up to 90%. This capacity to degrade lignocellulose relies on both mechanical and enzymatic machinery of the termite host, together with the action of intestinal symbiont enzymes. This metabolic potential makes termites an ideal target to search for microbial lignocellulosic enzymes that might be used in the textile, food, animal feed, paper and biofuel industries. The aim of this work was the molecular cloning, heterologous expression and activity evaluation of a endo-1,4-beta-xylanase (Xyl10B) from termite gut microbiome. Xyl10B was identified in a previous study by our group. The BLAST analysis of the amino acid sequence of Xyl10B against Genbank showed 59% identity and 97% coverage with a GH10 from an uncultured bacterium (AGS53960). In addition, a comparative computational modeling was performed using ITASSER. That structural-based modeling analysis indicated that this xylanase possesses a typical eight-fold TIM-barrel characteristic of GH10. The complete Xyl10B coding sequence was cloned into the plasmid pET-28b(+). The recombinant protein expressed with a N-terminal 6xHis fusion tag and purified by immobilized metal affinity chromatography. By SDS-PAGE a protein of 46 KDa (Xyl10B), in agreement with the expected molecular weight, was obtained and identified. The recombinant purified enzyme showed xylanase activity by hydrolysis of beechwood xylan and generation of reducing sugars. According to enzymatic activity assays, Xyl10B had a specific endo-1,4-beta-xylanase of 255 IU/mg of enzyme, with an optimum activity at around 50 °C and pH 8. Enzymes adapted to very specific and regulated environments are very promising candidates for hemicellulose degradation within the constraints of a biotechnological process.

D36 – *Pseudoxanthomonas indica* strain H32 as an efficient biofertilizer for agricultural crops of chard, carrot and radish

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One of the main problems in agriculture todays is the reduction of chemical fertilizers and to replace them with bioferlizers composed of beneficial bacteria for soils and plants. Therefore the aims of the present work was to evaluate the effect of the strain Pseudoxanthomona indica H32, previously isolated from tomato rhizosphere, on the growth, development and yield of chard, carrot and radish crops. For this, the seeds were swollen in a suspension of a H32 culture at a concentration of 105 cfu / ml. The sowing was carried out in plots of 1m wide by 5m long and seven days after the germination of the seedlings, the bacteria were inoculated on the soil around their root zone. As a control, the same number of seeds of the three crops were sown, but without any contact with the bacteria. At the end of the growth cycle of each crop, the plant weight was determined and the yield in each plot was calculated. The increase in yield was calculated in the plots treated with the bacteria, with respect to the untreated plots. In the three crops, the positive effect caused by H32 on plant growth was observed and the yield increased by 15% for radish, 50% for chard and 38% for cultivation of the carrot. This fact can be attributed to the ability of H32 to colonize the root, to produce the auxin indolacetic acid and to solubilize the phosphate, properties previously demonstrated that confer characteristics of a plant growth-promoting bacteria with potential for use as a biofertilizer.

D37 - Evaluation of the antibacterial activity of marine actinobacteria extracts against *Staphylococcus epidermidis*

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Staphylococcus epidermidis frequently cause nosocomial bacteremia and skin diseases like acne vulgaris. The inappropriate antibiotic treatment causes multi-resistant strains. Therefore, the search for new antibiotics is needed. Here we evaluate the antibacterial potential of marine actinobacteria ethyl acetate extracts, as actinobacteria have been an important source of active compounds in the past decades. Twenty marine actinobacteria strains were obtained from the Bioprospecting group of the Universidad de La Sabana collection and screened against S. epidermidis. The growth curves were calculated according to the Baranyi and Roberts model using gentamicin as positive control and the medium with no extract, as a negative control. Significant antibacterial activity was observed in six isolates; B4-17 and B4-16 decreased S. epidermidis growth rates showing pharmaceutical or cosmeceutical potential.

D38 - A customized toluene dioxygenase platform for the production of cis-1,2-dihydrocatechol in *Escherichia coli* BW25113 lacking glycerol dehydrogenase activity

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One of the most studied and widely characterized Rieske non-heme iron dioxygenases in literature is toluene dioxygenase (TDO) from Pseudomonas putida F1. The fascinating features of this enzyme combine a large substrate scope along with an outstanding product formation and enantioselectivity. Nevertheless, in the last decades, in spite of the frequent utilization of recombinant Escherichia coli cells harboring TDO, neither the plasmid system was optimized, nor the E. coli strain was objectively selected. In this work, a robust and enhanced TDO-based platform for the selective cis-dihydroxylation of benzene was generated and designated as E. coli BW25113 pBAD18-TDO. The unforeseen dehydrogenation of the monocyclic cis-dihydrodiendiol to its corresponding catechol, performed by E. coli, was circumvented by opportunely identifying the enzyme glycerol dehydrogenase (GldA) as responsible for the downstream degradation. Based on this knowledge it was established the customized platform E. coli BW25113 ΔgldA pBAD18-TDO, which allowed to practically abolish the unwanted secondary reaction, enabling the formation of 9.0 mM (90%) of cis-dihydrocatechol from the simple and accessible substrate benzene, in analytical scale. These results settled the foundations to perform a semi-preparative biotransformation of benzene in 100 mL scale, resulting in the selective generation of 141 mg (31%) of the valuable synthon cis-dihydrocatechol. Furthermore, it was found that the substrate scope for the GldA-driven degradation only includes monocyclic cis-dihydrodiendiols but not bicyclic ones.

D39 - Diversidad microbiana durante la biofiltración de H_2S y NH_3 en condiciones transitorias de concentración

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La biofiltración es una biotecnología de alta eficiencia y bajo costo para la remoción de sulfuro de hidrogeno (H2S), amoniaco (NH3) y compuestos orgánicos volátiles emitidos en el tratamiento de aguas residuales. Sin embargo, en la biofiltración simultánea de H2S y NH3 se ha reportado que, cuando hay cambios drásticos en la concentración, la eficiencia de remoción de los gases disminuye debido a la inhibición de la oxidación biológica de estos compuestos. Por esto, el objetivo de este trabajo fue evaluar los cambios en la comunidad microbiana y en la oxidación de los gases durante la biofiltración de H2S y NH3 bajo condiciones transitorias de concentración usando biofiltros empacados con compost de pollinaza y bagazo de caña. Durante el proceso se cambió el tiempo de residencia (60, 45, 33, 25 y 18s) a dos niveles de concentración (52 mgH2S/m3 y 2 mgNH3/m3; 260 mgH2S/m3 y 10 mgNH3/m3). Al evidenciar cambios en la eficiencia de remoción de los gases, se tomaron muestras de lecho para analizar la comunidad microbiana mediante la secuenciación de amplicones del gen 16SrRNA, y los productos de la oxidación de H2S y NH3. La eficiencia de remoción del H2S y NH3 fue de 100% a 60 y 45 s en los 2 niveles de concentración, sin embargo no se evidenció aumento en la concentración de sulfato ni de nitrato, productos de la oxidación de H2S y NH3. Al disminuir el tiempo a 25s y aumentar la concentración de gases, la remoción disminuyó pero aumentó la concentración de sulfato y nitrato. Las clases más abundantes fueron Actinobacteria, Gammaproteobacteria, Alfaproteobacteria, Bacteroidia y Bacilli, siendo este último el de mayor variación durante la evaluación. También se observó la presencia de géneros alcalófilos y halófilos como Halomonas, que pueden estar relacionados con la acumulación de sulfato y amonio en el lecho.

D40 - *Bacillus thuringiensis* parasporin-6 associations in the context of uterine cancer

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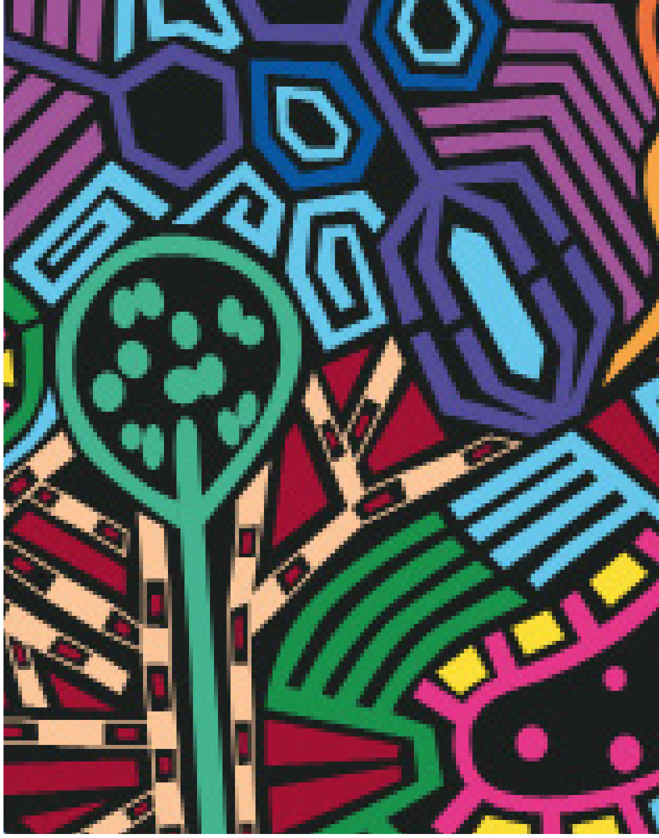
Uterine cancer appears after fourth decade of life, their risk factors include sexual promiscuity, human papillomavirus, human leukocyte antigen, some contraceptives, or cigarettes. Uterine cancer is classified as squamous cell carcinoma, adenocarcinoma, adenosquamous carcinoma, and neuroendocrine carcinoma. Treatments are very aggressive and include surgical excision, hysterectomy, radio and chemotherapy. Bacillus thuringiensis is a bacterium that is used as biopesticide in commercial agriculture as pathogen of insects. Their principal virulence factor is a class of proteins named Cry, these three domain proteins are very specific because they interact with protein receptor in host cells. A special type of Cry proteins with anticancer activity are parasporins (PS) including PS1, PS3 and PS6. PS6 has activity against uterine cancer cells, but the proteinic receptor is unknown yet. Cry proteins interact with cadherin (CADR), aminopeptidase N (APN) or alkaline phosphatase (ALP) receptors in insect midgut epithelium, particularly through domain II. This work shows an in silico characterization of the networks of PS6 with human proteome, and note that the study uses a yeast two hybrid (YTH) assay for determination of cervical cancer proteins responding to PS6 domain II. PS6 domain II has determinants related to receptor recognition (residues 453-520). STRING 11.0 was used to find human proteins that interact with CADR, APN or ALP receptors encountered in human genome by analogy with their insect equivalents, so, 30 proteins associated with signaling pathways and transcription factors were determined including the HeLa cell-related protein leucine aminopeptidase 3. The YTH assay showed that 11 proteins specifically from cervical cancer cells interacted with PS6 domain II such as COPS5, ATP6V1B2 and EIF4G1 (related to HeLa cell proteome). This is the first research that exposed protein-protein interactions between PS6 and human proteins associate to uterine cancer.

POSTER SESSIONS



E

METHODS APPLIED IN MICROBIAL ECOLOGY AND COMPUTATIONAL TOOLS

E1 - Comparative genomics reveals *Bacillus velezensis* genes and their importance in the ecological relationship with plants

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The Bacillus amyloliquefaciens operational group has three species, B. amyloliquefaciens, B. velenzesis and B. siamensis. B. amyloliquefaciens had two ecotypes, non-plant associated (subspecies amyloliquefaciens) and plant associated (subspecies plantarum), where the latter was renamed as B. velezensis. But, currently there are reported strains of B. velezensis as non-plant associated and strains of B. amyloliquefaciens that are beneficial to plants. The genomic comparison between members of these species would allow the knowledge of their genetic characteristics and their ecological relationship with plants. The objective of this work was to carry out a comparative genomic analysis of strains of B. amyloliquefaciens and B. velezensis to determine distinctive genes of both species that allow explaining their attributes as plant growth promoters and biological control agents. 44 genomes of B. amyloliquefaciens and B. velezensis reported as associated with plants or not, were used in the comparative analysis with the ROARY software, including the Colombian biocontroller strain IBUN 2755. Later, distinctive genes were determined for the groups obtained and classified in orthologs. The genomic comparison allowed the separation of the strains into two clades, one that groups strains associated with plants or close to B. velezensis FZB42 and the other with those non-plant associated or close to B. amyloliquefaciens DSM7. According to the ANIb index, it was found that strains of B. amyloliquefaciens associated with plants should be renamed as B. velezensis. The IBUN 2755 strain was located within B. velezensis. Those plant associated strain present distinctive genes related to biological control, biofilm formation, colonization and competition, metabolism of carbohydrates, inorganic ions and amino acids, and a large number for the production of antimicrobial compounds. This suggests a close ecological relationship of these strains with plants. Both groups have a many of hypothetical and unknown genes.

E3 - Estandarización de una PCR en tiempo real para la detección de *Ralstonia solanacearum* filo IIB4 a partir de muestras de suelo rizosférico

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La bacteria Ralstonia solanacearum es el agente causal de la enfermedad del Moko, uno de los problemas fitosanitarios más limitantes en plantaciones de plátano y banano, generando importantes pérdidas económicas y largos tiempos de cuarentena en unidades agrícolas productivas. El desarrollo de un método de diagnóstico temprano, específico y sensible de este patógeno en el suelo y tejidos de plántulas, previo al establecimiento del cultivo, es prioritario para evitar sus efectos negativos en plantas adultas. En este trabajo, se propone una metodología basada en PCR en tiempo real para la detección de la bacteria a partir de muestras de suelo rizosférico. Se diseñaron cebadores con base en el gen que codifica para la endoglucanasa (egl) del filo IIB4 de R. solanacearum y se estandarizaron condiciones óptimas de qPCR empleando SYBR Green para la amplificación de un fragmento de 108pb. Se determinó que el método es altamente sensible, llegando a amplificar hasta 9.6x10-5 ng/μL de ADN obtenido de células de cultivo de la bacteria. Posteriormente se confirmó una alta sensibilidad experimental mediante el análisis de muestras de ADN de suelo sin bacteria y muestras inoculadas con concentraciones conocidas de la bacteria. En todos los casos las muestras provenientes de muestras de suelo sin bacteria no presentaron amplificación, mientras que todas las muestras de suelo rizosférico infectado con R. solanacearum fueron positivas. La especificidad de la reacción se determinó empleando ADN obtenido de los fitopatógenos Xanthomonas spp. y Pectobacterium spp., sin obtener ninguna amplificación. Este método de detección y cuantificación de R. solanacearum aplicado a muestras de suelo, previo al establecimiento de cultivos de banano y plátano, puede ser implementado como una medida de prevención de la enfermedad del Moko con sus efectos benéficos en la sanidad vegetal y en la productividad.

E4 - Exploring microbial production of mycosporine-like amino acids in metagenomes from soda lakes of Brazilian Pantanal

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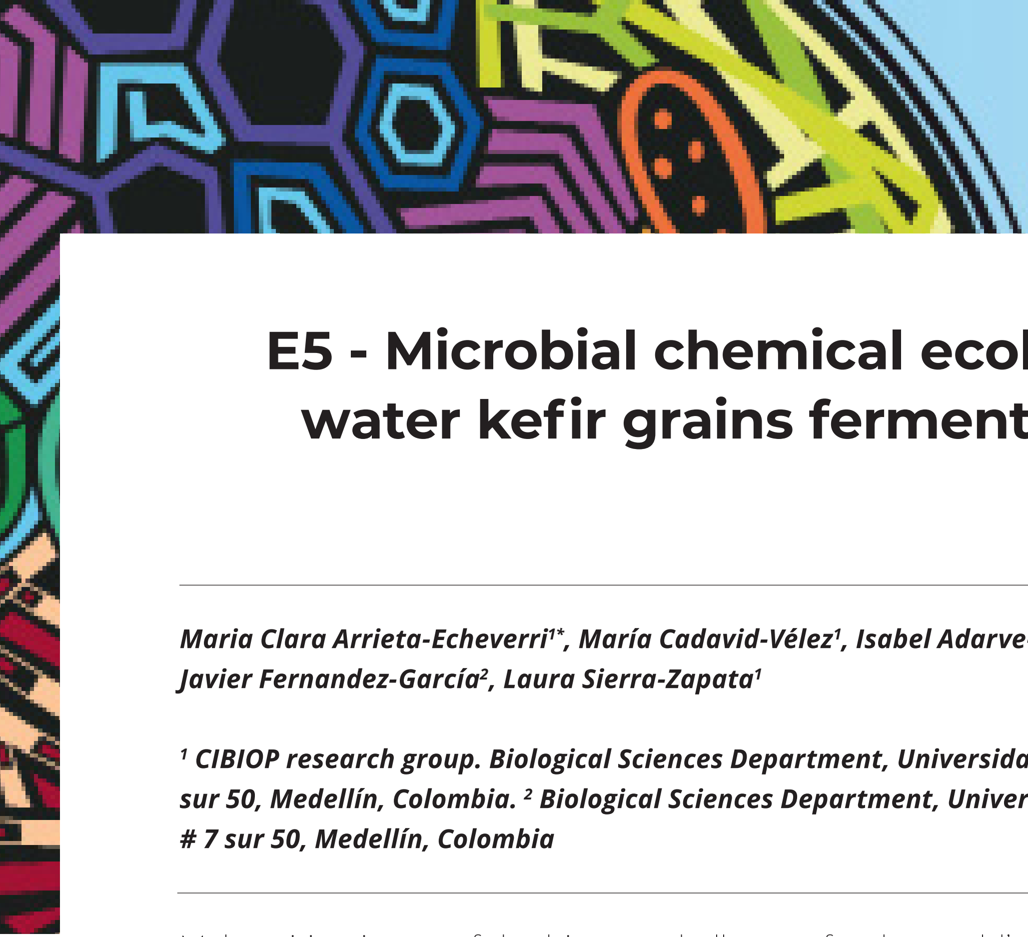
Soda lakes are hypersaline aquatic environments with elevated pH (9 and above) and high concentrations of NaHCO3. These lakes occur in several locations around the globe, but in tropical latitudes such as Brazilian Pantanal, Africa and Australia, their physicochemical settings are similar, fostering the growth of diverse microbial communities that resist the saline condition. The phytoplankton of these lakes are continuously exposed to high levels of UV radiation and temperatures, which may be stressing factors. In these communities, cyanobacteria are the main microorganisms responsible for the production of photo-protective pigments, such as mycosporine-like amino acids (MAAs), which can protect themselves and possibly be used by other bacteria. By applying metagenomics, it was possible to evaluate the presence of specific genes associated with MAAs in a soda lake from Pantanal (identified as 04SR). This lake is nutrient rich (nitrogen and phosphorus), with average water temperature of 26°C and pH 10. The biosynthesis pathway of porphyra and shinorine, two of the most explored MAAs, involve the genes DHQS, SAM-dependent/O-methyltransferase, ATP Grasp/D-ala D-ala ligase and AMP-binding from a non-ribosomal peptide (NRPS). A manual library was created using sequences of these genes from strains that are described as MAAs producers. The analyses of the sampled metagenome was then carried out in MGRast using as reference databases RefSeq for taxonomy and COG for metabolites hierarchy. Out of the four genes evaluated, two of them (SAM-dependent/O-methyltransferase and AMP-binding) presented more hits associated with cyanobacterial sequences. Other bacterial phyla, such as proteobacteria, bacteroidetes and actinobacteria, had significant hits, possibly related to orthologous genes. The presence and abundance of the specific genes associated with the biosynthesis of MAAs at the soda lake 04SR demonstrates the potential of the phytoplankton, specifically the cyanobacteria, from this environment to be used in biotechnological applications.



E5 - Microbial chemical ecology of water kefir grains fermentation

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Malnutrition is one of the biggest challenges for the world's population, being the leading causal agent of mortality and morbidity worldwide. Improving the food system with an adequate amount of micro and macronutrients is considered a priority. In this way, fermented foods offer nutritional benefits, increased food safety and a longer shelf life. One of these is water kefir – symbiotic colonies of yeast and bacteria –. We aim to characterize the dynamic communities and associated metabolites production of a water kefir fermentation, using a multi-OMICS approach: compositional metagenomics, directed culturomics, and untargeted metabolomics. We collected two types of samples: fermentation grains and liquor at different times. For the culturomics approach, four semi-selective culture media were used for different microbial groups: yeast (YMA), lactic-acid bacteria (MRS), acetic-acid bacteria (WL), and total molasses degrading microbial biomass (MM). In addition, sequencing of the 16S rRNA gene and ITS region were performed. Growth patterns and microbial composition in relative abundance were obtained for the kefir fermentation for culturable strains belonging to the microbial groups and for total bacteria and yeast sequences by metabarcoding analysis. Besides, 99 strains have been isolated using the culturomics approach and stored in the collection for ongoing molecular identification. Metabarcoding analysis suggested that the fermentation can be classified as water kefir as the abundance of the groups is similar to the genera reported: Lactobacillus and Acetobacter. Monitoring fermented foods through multi-omics approaches enables the identification of microbial population patterns and detection of specific points of enrichment of the most favored microbial groups and metabolites during the fermentation process. This allows the integration of biological (microbial biodiversity/cultured species) and chemical data for the ulterior design and formulation of synthetic consortia that can be further used as active pharmaceutical ingredients (APIs) or probiotics supplements for specific metabolic enhancements in the host.

E7 - Metabolic pathway of terpenes in metagenome-assembled genomes from Brazilian soda lakes

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The Brazilian Pantanal is the largest tropical wetland in the world with hundreds of soda lakes, an extreme environment due to its high pH and salinity. In several of these lakes occur blooms of cyanobacteria, which are photosynthetic oxygen bacteria that, like other organisms, produce several specialized metabolites, such as toxins and pigments, many of which have biotechnological applications. Among these compounds is the terpenes group, which are involved in activities related to photosynthesis, electron transport and antimicrobial activity. Despite being a diverse group of compounds, the precursor of all the terpenes is the same isopentenyl diphosphate carbon, which can be produced from two different pathways, being the methylerythritol-4-phosphate (MEP) pathway present in cyanobacteria. Genome mining tools have contributed to the discovery of new natural products with potential for biotechnological application, mainly through the identification of gene clusters and prediction of metabolic pathways, facilitating the process of bioprospecting. This study aimed to identify the genes of biosynthetic pathway and terpenoid gene clusters in metagenome-assembled genomes (MAGs) of cyanobacteria from saline-alkaline lakes of Brazilian Pantanal. The metagenomic sequencing of water samples from six lakes was carried out at two periods (October/2017 and September/2018), the sequences were filtered for quality and the MAGs were assembled. Functional annotation of the MAGs was performed with PROKKA and the gene clusters potentially involved in terpene syntheses were analyzed using the antiSMASH program. The terpenoid metabolic pathway was analyzed by KEGG and BLAST using the amino acid sequences. Gene clusters of scalene/phytoene synthase precursors of pigments such as carotenoids, zeaxanthin and astaxanthin were predicted by the antiSMASH and KEGG platform. However, in four MAGs among 11 evaluated, only few genes for terpene biosynthesis were not found. This genome mining study showed that cyanobacteria MAGs from soda lakes are an important source of potential terpenoid exploration.

E8 - Modelado y simulación de consorcios microbianos para la producción de polihidroxialcanoatos empleando balances de flujo dinámicos y restricciones termodinámicas

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Bajo el marco conceptual de la Biología Sintética se busca rediseñar vías metabólicas ya existentes o generarlas de novo con el objetivo de producir metabolitos químicos de interés industrial. Las mejoradas técnicas de biología molecular hacen cada vez más posible la implementación en chasis microbianos de redes metabólicas diseñadas in silico. Los polihidroxialcanoatos (PHA), son poliésteres intracelulares sintetizados por diferentes especies de bacterias con alto potencial para ser empleados en la fabricación de plásticos que puedan ser sustitutos de los polímeros de origen petroquímico. Para mejorar su selectividad se requiere el uso de rutas bioquímicas específicas. En estado natural, consorcios de microorganismos participan en la generación de PHA y según el sustrato y las restricciones metabólicas emplean diferentes rutas para su producción. En este trabajo, empleando un modelo de equilibrio de flujo dinámico para el análisis de redes metabólicas, y haciendo uso restricciones termodinámicas para la identificación de la viabilidad de rutas bioquímicas, se modelaron y simularon consorcios binarios de microorganismos para emular la producción de PHA bajo condiciones de estrés nutricional, se encontró que los consorcios diseñados bajo el supuesto de crecimiento limitado de C:N en relación 20:1 mostraron las más altas concentraciones intracelulares del biopolímero, también se identificó que las interacciones de consorcios dieron como resultado la propiedad emergente de mejorar la productividad del sistema comparado con simulaciones de microorganismos individuales. Los modelos obtenidos representan un primer paso en el diseño in silico de consorcios microbianos para la producción eficiente de PHA. Los modelos pueden ser mejorados al considerar condiciones como pH y Temperatura al estimar la termodinámica. Este trabajo permite crear un mapa inicial de potenciales rutas útiles entre dos compuestos dados. Las vías identificadas deben ser optimizadas en análisis más profundos antes de que se pueda intentar implementación experimental in vitro o in vivo.

E9 - Cyanobacteria circadian mechanism: multicellularity and environment as a modulating factor

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Cyanobacteria are the oldest known organisms with a functional circadian clock. KaiABC is the central oscillator, which together with CdpA, IrcA, LdpA, NhtA, Pex, PrkE, CikA (signal detection proteins - input pathway), and CpmA, Crm, LabA, LalA, RpaA, RpaB, SasA (transcriptional regulators - output pathway), coordinate an adequate response to light-dark cycles. The circadian regulation is well described in unicellular cyanobacteria, but is rather unknown in filamentous organisms. In this work, we focused on determining the relationship between the presence/absence of 17 circadian genes and cellular phenotype, as well as considering the environment as a modulating factor. Using BLASTP and InterProScan, we searched for homologous sequences of these genes in 868 cyanobacterial genomes (NCBI RefSeq database), which had to have certain sequence similarity parameters and critical functional domains to be selected. Our analysis showed that only 12.4% (108) of the genomes have at least one copy of these 17 genes, corresponding mainly to filamentous members of the Nostocaceae family. Furthermore, when relating morphology and gene presence, we found that some genes are more abundant in filamentous than unicellular cyanobacteria (pex, prkE, cikA, labA, lalA), while others are reduced (crm). On the other hand, the study of different habitats (marine, freshwater, terrestrial, among others) suggests that marine environment favors the reduction of the number of the circadian genes kaiA, cdpA, pex, prkE, cikA in unicellular organisms, however the presence of crm is favored in thermal environments. This suggests that the cellular phenotype (unicellular vs multicellular) and the environment could be modulating the circadian mechanism. Further statistical correlation analyses are still needed to demonstrate this. In addition, the effect of gene absence on circadian dynamics needs to be determined.

E10 - A novel pipeline for taxonomic and diversity analyses using QIIME 2

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Taxonomic assignment and diversity analyses of amplicon sequencing are fundamental steps in microbial ecology studies. QIIME 2 is one of the most-used packages facilitating microbiome studies as provides data standards, wrapped tools, and a visualization environment. Automation of usual amplicon processing steps in QIIME 2 is frequently required in studies following more or less fixed procedures wherein command line execution becomes almost repetitive, laborious and prone to user mistakes. Furthermore, operating time and calculation are reasons of concern during the processing of datasets proceeding from several sequencing runs since denoising of reads is recommended to be done on a per-run basis. Here, we implemented a fast QIIME 2 (version 2020.11) execution-based pipeline for taxonomic and diversity analyses of 16S rRNA paired-end reads. This pipeline uses Bash scripting to automate usual steps while processing datasets of multiple sequencing runs in a single execution and maintaining parameter customization as required. As tested with two microbial community datasets from the public resource mockrobiota (https://github.com/caporaso-lab/mockrobiota) and the QIIME 2 tutorials (https://docs.qiime2.org/2021.4/tutorials/atacama-soils/), this pipeline reduced up to 57% the execution time of microbial analyses encompassing the following steps: Demultiplexing, trimming and denoising, merging data, taxonomy classification, exclusion of samples, and diversity analysis. Default QIIME 2 output data is retrieved for each step. The pipeline resources are currently available in GitHub (https://github.com/mdelacuba/pipeline-qiime-2) and prone to updates. In conclusion, this pipeline contributes to optimizing execution time for microbiome analyses of several sequencing runs using QIIME 2.

Acknoledgment: This work was supported by Agencia Nacional de Investigación y Desarrollo (ANID) doctoral scholarship N° 21211164.

E11 - Combining molecular primer design and Ecological Niche Models for the arbuscular mycorrhizal fungi *Rhizophagus clarus*

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Rhizophagus clarus is a species of arbuscular mycorrhizal fungi (AMF) with wide occurrence and beneficial interaction with several plant species, agricultural crops such as soybean and maize or forest species. As AMFs have a preference for certain environmental gradients, predictive models of environmentally suitable areas for their inoculation can assist in decision making. Here, combining molecular and biogeographical analyses, we developed a pair of ITS primers for identification and Ecological Niche Models (ENMs) to model environmental suitable areas for R. clarus. Nine AMFs species were tested by PCR to show specificity of our primers. For ENMs, occurrence data were filtered from the Global Biodiversity Facility (GBIF), germplasm banks and literature review. We generated three models (Climate; Climate + Soil; Soil) with 10 replications and cross-validation data partition. Our results showed that the DNA of R. clarus and R. intraradices were amplified, so we consider that the designed primers may be useful to identify R. clarus in field conditions. All ENM models showed good performance reaching mean values of AUC higher than 0.8 and omission errors less than 0.12. According to the Jackknife test, the climate variables mean temperature of driest quarter; temperature seasonality and annual precipitation had the greatest influence on distribution in both Climate and Climate + Soil models. Soil model indicated that cation exchange capacity, pH, and percentage of silt particles as the most important variables. ENM models predictions indicated environmental suitable areas for the use of the species as inoculant in several countries, especially in Brazil (16,55% of the total). As a result of the amount of environmental suitable areas and the identification method developed here, we hope that our results can contribute to encourage the use of the species R. clarus as a mycorrhizal inoculant, as it may help reaching an agriculture less environmentally harmful.

E13 - Metabiome: a flexible and modular pipeline for metagenomic analysis

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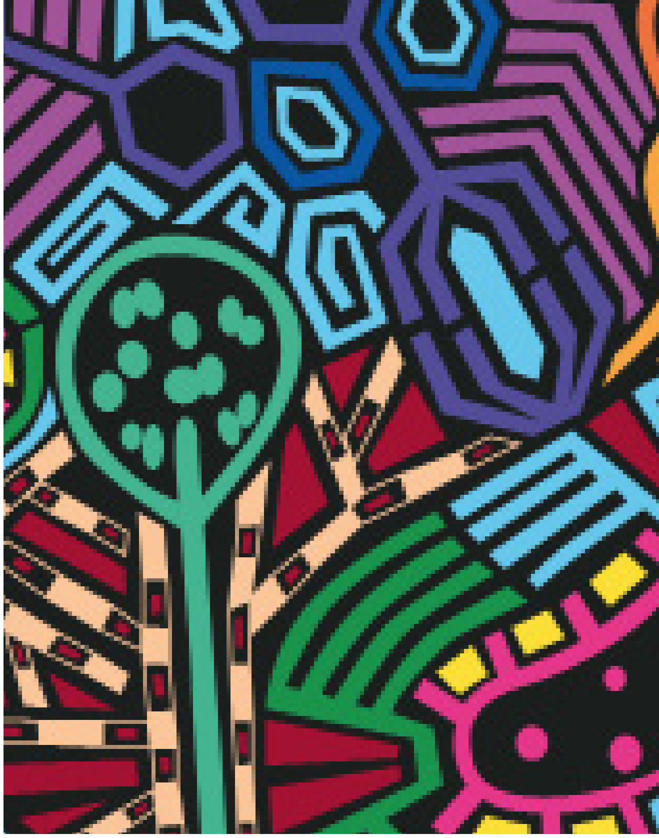
Analysis of metagenomic data is often a complex task that involves the use of a set of different bioinformatic software in order to go from raw reads to interpretable and useful information about a microbial community. Although these software packages can be integrated into bioinformatic pipelines to facilitate their use to the scientific community, most of the bioinformatic pipelines to date do not show greater flexibility. And sometimes they require previous knowledge in different programming languages. Therefore, we present Metabiome, an easy-to-use, open-source metagenomic pipeline that performs preprocessing, functional and taxonomic profiling, genome assembly and binning of short sequencing reads from Next-Generation-Sequencing (NGS) technologies. Metabiome is a command-line tool that consists of Bash wrapper scripts that are contained in different Conda environments (modules). It is easily installed through Conda and can work with different GNU/Linux distributions. Moreover, Metabiome has an easy command-line interface that does not require deep knowledge in Bash programming. Each of the Metabiome's modules contain up-to-date bioinformatic software that perform specific tasks of the metagenomic analysis. The modules also provide flexibility because the user is free to choose which of them to use. Likewise, the user is also free to choose the options to run each of the bioinformatic software that are contained within the modules. Metabiome has been tested on a previous mouse gut microbiome study showing similar results, and including the detection of novel microorganisms which were not reported in the original article. Taken all together, Metabiome will ease the work in metagenomic analysis for non-bioinformaticians, by providing an easy-to-use, module-based and customizable metagenomic pipeline.

POSTER SESSIONS



F

EXTREMOPHILES

F1 - An antarctic *Rahnella inusitata* showed polyextreme adaptability and cold-active β-galactosidase enzymes based on genomic analysis.

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Antarctica is a hostile habitat that can be defined as a polyextreme environment, given the multiple harsh conditions for life –low temperatures, limited water bioavailability, high solar radiation, presence of heavy metals and others–. There is a great interest in discovering new enzymes from polyextremophile microorganisms, also called extremozymes, for industrial purposes. Exploration of cold-active β-galactosidases has increased since it offers new alternatives in the dairy industry for lactose-intolerant consumers (~65% of the world's population). Then, this work aimed to study the genomic features related to the polyextreme adaptability of an Antarctic Rahnella inusitata Se8.10.12, a cold-active β-galactosidase producer. Based on whole-genome sequencing and molecular characterization, this is the first report of R. inusitata species on the Antarctic continent. Gene ontology showed that absent genes on this Antarctic strain are related to two biological processes: sporulation and response to zinc ion. Comparative analysis of orthologous clusters revealed the presence of 101 protein families in the Antarctic strain that is absent in the reference R. inusitata genome. The unique clusters are mostly related to heavy metal resistance, including copper, silver, cadmium, and cobalt. Also, our data suggest a gene loss of R. inusitata species related to zinc resistance, which may have been kept in the Antarctica strain by selective pressure due to heavy metals in the environment. Three β-galactosidases genes were found in the R. inusitata genome, which belongs to the glycoside hydrolase families GH2 (LacZ and EbgA) and GH42 (BglY). Based on modeling and molecular docking, some of these enzymes exhibited higher lactose predicted affinity than a commercial control enzyme. Its predicted secondary structure might support its cold activity. Hence, this work reports a new Rahnella inusitata strain from the Antarctic continent as a polyextreme-adapted strain and prominent cold-active β-galactosidase producer.

F2 - Drenajes ácidos en pasivos mineros de la Puna Argentina: microorganismos responsables y su inhibición

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El drenaje ácido de minas (DAM) es generado por la oxidación de minerales sulfurados en un proceso que es catalizado y amplificado esencialmente por la acción de microorganismos hierro y azufre oxidantes entre los que se destacan diferentes especies de Acidithiobacillus. La inhibición de la acción microbiana es una estrategia adecuada para el control de la generación de DAM. Recientemente hemos reportado la acción inhibitoria que el extracto acuoso de Parastrephia quadrangularis -una planta que crece sobre los pasivos mineros en la puna argentina- ejerce sobre el crecimiento de Acidithiobacillus ferrooxidans, una de las especies bacterianas mesófilas que usualmente tiene un rol relevante en la generación de DAM. El pasivo minero Concordia y La Planta de Tratamiento de La Poma están ubicados en el noroeste de la provincia de Salta (Argentina) a 4200 msnm. La Planta de Tratamiento de la Poma funcionó hasta el año 1985 mientras que el pasivo minero Concordia cesó su actividad en 1986. En la actualidad, todavía se acumulan sus residuos sobre cauces de arroyos y ríos con un fuerte impacto sobre la población de San Antonio de los Cobres. En este trabajo, presentamos los resultados del aislamiento mediante el método de doble capa de tres cepas de Acidithiobacillus que serían las principales responsables de la generación de DAM, estrechamente relacionadas con las especies: A. ferriphilus (AFP), A. ferridurans (AFD) y A. thiooxidans (AT). También se incluyen las experiencias de inhibición de estos microorganismos utilizando distintas concentraciones del extracto acuosos de P. quadrangularis en medio liquido MAC y su comparación con el efecto observado sobre A. ferrooxidans. Se observó que AFP es más sensible a su acción inhibitoria mientras que AT es el más tolerante. Los resultados obtenidos muestran el potencial de este extracto para mitigar la generación de DAM en pasivos mineros del noroeste argentino.

F3 - Tracking arsenic metabolism in the Salar de Huasco - Altiplanic environment, via genome-resolved metagenomics

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Arsenic is a toxic natural component of Earth crust and a major contaminant of aquatic ecosystems. In nature, microorganisms cope with arsenic toxicity through precipitation, chelation, sequestration, expulsion and biochemical transformation (redox processes or methylation). In extreme environments with arsenic, such as the Salar de Huasco (SH), the inhabiting microorganisms presenting these capacities abound. The genes and mechanisms responsible for these phenotypes are not yet fully clarified, and the vast majority of these communities members are little characterized, unknown and uncultured, which limits our understanding. Hence, we set to address this using genome-resolved metagenomics, this approach allows us to identify and characterize unknown microbial species from metagenomes, getting insights of their functional potential. Therefore, starting with sediment samples from five different SH sites along an arsenic gradient (9 to 321 mg/kg), we carried out shotgun metagenomic sequencing. Here, we use 96 million reads from the 5 metagenomes to reconstruct and manually curate 195 metagenome-assembled genomes (MAGs), from which 18 were high-quality ones. The taxonomy affiliation of these non-redundant MAGs resulted in 9 Proteobacteria, 7 Bacteroidetes, 1 Cyanobacteria and 1 Gemmatimonadota phylum members, only 4 of those were assigned to a known genus. Moreover, the global functional potential of reconstructed MAGs broadly showed some level of variability, a total of 267 KEGG modules were detected, presenting differential absence/presence and completion patterns. Particularly, in relation to their repertoire of arsenic associated genes, a considerable number was detected with a clear dominance of those related to arsenic expulsion (acr3, arsA, arsJ), followed by reduction (arsC) and methylation (arsM) being the most recurrent widespread mechanisms in the SH to cope with the high arsenic concentrations. This study has contributed to the knowledge of the microbial “dark matter” that inhabits this special and fragile ecosystem, harboring candidates for advancements in science and technology applications.

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F4 - Biogeoquímica en el Río Amarillo: rol de microorganismos autótrofos y heterótrofos

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El río Amarillo, (La Rioja, Argentina) es un ecosistema extremófilo debido al carácter acido de sus aguas, (pH promedio 3), alta concentración de metales/oides (Fe, Mn, Cu, Zn, Co, As, Mo, V, Cd, Pb, etc.) disueltos y amplitud térmica. A lo largo de su trayecto se observa el depósito de sedimentos de color ocre asociados con la precipitación de compuestos de Fe(III) y el pH se mantiene aproximadamente constante mientras que la concentración de metales disueltos disminuye significativamente. El objetivo de este trabajo es evaluar la biodiversidad y el rol de los microorganismos habitantes del río Amarillo en la geoquímica de este ecosistema. A partir de muestras de agua y sedimentos del río se extrajo DNA genómico y se realizó el análisis metagenómico mediante la secuenciación de genes marcadores específicos: región V3-V4 del gen 16s rRNA (biodiversidad procariota) y ITS1-ITS2 (biodiversidad fúngica). Se estableció un consorcio favoreciendo el crecimiento de microorganismos acidófilos oxidantes de hierro y se evaluó su capacidad para catalizar la oxidación de Fe(II) y para favorecer la bioprecipitación en aguas tomadas del río previamente esterilizadas. Los resultados muestran la presencia de microorganismos acidófilos autótrofos y heterótrofos tanto en las muestras tomadas en el río como en el consorcio establecido. Además, el consorcio fue capaz de acelerar la oxidación de Fe(II) y de formar una abundante cantidad de precipitados ocres disminuyendo simultáneamente la concentración de Cu, Fe y Zn disueltos en comparación a los controles abióticos. Se concluye que la acción microbiana involucra principalmente la catálisis de la oxidación de Fe(II), permitiendo mayor disponibilidad de ion Fe(III) o y contribuyendo a la precipitación de fases sólidas similares a las encontradas en este ecosistema. Al mismo tiempo se observa la disminución en la concentración de otros metales, probablemente debido a procesos de coprecipitación.

F5 - Análisis de las comunidades procariontes de tapetes microbianos y estructuras órgano-sedimentarias asociadas de cuevas pseudokársticas en la Sierra del Chichinautzin, México

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Los tubos de lava están clasificados como cuevas pseudokársticas y son considerados ambientes extremos para la vida, ya que son sitios afóticos y con poca disponibilidad de nutrientes. Los microorganismos desempeñan un papel importante en el mantenimiento de los ecosistemas subterráneos a través de su participación en los ciclos biogeoquímicos y en la formación de depósitos sedimentarios secundarios. La Cueva de la Iglesia y el sistema de Tubo de Lava de Chimalacatepec en el Campo Volcánico Chichinautzin (Morelos, México), son cuevas con diferentes características geomorfológicas cuyo microbioma no ha sido explorado. El objetivo de este estudio fue determinar la composición, estructura y potencial funcional de las comunidades procariónticas de los tubos de lava de Chimalacatepec e Iglesia, México. Para ello, se muestrearon tapetes microbianos, depósitos sedimentarios secundarios y suelo. Se estudiaron a las comunidades procariotas de ambas cuevas a través del análisis la región hipervariable V4 de la subunidad 16S rRNA. Asimismo, se realizó el análisis potencial de las comunidades procariotas para la fijación de carbono en obscuro mediante tres ciclos: el ciclo de las pentosas fosfato, el ciclo del 3-hidroxipropionato/4-hidroxibutirato y el ciclo reductivo del ácido cítrico. Los resultados obtenidos no muestran diferencias significativas en la composición, diversidad ó estructura de las comunidades procariotas entre cuevas. Estos resultados sugieren que los mismos organismos se adaptan a diferentes matrices dentro de las cavidades. Además, existe el potencial para la fijación carbono en ausencia de luz, sin mencionar que, se detectaron géneros clave capaces de degradar compuestos orgánicos complejos, lo que sugiere la importancia de estos organismos para el mantenimiento de las comunidades en estos sistemas.

Agradecimientos: Esta investigación se realizó gracias al financiamiento otorgado por el Programa de Apoyo a Proyectos de Investigación e Innovación Tecnológica UNAM-DGAPA-PAPIIT IN121420, otorgado a la Dra. Rocío Jetzabel Alcántara Hernández.

F6 - Diversidad y distribución del filo *Chloroflexi* en tapetes microbianos de 14 fuentes termales de Costa Rica

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El filo Chloroflexi está conformado por bacterias filamentosas fotoheterótrofas que se caracterizan por tener amplia diversidad metabólica y ecológica. Se pueden encontrar en distintos ambientes. Hasta el momento, no existe información acerca de su diversidad y distribución en fuentes termales de Costa Rica. El objetivo de este trabajo fue determinar la similitud y relaciones filogenéticas entre los MAGs (genomas obtenidos a partir de datos metagenómicos) de estos ambientes y genomas de referencia. Los sitios de estudio corresponden a 14 tapetes microbianos de fuentes termales con rangos de temperatura entre 35°C y 75°C. Los MAGs fueron generados mediante el binning de metagenomas. Se realizó el análisis de similitud de secuencias utilizando ANI, el análisis de calidad mediante CheckM y el programa GTDB-Tk, para obtener la clasificación taxonómica. Para la anotación y construcción del árbol se utilizó Prokka v1.14.5 y Orthofinder v2.3.3. Se construyó una base de 143 genomas afiliados a Chloroflexi utilizando como referencia GenBank y Ensembl-Bacteria (EMBL-EBI).Se ensamblaron 68 MAGs clasificados en las clases Anaerolineae (40), Chloroflexia (8), Thermoflexia (7), Dehalococcoidea (7), Caldilineae (5) y Ktedonobacteria (1).Con respecto a la temperatura, Ktedonobacteria se encontró a 50°C en la fuente termal Hornillas, Dehalococcoidea y Anaerolineae se encontraron en un rango de temperatura 35°C a 60°C. Chloroflexi y Caldilinea principalmente a 60°C. Thermoflexia, específicamente Thermoflexus hugenholtzii JAD2, se encontró en la fuente termal Las Lilas (75°C, conductividad > 13 000 uS). En este estudio, se identificaron seis clases del filo Chloroflexi, contribuyendo al conocimiento de este filo a nivel de diversidad y distribución en los tapetes microbianos de fuentes termales de Costa Rica. A partir de los resultados obtenidos, se sugiere una nueva diversidad del filo en estos ambientes, ya que el análisis filogenómico resulta en la presencia de clados distintos a los reportados en la literatura.

F7 - First steps in the quest for actinobacteria in Ecuadorian Amazon oil-ponds

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Mismanagement of oil extraction sites in the Ecuadorian Amazon region has led to the existence of oil-ponds, small areas where crude oil is deposited in unlined pits. These areas can be considered as an extreme environment for life, as the high hydrocarbon concentration does not favor the existence of most species. However, given that actinobacteria are ubiquitous in extreme environments, our research aims to find out the diversity of species that have adapted to hydrocarbon polluted environments, and the biochemical characteristics that enable their survival. For this purpose, soil samples from two sites, one in Belgium and one in Ecuador, have been used to isolate these bacteria. Both places show hydrocarbon pollution, but the site in the Ecuadorian Amazon is quite singular, as it is an oil-pond that is currently covered with a layer of soil and dense vegetation. Preliminary tests were performed with the soil collected in Belgium, in order to establish the best culturing conditions for isolation of hydrocarbonoclastic actinobacteria; factors tested included growth-medium composition, hydrocarbon concentration and inoculation techniques. In addition, PCR procedures were optimized for amplification of a selection of six housekeeping genes, to facilitate further robust phylogenetic analysis. So far, we have been able to develop protocols that favor the isolation and characterization of actinobacteria from environmental samples polluted with hydrocarbons, particularly those with the ability to metabolize these compounds.

F8 - *Frigoflavimonas asaccharolytica* gen. nov. sp. nov., isolated from Antarctica

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In the course of evaluating the number and diversity of cultivable and non-cultivable prokaryotes in the air of the Fildes peninsula, King George island (South Shetland islands, maritime Antarctica) a total of 16 samplings were carried out in summer of 2017 and 2018. A rod-shaped and Gram-stain-negative bacterial strain, designated 16FT, was isolated and selected to determine its taxonomic status. Strain 16FT is strictly aerobic, catalase positive, oxidase positive and non-motile and grows at 0–20 °C (optimum 10 °C), pH 5.0–8.0 (optimum pH 6.0), and in the presence of 0–2.0% NaCl (optimum 0.5%). The predominant menaquinone is MK-6, and the major fatty acids (> 10%) comprise anteiso-C15:0 and iso-C15:0. The major polar lipids are phosphatidylethanolamine, ornithine lipid OL2, unidentified phospholipid PL1 and the unidentified lipids L3 and L6 lacking functional groups. The DNA G+C content based on the draft genome sequence is 32.3 mol%. Sequence analysis of the 16S rRNA gene indicates the highest similarity to Kaistella palustris 3A10T (95.4%), Kaistella chaponensis Sa 1147-06T (95.2%), Kaistella antarctica AT1013T (95.1%), Kaistella carnis NCTC 13525T (95.1%) and below 95.0% to other species with validly published names. Phylogenetic analysis based on 16S rRNA gene and whole-genome sequences places strain 16FT in a distinct branch, indicating a separate lineage within the family Weeksellaceae. It shows less than 78% average nucleotide identity and less than 68% amino acid identity compared to the type strains of related genera within the family Weeksellaceae. Based on the data from our polyphasic approach, 16FT represents a novel species of a new genus, for which the name Frigoflavimonas asaccharolytica gen. nov, sp. nov. is proposed.

F9- Caracterización metagenómica de la comunidad procariota planctónica de lagunas hipersalinas de la región pampeana occidental, Argentina

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Las lagunas son elementos distintivos del paisaje de la región pampeana y están íntimamente asociadas al desarrollo económico regional. Se destacan las lagunas hipersalinas, principales yacimientos no metalíferos de la región. Las bacterias y arqueas que allí se desarrollan cumplen roles ecológicos fundamentales y tienen un impacto directo en la calidad y cantidad de sales producidas. Conocer su estructura comunitaria y función resulta relevante, no sólo por el valor intrínseco de estos sistemas, sino por el potencial de aplicación de los resultados en áreas como la biorremediación, la bioprospección y en el desarrollo de nuevas estrategias de manejo sustentable de estos ecosistemas. Se presentan los resultados preliminares de la caracterización a través de secuenciación metagenómica shotgun del ADN ambiental de las comunidades procariontes planctónicas de tres lagunas hipersalinas localizadas al SO de la región pampeana: Laguna Guatraché (G), Colorada Grande (CG) y Colorada Chica-(CCH). Estos sistemas constituyen importantes yacimientos de sales actualmente bajo explotación y los estudios sobre la diversidad procariota de estos sistemas es prácticamente nula. Las lagunas presentaron baja turbidez y pH ligeramente alcalino. Sodio, cloruros y sulfatos dominaron la composición iónica, con salinidades superiores a 30%. El recuento citométrico indicó densidades celulares dentro del rango descripto para otros ambientes hipersalinos, con los mayores valores en G (3.9 10 7 células/mL). La extracción y anotación de fragmentos del gen 16s rARN permitió identificar un total de 946 OTU's, con mayor diversidad en G. En conjunto, Halobacterota, Nanohaloarchaeota, Bacteroidota y Proteobacteria fueron los phyla dominantes. A nivel de género, Haloquadratum dominó en CCH y CG. En G, el género dominante fue Halorubrum, acompañado por Natronomonas. Finalmente, se lograron extraer y ensamblar 71 genomas de calidad a partir de los metagenomas de las lagunas. Los valores de ANI obtenidos indican que una fracción relevante de genomas resultan novedosos.

F10 - CRISPR-CAS type IVB in *Rhodococcus* sp. strain ADH, an actinobacterial antarctic isolate

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Virus-host co-evolution is a topic of special scientific interest. Antarctica is a poorly explored extreme environment and the study of extremophilic organisms is of interest at both basic and applied scientific levels. Our work studies the virus-host co-evolution of Rhodococcus sp. strain ADH (NZ_LJIS00000000.1) and a parasitizing prophage. In silico analysis of the ADH genome, using ACLAME Prophinder, revealed the existence of a prophage on contig 10 (accession LJIS01000120.1, 227198bp). In parallel, a CRISPR-Cas type IVB system was detected on contig 38 (access LJIS01000092.1, 54009bp) of the ADH genome (congruent with previous work). Our objective question was, what is the degree of conservation of the type IVB CRISPR-Cas system in actinobacteria?. Previous work determined that the phosphoadenosine phosphosulfate reductase (CysH) gene is a marker for the CRISPR-Cas IVB operon. Blastp analysis of the Joint Genome Institute database showed 139 CysH homologues in actinobacterial scaffolds. These genes were found to be associated with other components of the cas operon of the IVB system but not with CRISPR sequences (analysis performed using CRISPRCasTyper). In addition, the organisation of the cas-IVB operon in actinobacteria showed the csf2 gene to be ubiquitous. Phylogenetic reconstruction of CysH showed the formation of 14 clades (≥ 91% bootstrap) and of csf2 (PHYML) 14 clades (≥ 82% bootstrap). Both topologies were shown to be partially congruent (Tanglegram, Dendroscope). Synthesizing: a) the cas-IVB operon in actinobacteria presented 11 rearrangements in 139 genomes analyzed; b) the molecular phylogeny of the cysH and csf2 genes showed great diversity and c) the comparison of those molecular phylogenies suggests that both vertical and horizontal transmission of both genes would be possible in the cas-IVB operon of actinobacteria. Finally, our results suggest that IVB-type systems are poorly conserved among the actinobacteria studied.

F11- Novel hot spring cyanobacterial genomes from metagenomes unveil genetic adaptations to the high temperature environment

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Several cyanobacterial species are dominant primary producers in hot spring microbial mats. However, their genomic taxonomy and the evolution of their adaptations to high temperatures are poorly understood, and genomic information is currently available for only a few dominant thermophilic genera. We recovered cyanobacterial genomes from hot spring metagenomes determining their genomic taxonomy with the aim of tracking the phylum-wide genomic consequences of evolution in high-temperature environments. A total of 57 medium- and high-quality cyanobacterial metagenome-assembled genomes (MAGs) were obtained from 21 hot springs worldwide, with temperatures between 32 and 75°C. For these MAGs, the genomic taxonomy revealed a high degree of novelty, representing potential new orders (1), families (3), genera (15), and species (36) within the phylum Cyanobacteria. Comparative genomics showed differences between 93 hot spring cyanobacterial genomes (including the 57 novel MAGs) and 66 non-thermal reference genomes. Hot spring genomes are smaller and have higher GC content, with shorter and more hydrophilic and basic proteins. In addition, few genes were shared among members of some hot spring genera and were more related to unknown functions than non-thermal ones. Finally, hot spring genomes showed greater dependence on the CRISPR-Cas defense system against exogenous nucleic acids and reduced secondary metabolism biosynthetic gene clusters. These results suggest differences in cyanobacterial response to biotic and abiotic factors and provide new insights into genomic adaptations to a specific niche such as the thermal environment, where cyanobacteria are essential and dominant members of microbial communities.

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F12 - In the dark: microorganisms of microbial mats and terrestrial stromatolites in lava tubes

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Microbial mats are one of the most interesting matrixes to study microorganisms, further these microbial assemblages can be found in organosedimentary structures such as stromatolites, playing an essential role in mineral bioprecipitation. Caves and underground environments offer a unique opportunity to know how microorganisms drive in the absence of light. In this study, we surveyed the prokaryotic composition of microbial mats and terrestrial stromatolites from a lava tube system, analyzing its 16S rRNA fingerprint by Next-Generation Sequencing. These stromatolites are mainly composed of ferrihydrite and allofane as a secondary mineral. Drop water contains nitrate (9.5-124 mg/L) rather than ammonium, and bicarbonate (up to 58 mg/L), with some Fe (up to 0.16 mg/L). Microbial mats were separated in two types according to their microbial composition: i) Firmicutes/Actinobacteria-dominated and ii) Proteobacteria-dominated. In contrast the stromatolites were mainly composed by Crenarchaeota and Methylomirabilota. Further, stromatolites contained the largest number of observed Amplicon Sequences Variants (or nucleotide sequences with 100% nucleotide identity) with 861-1015, while the microbial mats had 199-799, suggesting a larger diversity in the stromatolite assemblage than in the microbial mats. The main genera identified in the microbial mats were Lactococcus, Crossiella and Acinetobacter. In the stromatolites, we found unassigned members of the Rokubacteriales and Nitrosotaleaceae. Ferritrophicum, Acidithiobacillus ferrooxidans, Leptospirillum ferrodiazotrophum and Alicyclobacillus ferrooxydans were found, which surely play an important role in the Fe-cycle and possibly, in its bioprecipitation. Acinetobacter has been found in terrestrial stromatolites from other lava tubes (Luis-Vargas et al. 2019). These first results give light to the microbial diversity of organosedimentary structures in the dark, developing in pseudokarst caves with Fe-minerals.

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F13 - Análisis del metagenoma de una poza hidrotermal del sistema Lirima, Chile: una nueva fuente de compuestos promotores del crecimiento vegetal

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Los microorganismos de ambientes extremos presentan estrategias adaptativas que les permiten desarrollarse en ambientes únicos. Han demostrado potencial biotecnológico al ser fuente prometedora de compuestos bioactivos. En la búsqueda de nuevas estrategias para una agricultura sustentable, los compuestos derivados de extremófilos podrían actuar promoviendo el crecimiento vegetal (PGP) y ser una alternativa a los agroquímicos. Las termas de Lirima del altiplano Chileno (Región de Tarapacá; 4.200 msnm) es un ecosistema extremo con pozas de agua dulce, caracterizadas por escaza materia orgánica, con temperaturas y pH variables. El objetivo del estudio fue analizar el metagenoma de una poza hidrotermal de Lirima, en busca de enzimas asociadas a caracteres PGPs y de la descripción de la diversidad taxonómica asociada a familias de bacterias descritas como PGPB. Para la búsqueda de los genes con potenciales PGPs y el análisis de la taxonomía bacteriana se utilizó la plataforma MG-RAST. Los resultados muestran 28 familias potenciales promotoras del crecimiento vegetal en el metagenoma, clasificadas en los filos Firmicutes, Bacteroidetes, Actinobacteria y Proteobacteria. El análisis del metagenoma reveló enzimas asociadas a la síntesis de metabolitos promotores del crecimiento vegetal, encontrándose 8500 secuencias relacionadas con la síntesis de poliaminas, enzimas antioxidantes, indol, vitaminas, ácidos orgánicos, fosfatasa, ácido indolacético (IAA) y genes nif. Sin embargo, no detecto genes que participen en la síntesis de IAA dependiente de triptófano y de sideróforos, lo que podría relacionarse con la gran cantidad de secuencias (20,4% del total) de proteínas predichas de función desconocida. Estos resultados sugieren que las bacterias analizadas presentan nuevas vías metabólicas que no han sido estudiadas. La gran cantidad de genes y familias relacionadas con la promoción del crecimiento vegetal encontradas en el metagenoma ubica a la diversidad bacteriana de la poza hidrotermal de Lirima como foco de atención para búsqueda de alternativas sustentables a los fertilizantes químicos.

F14 - Genomic diversity of themoacidophilic bacteria from Los Azufres geothermal field and their implications in biotechnology and astrobiology

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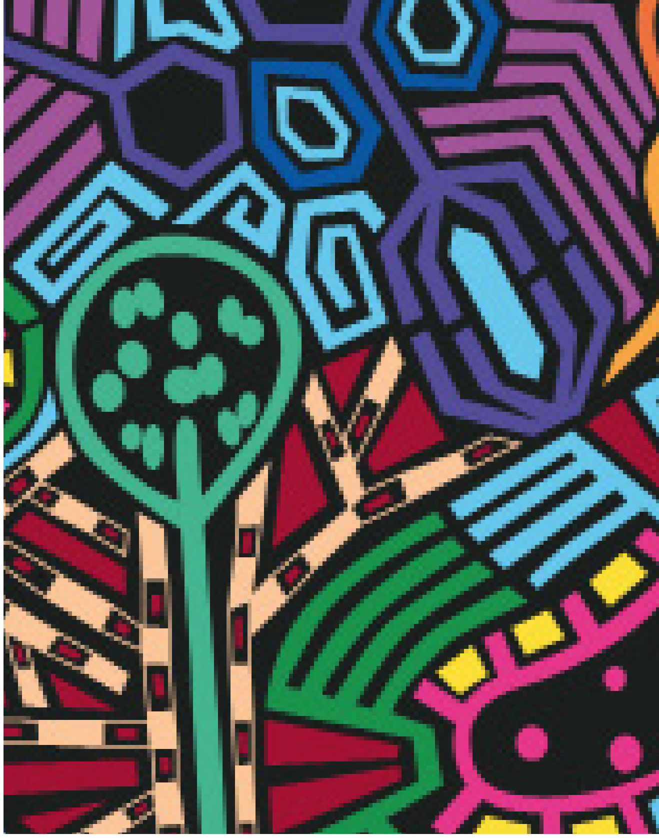
The thermoacidophile microorganisms have several adaptation mechanisms to the hostile acidic thermal environments where they live. The study of this kind of microorganisms has been one of the biggest challenges for understanding their evolution, and ecological function. Therefore, their metagenomic study has been a way to explore new biological resources with biotechnology interest. In addition, those microorganisms usually have primitive features, for this reason, its study could contribute to understanding the origin and evolution of life's earth. In Mexico, into the TransMexican Volcanic Belt, is located the geothermal field of “Los Azufres”, an ecosystem still unexplored. Hence, the aim of this study is to present the advances in the metagenomic analysis of the bacterial diversity and the metagenome annotation of thermal sediments samples in unexplored areas on the Los Azufres geothermal field. The sample area consists of hot springs located in the Maritaro zone. For this, new generation sequencing techniques and bioinformatic analysis were used to obtain a taxonomic description and the potential functions that the microbial communities have developed in this geothermal environment. The preliminary results show that in the metagenome were detected genes related to heat and cold shock resistance, synthesis and antibiotic resistance, and heavy metals tolerance, etc. The taxonomic analysis shows that in Maritaro we found a dominance of the Bacteria domain and in less proportion Eukarya and archaea, With a high abundance of Proteobacteria, Firmicutes, Acidobacteria, Actinobacteria, Bacteroidetes, and Nitrospirae phyla. The findings in this research show that the Maritaro Zone contains a high bacterial taxonomic and functional diversity with a great potential for obtaining microorganisms that could be used for bio-remediation, and industrial applications and could help us to understand better the evolution of microbial communities in those environments.

POSTER SESSIONS



G SYNTHETIC MICROBIAL ECOLOGY

G2 - Reconstruction of metabolic models from the assembled genomes of the metagenome associated with a lignocellulolytic bacterial consortium

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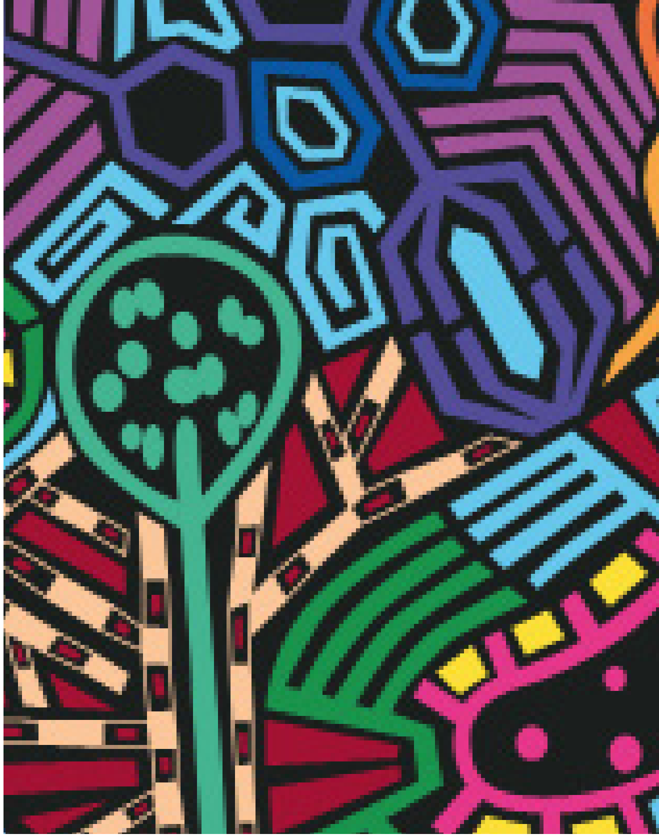
In the context of energetic transition, depolymerization processes are one of the highest challenges for using agricultural residues as an alternative resource. That is because they are highly recalcitrant materials. Among the most sustainable alternatives to overcome that issue, is the use of microorganisms both, in pure cultures and, in consortiums made of several species. However, the role of each of the members and the ecological interactions present among them are not completely understood yet. Thus, this work aims to characterize the most abundant species present in a minimal consortium with lignocellulolytic activity. It was constructed using samples taken from Andean Forest soil by reconstructing the metabolic models generated associated with the assembled genomes obtained from the metagenome of that consortium. For reconstructing metabolic models, we used the webserver ModelSEED by taking as input high-quality assembled genomes with the completeness of more than 90% and with contamination levels of less than 5%. Specifically, we generated three genomes using the Flye software, which was taxonomical and functionally described using CheckM software and the MIGA, RAST, and dbCAN databases, which resulted in genomes associated with the Bacillus, Pseudomonas, and Paenibacillus genera. The latter being the genus with the broadly enzymatic potential for the degradation capacity of lignocellulolytic material. In addition, we created metabolic models with more than one thousand reactions. After a flux balance analysis, it indicated that the Pseudomonas genus was the one with the highest growth rate in simple monomers, such as glucose despite its low enzymatic potential. Therefore, it is clear how these last two genera can coexist thanks to a specific ecological interaction where enzymatic synergism plays an important role.

POSTER SESSIONS



H MICROBIAL ECOLOGY OF MIXED COMMUNITIES

H1 - Seasonal and spatial variability in microbial composition from sediments across the Altiplanic Salar de Huasco

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Salar de Huasco, located in the Chilean altiplano, is an athalosaline wetland that comprises several abiotic pressures given its geochemical and topographical features. Therefore, it is an important reservoir for new and interesting microbial taxa. We used high-throughput sequencing (16S rRNA amplicon) for determining temporal and spatial changes in the microbial community's composition. We sampled sediments in five different sites along the ecosystem and measured the particular abiotic conditions found (pH, salinity, arsenic concentration, etc.), during the summer of 2017 and the winter season in 2018. This study revealed there are changes in terms of diversity and composition in the span of a year, that could be attributed to rain influx and seasonal changes. Alpha diversity analysis revealed significant differences in richness and phylogenetic diversity between seasons. Overall, there is little overlap in the composition between the five sampled sites, comparing the core microbiome determined for each sampled year, we detected only 1% is shared between the composition each season. Also, the co-occurrence network reveals several sub-modules but no keystone species in these communities, reflecting the fragility of the community. Additionally, we found that microbiota composition at phylum rank was dominated by Bacteroidota, Proteobacteria, and Desulfobacterota, consistent with other reports for the area. Moreover, one of the main abiotic drivers of diversity in this ecosystem is arsenic concentration, a relevant attribute due to the natural occurrence of this compound in the area. To the best of our knowledge, this is the first report on the composition and structure in a temporal scale for the Salar de Huasco; we found that there is a relevant dynamic that occurs that might be responding to great scale changes that need further research, as this ecosystem could be an interesting model for adaptation and changes required to face great disruptions such as climate change.

H2 - Valorisation of nitrogen-deficient wastewater treatment systems using sludge enriched with nitrogen-fixing bacteria

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We live in a world highly dependent on the use of nitrogen fertilisers produced with the Haber-Bosch process (HBP) but their production and deployment are unsustainable. Finding cheaper and greener alternative technologies that can sustain global agricultural production is therefore a research priority. In this study, we developed a new strategy of nitrogen fixation by enriching free-living nitrogen-fixing bacteria (NFB) found in the activated sludge from wastewater treatment plants in reactors fed with low nitrogen synthetic wastewater, similar to then effluents from paper mill industries. After 85 days of operation, these sequencing batch reactors (SBR) were able to fix nitrogen at an average rate of up to 11.8 mg of N L-1 day-1, contained sludge that was enriched by 13% with NFB and was able to treat the wastewater. Subsequently, the viability of this nitrogen-fixing sludge as a biofertiliser was assessed by estimating its nitrogen fixation rates under different ammonia concentrations; nitrogen fixation activity was reduced by 83% (compared to controls containing no N) when treating wastewater containing 78 mg of N L-1. Finally, the feasibility of using real effluent from pulp and paper mills as a source of carbon to culture NFB in SBR was evaluated. Effluent from this industry is produced in large volumes and contains high organic loads with little to no nitrogen. After 114 days of operation, the four reactors inoculated with sludge enriched with NFB, did not have any nitrogen-fixing activity and showed a decrease in the putative number of NFB; although they were able to reduce the organic load of the wastewater by up to 89%. Nitrogen fixation was only observed when sucrose in concentration of 3 g L-1 was added as a further supplement of carbon source, hinting at the energetic requirements of biological nitrogen fixation (BNF) within this type of environment. This study demonstrates the scope and magnitude of nitrogen fixation in wastewaters and could valorise the use of this organic matter low in nitrogen, as the sludge enriched with NFB could be potentially used as a biofertilisers.

H3 - High bacterial microdiversity within an Antarctic wetland complex

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The discrimination of amplicon sequence variants (ASVs), which can be further clustered into 97% similarity operational taxonomic units (OTUs, species proxy), allows the identification of strains or ecotypes within species and therefore the study of intra-species microdiversity. The study of microdiversity is key to understanding the ecological and evolutionary processes shaping the distributional patterns of microorganisms. Here, we studied bacterial microdiversity at one specific sampling time (summer 2018) and a relatively small spatial scale (1 square kilometer) encompassing the Punta Cierva wetland complex. This area has been long recognized as a macro-biodiversity hotspot within the Antarctic Peninsula. The analysis of high-throughput 16S rRNA gene amplicons uncovered 17 dominant OTUs (78% total reads), each containing from 17 to 460 ASVs. These dominant OTUs were ubiquitously distributed across the wetland complex. In contrast, most ASVs were specific to one wetland type. Accordingly, we observed significantly different ASV-community structures for each wetland type (Bray-Curtis based PERMANOVA, all pairwise comparison $P < 0.05$). Using rarefaction to decouple dominant OTU characteristics from their global abundance, we found that the increase of OTU effective microdiversity (i.e., number of ASVs) favored their persistence and reduced their abundance variability across samples. Studying the degree of diversification among dominant OTUs (i.e., OTU-population structure: Bray Curtis dissimilarities of ASV composition for each OTU) and the environmental distribution of their most abundant ASVs, two contrasting patterns were observed. Highly diversified OTUs appear to achieve their ubiquity through many specialist ASVs inhabiting specific wetland types, while less diversified OTUs may be ubiquitous due to a small number of ASVs inhabiting a broader range of wetland types. Overall, several bacterial taxa at Punta Cierva showed high intra-species microdiversity, which might ensure the survival of these taxa under changing environmental conditions.

H5 - Estudiar sistemas microbianos con bioimagen química acoplada a luz de sincrotrón

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Los microbios juegan papeles clave en la formación de biominerales. Estructuras microbianas-sedimentarias tan antiguas como 3,500 Ma han constituido una fuente de información fundamental para entender el papel de los microorganismos en la biosfera. Así mismo, hoy en día los microbios participan en la precipitación de lechos masivos de carbonatos en aguas naturales. Las interrogantes que han acompañado al proceso de formación y disolución de biominerales están ligadas a la naturaleza micrométrica de estos procesos, donde los microbios juegan papeles clave. La espectromicroscopía de infrarrojo acoplada a luz de sincrotrón (SR-FTIRs) fue la estrategia metodológica aunada esta investigación, ya que tanto los minerales como las biomoléculas son visibles al infrarrojo. Estas estrategia de imagen química no implica tinción, no es destructiva y ofrece información química con resolución espacial en microescala. Los métodos incluyeron además 16s metabarcoding, microscopía SEM y difracción de rayos-X. Los modelos de estudio son sistemas microbianos complejos que median la formación de minerales en ambientes de baja disponibilidad de nutrimentos y alta exposición a la radiación UV: 1) microbialitos (comunidades fundamentalmente procariontes) de aguas interiores y costeras de México y Cuba; y 2) algas coralinas de la Bahía de La Paz, México, donde el alga y su microbiota participan en la formación de un esqueleto carbonatado. Los resultados de bioimagen química revelaron rasgos estructurales y funcionales específicos de microbios con sitios de formación de minerales, e.g., de calcitas con cianobacterias filamentosas en microbialitos, o bien, han revelado segregación espacial en escala micrométrica de biomoléculas y minerales (e.g. de polisacáridos sulfatados) en células del epitalo de algas coralinas. Los hallazgos de estas preguntas de investigación pueden impulsar el conocimiento sobre materiales biogénicos, y sobre las estrategias para capturar carbono en materiales minerales, lo cual es una necesidad urgente en un mundo donde el CO2 atmosférico se está incrementando.

H6 - Caracterización taxonómica y fisiológico-bioquímica de cepas ambientales de *Cladosporium* conservadas *ex situ*

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El género Cladosporium Link. reúne alrededor de 218 especies consideradas hifomicetos dematiáceos con un amplio rango ecológico (saprobios, endófitos, fitopatógenos y patógenos oportunistas para humanos). C. cladosporioides, C. sphaerospermum y C. oxysporum son las principales especies relacionadas con alergias, asmas e infecciones en pacientes inmunodeprimidos, pues producen y secretan proteasas y metabolitos secundarios que constituyen atributos patogénicos. No obstante, tienen aplicaciones significativas en la salud, la industria, la alimentación, la agricultura y la biorremediación de diferentes ecosistemas. El objetivo de este trabajo fue caracterizar cepas de Cladosporium conservadas ex situ en la Colección de Cultivos Microbianos de la Facultad de Biología mediante criterios culturales, morfológicos y fisiológicos □ bioquímicos para un conocimiento más amplio de la micobiota de La Habana, Cuba. Se estudiaron 69 cepas provenientes de ambientes interiores y exteriores, que se identificaron a través de criterios culturales y morfológicos. Se analizó la posible penetración de los propágalos de las especies en el tracto respiratorio humano mediante el estudio morfométrico de conidios, ramoconidios y conidióforos. Además, se determinó la potencialidad patogénica mediante la evaluación del crecimiento a 33°C, 37°C y se realizó la detección semicuantitativa de proteasas, ácidos orgánicos y pigmentos extracelulares. En este estudio, se identificaron diez especies de Cladoporium, dentro de las cuales C. paracladosporioides, C. fusiforme, C. basiinflatum, C. exile, C. funiculosum y C. pseudocladosporioides constituyen nuevos registros para ambientes interiores de Cuba. Todas las especies identificadas tienen la potencialidad de penetrar a través del sistema respiratorio humano hasta el nivel de alveolos. Las cepas de C. cladosporioides presentaron al menos uno de los atributos patogénicos evaluados. Los resultados alcanzados contribuyen al conocimiento de la micobiota fúngica nacional y evidencian que Cladosporium debe considerarse como potencial agente causal de afecciones a la salud de humanos en Cuba.

H7 - Las bacterias asociadas a líquenes *Peltigera* del sur de Chile contribuirían a la simbiosis con la solubilización de fosfato

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Los líquenes albergan un microbioma diverso que incluye bacterias, virus, algas y hongos, por lo que actualmente son descritos como complejas asociaciones multiespecies. En esta simbiosis mutualista, cada integrante contribuye a la asociación: el micobionte proporciona refugio y minerales, mientras que el fotobionte fija carbono, y nitrógeno si es una cianobacteria. En cuanto al microbioma, se ha sugerido que podría contribuir con funciones esenciales, tales como resistencia a factores bióticos y abióticos, y suministro de vitaminas y nutrientes. En este trabajo analizamos el microbioma bacteriano asociado a talos y sustratos (i.e. suelo) de 4 especies de cianolíquenes Peltigera creciendo en la Reserva Nacional Coyhaique (Región de Aysén, Chile), y exploramos su potencial capacidad de solubilización de fosfato. Las comunidades bacterianas se caracterizaron mediante secuenciación masiva del gen 16S rRNA utilizando primers que excluyen al cianobionte, y los ASVs fueron inferidos siguiendo la tubería DADA2. Con estas secuencias se predijeron las posibles funciones del microbioma utilizando el software PICRUSt2 y se analizaron diversos genes funcionales relacionados al ciclo del fósforo. Además, cuatro de estos marcadores funcionales se cuantificaron por qPCR. Tanto con PICRUSt2 como con qPCR se obtuvieron resultados similares, aunque para algunos marcadores la información en las bases de datos o los primers representan sesgos para una u otra aproximación. En general, los solubilizadores de fosfato fueron más abundantes y diversos en los sustratos en comparación a sus respectivos talos, aunque muchos taxones se encontraron en ambos microambientes. Además, se pudo determinar que los marcadores de solubilización de fosfato orgánico (e.g. fosfatasas y fosfonatasas) fueron más abundantes que los marcadores de solubilización de fosfato inorgánico. Estos resultados sugieren que las bacterias solubilizadoras de fosfato orgánico son abundantes en el microbioma de líquenes Peltigera y podrían estar siendo reclutadas desde el ambiente en donde los líquenes crecen.

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H8 - Levaduras basidiomicetes en líquenes: ¿un nuevo componente de la simbiosis liquénica?

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Actualmente los líquenes se definen como simbiosis multiespecies que consideran tanto los simbiontes clásicos, como la gran diversidad de microorganismos en su microbioma. En 2016, se reportó por primera vez la presencia de levaduras basidiomicetes incrustadas en la corteza de diferentes especies de líquenes de varias regiones del mundo. En este trabajo realizamos una revisión bibliográfica de publicaciones sobre levaduras basidiomicetes asociadas a líquenes, para evaluar si estas pueden considerarse simbiontes fúngicos secundarios asociados de forma estable a una gran variedad de líquenes. La búsqueda bibliográfica se realizó a través de Google Académico considerando los artículos que citan al trabajo pionero en describir la presencia de levaduras basidiomicetes en líquenes. De los 384 artículos encontrados, solo 9 dan evidencias de la presencia de levaduras basidiomicetes en los líquenes. Estas levaduras pertenecen a dos subdivisiones y tres clases: Pucciniomycotina (Cystobasidiomycetes y Microbotryomycetes) y Agaricomycotina. (Tremellomycetes), incluyendo dos géneros de levaduras conocidos por habitar exclusivamente líquenes: Cyphobasidium y Lichenozyma. En cuanto a los líquenes, todas las especies donde se han reportado estas levaduras, excepto una, corresponden a la clase Lecanoromycetes, y si bien la presencia de las levaduras se evidencia en 58 géneros liquénicos distribuidos en 17 familias, la familia Parmeliaceae es la más representada en estos estudios (67,2%). De todos estos géneros de líquenes, se reportó la presencia de levaduras Cystobasidiomycetes en 98,3% de los casos, Microbotryomycetes en 10,3% y Tremellomycetes en 8,6%, encontrándose en algunos casos representantes de 2 o 3 de estas clases de levaduras en el mismo género de líquenes. Estos resultados indican que para confirmar que estas levaduras basidiomicetes forman parte estable de la simbiosis, todavía son necesarias más investigaciones que incluyan representantes de especies liquénicas aún no estudiadas y que consideren otras clases de levaduras además de las hasta ahora reportadas.

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H9 - Taxones bacterianos claves en líquenes *Peltigera rufescens* creciendo en dos praderas en la región de Aysén, Chile

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Los líquenes son comunidades complejas compuestas por dos o tres simbiontes principales (un hongo y un alga verde o cianobacteria) y un microbioma asociado, el cual se propone cumpliría funciones esenciales para la supervivencia del holobionte. En este trabajo caracterizamos mediante secuenciación masiva del gen 16S rRNA, el microbioma bacteriano de líquenes Peltigera rufescens creciendo en dos praderas de la región de Aysén distantes ~200 Km (Coyhaique y Tamango). Se definieron variantes únicas de amplicón (ASVs) mediante la tubería DADA2 y se realizó su asignación taxonómica con el paquete DECIPHER y la base de datos GTDB. Se filtraron las ASVs presentes ≥90% de las muestras (i.e. "core") y se realizaron análisis de co-ocurrencia para definir los taxones bacterianos claves mediante la topografía de las redes. Se pudo determinar que los taxones claves más representados fueron similares al comparar los líquenes de ambos sitios, tanto a nivel de filo (Proteobacteria [20-21 taxones en Coyhaique y Tamango, respectivamente], Actinobacteriota [5-6]), como a nivel de orden (Rhizobiales [5-8], Sphingomonadales [6-3] y Burkholderiales [4-4]). A nivel de género, la mayoría de los taxones claves no se lograron asignar taxonómicamente dentro de la base de datos, pero fueron diferentes en ambos ambientes, lo que da cuenta de la alta novedad taxonómica de las comunidades estudiadas. El único taxón clave que se detectó en ambas praderas fue de la familia Sphingomonadaceae, el cual se ha propuesto previamente sería transmitido verticalmente en líquenes y podría estar llevando a cabo funciones clave dentro del microbioma liquénico. Además, de los taxones clave identificados a nivel de género, algunos se ha reportado que posiblemente serían reclutados desde el sustrato de los líquenes, e.g. Fimbriiglobus, Roseomonas, Methylobacterium y Rubrivivax. Estos resultados sugieren que líquenes de la misma especie estarían seleccionando taxones claves dependiendo de las condiciones del ambiente.

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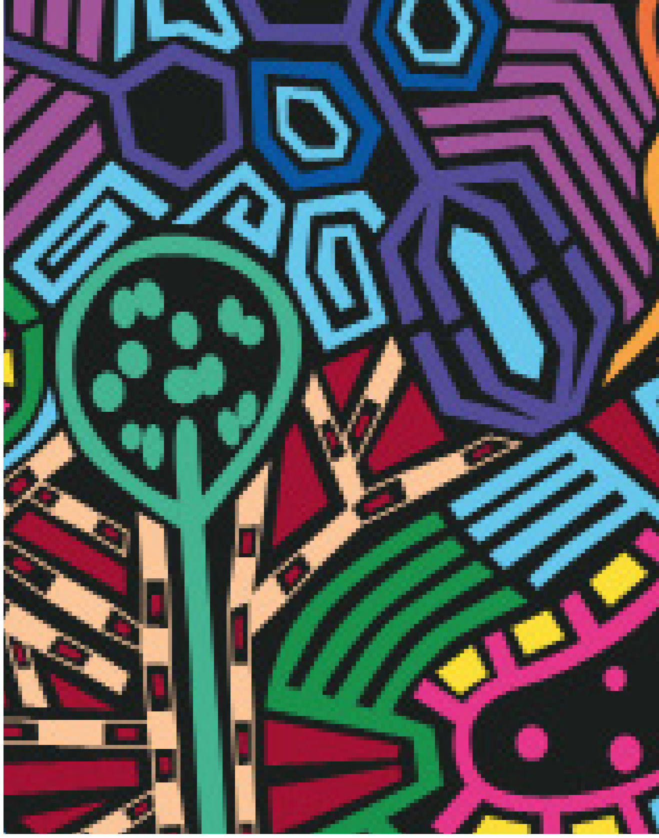
POSTER SESSIONS



I

PLANT-ASSOCIATED MICROBIOMES

I1 - The seed-associated microbiome of four cactus species from Southern Chihuahuan Desert

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The seed-associated microbiome is essential for the development of plants in their first stages of life, particularly in cactus that inhabit harsh environmental conditions. Although evidence indicates the relevance of the seed-associated microbiome during this stage, little is known about its structure and function. This knowledge is relevant to improve the propagation and conservation of this natural resource. Our main objectives were: 1) to describe and compare the episeminal (surface) and endoseminal (internal tissues) microbial communities, including bacteria and fungi, of Echinocactus platyacanthus, Ferocactus latispinus, Ferocactus pilosus, and Stenocereus queretaroensis. 2) To determine the growth-promoting abilities of the cultivable bacteria isolated from their seeds, and 3) finally to determine the episeminal community's role in the germination of seeds and protection of the emerging embryo using as model seeds of E. platyacanthus. We characterized the episeminal and endoseminal microbial communities sequencing by Illumina, the 16S rRNA gene for Bacteria, and the ITS1/ITS4 region for fungi. We isolated cultivable microorganisms and characterized their plant growth-promoting abilities to produce indol acetic acid by Salkowski method, siderophores production, chitinolytic activity, potential nitrogen fixation by acetylene reduction test, and organic acids by measuring changes in the culture medium's pH. We determined that microbial communities associated with cactus seeds have high richness but are dominated by few taxa, and in most cases, there are clear differences between episeminal and endoseminal microbial groups, especially for fungi. We can highlight bacterial groups such as Kluyvera, Bacillus, Paenibacillus, and Stenotrophomonas. For fungal groups, the classes Tremellomycetes, Dothideomycetes, Eurotiomycetes, Leotiomycetes, and Sordariomycetes. Our result suggested the coexistence of two strains of Aspergillus in the seeds of E. platyacanthus, where a beneficial strain can regulate the populations of a pathogenic strain. The cactus seed microbiota comprises potential pathogens and beneficial microorganisms that could influence germination and seedling development.

I2 - Genomics of cycads' coralloid-root bacterial microbiome suggests adaptation from bacterial symbionts allowing holobiont to thrive in contrasting environments

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The relationships between eukaryotes and prokaryotes have played a pivotal role in the evolution of macrobes. Cycads are an ancient lineage of gymnosperms distributed in a myriad of environments around the globe. These plants develop a special organ called coralloid root where symbiotic bacteria thrive and which is considered a key trait for its survival. This bacterial microbiome can perform diverse processes for the plant by diverse metabolic functions encoded in their genomes as biosynthetic gene clusters (BGCs). BGC diversity is related to chemical-structural variations of their molecular products, resulting in different biological activities that can serve as adaptations for the holobiont. We chose Dioon edule as a model to search for the relationship between the environmental differences where cycads thrive (soil type and pH), and the coralloid root microbiome's genomic diversity (BGCs) across two contrasting environments. Using a culture-independent methodology, we found that Nostoc populations dominate over other bacterial lineages, contrary to previous observations. Differences in nitrogenase GCs and siderophore BGCs among the two environments suggest metabolic adaptation from the microbiome to the respective soil characteristics. Moreover, signatures of selection found in the dN/dS ratio point out that differences in the BGCs genomic sequence can be the result of positive selection acting on critical parts of the cluster. A terrestrial-symbiotic Nostoc lineage comparison suggests that these changes in dN/dS ratio are not balanced by genetic drift, expected in obligate symbionts. Together, this evidence confirms the main role that bacterial populations have to help cycads in coping with the environment and holobiont adaptation to different niches.

I3 - Análisis del microbioma endófito bacteriano radicular y su relación con el comportamiento hospedero-dependiente de la bacteria endófita diazotrófica SOG26 durante la interacción con las especies *Oryza glumaepatula* y *Arabidopsis thaliana*

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Los microorganismos endófitos promotores del crecimiento vegetal representan una alternativa sustentable al uso de agroquímicos para promover la productividad de cultivos alrededor del mundo. Sin embargo, su implementación en aplicaciones agrícolas requiere de más estudios que ayuden a comprender aspectos clave de la interacción planta- endófito; entre estos resulta importante abordar las dinámicas de interacción de estos microorganismos con las comunidades endófitas que componen el microbioma de cada hospedero. SOG26 es una bacteria diazotrófica, aislada de semillas de Oryza glumaepatula, capaz de promover el crecimiento y productividad vegetal de manera genotipo-dependiente, aumentando la productividad únicamente en hospederos nativos. En Arabidopsis thaliana, la interacción con SOG26 disminuye la productividad. Estos efectos diferenciales son interesantes para estudiar aspectos clave del endofitismo. En este proyecto se evaluó, mediante un análisis filometagenómico del gen 16S rRNA, el impacto temprano de SOG26 sobre el microbioma endófito bacteriano de dos genotipos (nativo y no nativo) de O. glumaepatula y uno de A. thaliana, y su relación con los patrones diferenciales de crecimiento y productividad mencionados previamente. Nuestros resultados demostraron que SOG26 afectó la composición del microbioma de ambos genotipos de arroz, convirtiéndose en un miembro abundante en la endósfera, posiblemente mediante competencia con los grupos innatos más representativos y promoviendo la proliferación de otros promotores del crecimiento. Sin embargo, este efecto fue mayor en el hospedero nativo, validando el rol del microbioma como un componente determinante del desenlace de la interacción planta-endófito. En A. thaliana, SOG26 no se integró al microbioma, pero su inoculación se asoció a una disminución de la productividad vegetal, lo cual sugiere la activación de costosos mecanismos de defensa en la planta que bloquean la colonización por SOG26. Nuevos estudios que incluyan las dinámicas del microbioma considerando otros modelos son necesarios para comprender la globalidad de estas interacciones.

I4 - High beta-diversity in cultivable yeast communities in leaves and fruits of *Bromelia* sp. in the Dry Tropical Forest in Northeast Brazil

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The plant phyllosphere is formed by several compartments, such as flowers (antosphere), fruits (carposphere) and leaves (phylloplane). Even within the same species of plant or the same individual, these compartments have their own configuration. The divergences are both in terms of chemical composition and its microbial dynamics of colonization, competition and extinction. These particularities provide unique communities in each of these compartments and make plants a mosaic of microbial communities. Therefore, the objective of this study was to verify the diversity and composition of cultivable yeasts associated with leaves and fruits of Bromelia sp. in a semiarid region of northeastern Brazil. For this purpose, leaves and fruits were collected between August 2016 and September 2017 in the state of Alagoas, Brazil. Twenty-nine yeast isolates (grouped into 21 species) were obtained from 8 samples of leaves and fruits. Leaves were richer than fruits, 14 and 12 species, respectively. The vast majority of species (76%) have a single occurrence record in the samples. However, the only species shared between the two compartments were Vishniacozyma alagoana and Kwoniella dejecticola, being also the most frequently found species, 50% and 37.5% of occurrence respectively. As such, the two compartments have accumulated a beta-diversity of over 90%. Both compartments showed greater richness of basidiomycetes (84-86%). In fruits, in addition to V. alagoana, the species with the highest occurrence were Clavispora lusitaniae and Meyerozyma guilliermondii, two species often associated with flowers, nectar and with a typically copiotrophic nutritional strategy, that is, associated with rapid growth and environments rich in simple sugars. Through these results, our study reinforced the diversity and particularity that the microbial community can have in different compartments of the same plant and how the yeast community is diverse in bromeliads.

I5 - Caracterización química de sobrenadantes de un aislado de cianobacterias con efecto promotor del crecimiento de la gramínea *P. australis*

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Las cianobacterias han causado gran interés por la capacidad de algunos aislados para promover el crecimiento de plantas mediante la producción de compuestos bioquímicos que influyen directamente sobre el desarrollo vegetal. En el estudio de esta interacción, una de las dificultades es discernir los efectos sobre las plantas causados por dichos compuestos y por los nutrientes del medio de crecimiento de las cianobacterias. En este trabajo se comparó la composición química en el tiempo del medio de cultivo BG-11 y de sobrenadantes de un cultivo de la cianobacteria Trichormus sp., que tienen un efecto promotor sobre el desarrollo de la gramínea nativa chilena Polypogon australis. Se realizó la caracterización de la curva de crecimiento mediante determinación de clorofila a, en cultivos de 800 y 2400 mL de Trichormus sp. durante 45 y 11 días, respectivamente. Paralelamente, se cuantificó los principales elementos del medio líquido mediante ICP-MS, los nitratos por el método del ácido salicílico y el contenido de proteínas por el método del ácido bicinconínico. El sobrenadante del cultivo de cianobacterias en la condición 2400 mL y un medio BG-11 modificado con las concentraciones de nutrientes de la condición 800 mL fueron usados en un bioensayo sobre plantas de P. australis de 31 días. Los resultados mostraron que las dos condiciones de cultivo evaluadas en la fase exponencial tardía presentaron menor concentración de nutrientes que el medio BG-11, destacando la condición 800 mL, con menores valores de fósforo (-100%), manganeso (-83%) y nitratos (-42%). El bioensayo mostró que las plantas tratadas con el sobrenadante de la condición 2400 mL, después de 4 días, presentaron un 16% de aumento en la longitud radicular respecto al medio BG-11 modificado. Los resultados permiten concluir que los efectos del tratamiento se deben a compuestos presentes en el sobrenadante no relacionados con los nutrientes remanentes.

I6 - Comunidade de leveduras do filoplano e a predileção por hábitos de vida em *Bromeliaceae*

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Bromélias são o quarto grupo mais abundante de plantas na Mata Atlântica e abrigam uma vasta diversidade de organismos. As leveduras, podem estar associadas ao filoplano como comensais, saprófitas ou mutualísticas, participando de processos ecológicos importantes, entre eles como inibidores de agentes fitopatogênicos. O objetivo do presente trabalho foi analisar as relações entre as comunidades de leveduras presentes em bromélias com diferentes hábitos de vida (epífitas e terrícolas) na Mata Atlântica da região nordeste do Brasil. Foram coletadas 56 amostras de folhas das bromélias, entre o período de 2013 a 2017, nos municípios de Maceió, Murici, Quebrangulo e União dos Palmares, estado de Alagoas, Brasil. Do total de amostras, 28 são de bromélias com hábito epífita e 28 bromélias terrícolas. Foram identificadas 71 espécies de leveduras, utilizando o sequenciamento da região D1/D2 do gene 26S rDNA. Destas, 31 foram encontradas em bromélias epífitas, 22 foram encontradas em bromélias terrícolas e 18 espécies estão presentes em bromélias dos dois tipos de hábitos de vida. Assim, os dois hábitos apresentaram uma beta-diversidade de 25% e ambos apresentaram maior riqueza de basidiomicetos (84%). A maior ocorrência foi das espécies Carlosrosaea hohenbergiae e Papiliotrema leoncinii. espécies frequentemente associadas ao filoplano, cumprindo um papel na distribuição de nutrientes necessários para a bromélia, o que favorece a sua fisiologia funcional. Através desses resultados, o estudo corroborou com a importância e a particularidade que as comunidades de leveduras podem ter nas bromélias com diferentes hábitos de vida, além da sua importância na interação micro-organismo-plantas.

I7- Análisis de comunidades bacterianas rizosféricas asociadas a dos genotipos de *Persea americana* cv. Hass, en dos localidades del Departamento de Antioquia, Colombia

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Colombia es el quinto productor mundial de aguacate, donde el cultivar Hass representa el 38% de la exportación total y especialmente, el departamento de Antioquia produce aproximadamente el 50% de la producción nacional. Para el departamento, el cultivar Hass presenta alto polimorfismo genético y se desconoce qué impacto pueden tener estos genotipos sobre las comunidades bacterianas de la rizósfera. Teniendo en cuenta la importancia de estas comunidades bacterianas en la salud y productividad del cultivo, este trabajo tuvo como objetivo analizar el efecto de la variabilidad genética de dos genotipos de Persea americana cv. Hass sobre la estructura de las comunidades bacterianas de la rizósfera, en dos localidades. Para cumplir este objetivo, se tomaron 8 muestras de suelo rizosférico por cada genotipo (dos genotipos en total) en dos fincas ubicadas en los municipios de San Pedro de los Milagros y Rionegro, para completar así un total de 32 muestras. A cada muestra se le realizó metagenómica dependiente de PCR (16S) mediante Illumina MiSeq y las secuencias fueron agrupadas en ASVs. Se encontraron marcadas diferencias en las comunidades bacterianas entre fincas, principalmente en las métricas de alfa y beta diversidad ($P < 0.05$), así como en las redes de co-ocurrencia. No se detectaron diferencias asociadas a los genotipos. Entre las variables asociadas al suelo que pueden influir en la estructuración de estas comunidades bacterianas, se encontró que la respiración del suelo, contenido de Fósforo y proteína son determinantes. También, la predicción del metagenoma sugiere un microbioma consumidor de los rizodepósitos. Este análisis describe la composición y estructura de estas comunidades bacterianas. También, se reportan variables influyentes en los procesos que tienen lugar en la rizósfera. Finalmente, este estudio permitirá profundizar en los mecanismos que influencian la salud y productividad de plantas con potencial agroindustrial como lo es el aguacate Hass.

I8- Simulated climate change in a semiarid shrubland decreased the phylogenetic diversity of arbuscular mycorrhizal fungal communities

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In this study, we carried out a 9-year manipulative field experiment in a semiarid shrubland in Southeastern Spain (Sorbas, Almería) dominated by several shrub species, such as Helianthemum squamatum, Helianthemum syriacum, Teucrium turredanum, Santolina viscosa, Coris hispánica and Gypsophila struthium. The AM fungal community associated with soil was characterized by DNA sequencing using Illumina technology. We simulated the warmer and drier climate conditions (~2-7°C temperature increase by using open top chambers and ~30% rainfall reduction using rainout shelters), in order to investigate the effect of increased temperature, rainfall reduction and their combination on the taxonomic and phylogenetic diversity of arbuscular mycorrhizal fungi communities in these areas. Warming factor had a significant effect on AMF community composition, favoring the presence of Glomeraceae family members mostly under the W+RR treatment. Rainfall reduction and its interaction with warming did not show a significant effect on AMF community composition. Indicator species analyses found that six VTs were indicators only for the W+RR treatment, the majority belonging to Glomeraceae family. In the phylogenetic diversity index, the W+RR treatment had the smallest and more negative value than rest of climate change treatments (-1.07 ± 0.41) and it was found to be significantly different from the generated null values ($t = -2.70$, $p < 0.05$). This means that the AM fungal communities associated with W+RR treatment exhibited a significant phylogenetic clustering. In conclusion, the combination of experimental warming and rainfall reduction significantly reduced the AMF phylogenetic/functional diversity with predominance of Glomeraceae members which were linked to decreased water content in the soil. This finding indicates that environmental filtering has selected AMF species with functional traits well-suited to cope with environmental stresses, which allowed them to survive under future climate changes in semiarid conditions.

I9 - Partners to survive: plant microbiome recruitment at the Atacama Desert

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Under the current global climate change scenario, the discovery and characterization of plant species adapted to extreme environmental conditions have become increasingly important. Hoffmannseggia doellii ("mutukuru") is a perennial herb endemic to the Chilean Atacama Desert that grows between 2.900 and 3.800 meters above sea level (m.a.s.l.) in the western Andes. Its growing habitat is characterized by high radiation (≥620 watts / m2), low water availability (~ 76 mm per year), rich in toxic mineral soils and low nutrients availability. Under these conditions, H. doellii can grow, reproduce, and develop a tuberous root. To understand the biotic factors that could be linked to their surprising ability to survive, we characterize the soil plant microbiome under the knowledge that bacteria could play an essential role. We sample on the field the soil microbiome between 1 to 2 cm close to their root and compared the soil DNA r16S and ITS profile at three different locations with 200 m of altitude difference and more than 2 Km of linear distance. It was found a correlation between H. doellii soil microbiome samples profile that differs from the bare soil profile that clusters as a group. Also, measured alpha diversity indexes were consistent with a mayor diversity on H. doellii soils than on bare soil overall sites. These findings suggest a mechanism of microbial diversity modulation under H. doellii influenced soil. We also compare the nifH soil profile of H. doellii close to the root-soil and the bare soil, where it was found distinctive signals on several known and unclassified species at the genus level.

Under natural conditions, H. doellii possesses a soil microbiome with distinctive signatures on Bacteria and Fungi species. Currently, we are exploring the significance of these differences perturbing the soil-plant system in vitro.

I10 - ¿Afecta la endozoocoria la diversidad de bacterias endófitas en semillas?

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Los microorganismos endófitos se han diversificado en varios microbiomas, ocupando un rol fundamental para el establecimiento de las plantas. Sin embargo, existen interacciones ecológicas en las que su participación ha sido poco abordada, por ejemplo, el efecto del proceso de dispersión de semillas y el paso por el tracto digestivo de los dispersores (endozoocoria) podrían moldear la comunidad de microbiota endófita de las semillas y generar un impacto sobre el desarrollo de las plantas. Se ha establecido que la endozoocoria promueve la germinación de las semillas. Este efecto podría relacionarse con la colonización de microorganismos endófitos. Por lo tanto, nuestro objetivo fue determinar el efecto del paso por el tracto digestivo de las aves, en la microbiota endófita y en la germinación de semillas dispersadas. Para ello, se comparó la diversidad microbiana endófita entre semillas de Vaccinium meridionale que pasaron por el tracto digestivo de tres especies de aves (Stilpnia cyanicollis, Stilpnia vitriolina y Tangara gyrola) y semillas obtenidas directamente de los frutos. Todas las semillas fueron procesadas para el aislamiento de bacterias y posteriormente se determinó su relación en la fijación de nitrógeno y solubilización de fosfatos. Los morfotipos potenciales promotores de crecimiento vegetal fueron identificados mediante la amplificación y secuenciación del gen que codifica para el ARN ribosomal 16S. Adicionalmente, se evaluó la germinación, viabilidad y latencia de las semillas. Encontramos que las semillas que pasaron por el tracto digestivo de las aves tuvieron una mayor diversidad de microorganismos endófitos. De estos microorganismos, el 80% de los morfotipos aislados son potencialmente promotores de crecimiento vegetal. Además, comprueban diferencias en la germinación y viabilidad de los tratamientos. Nuestros resultados indican que la endozoocoria promueve la colonización de las semillas por parte de bacterias con el potencial de promover el crecimiento vegetal. Se recomiendan futuros estudios con variables in vivo.

I11- The rhizosphere microbiome of the Andean blueberry (*Vaccinium floribundum* Kunth) is modulated by soil and plant genetics

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Bacterial and fungal communities present in the rhizosphere influence pathogen resistance, stress tolerance, and nutrients acquisition in plants. These processes affect their survival, adaptation, and distribution. Different abiotic and biotic factors have been pointed out to impact the rhizosphere microbiome structure, particularly in crop species in agricultural setups. However, how these factors govern the plant microbiome assembly in the wild has not been thoroughly addressed. Here, we contrasted how soil, an abiotic factor, and plant genotype, a biotic factor, affect the rhizosphere microbiome of Vaccinium floribundum Kunth. This species is endemic to the Andean region and has not been domesticated nor cultivated. Using high-throughput sequencing of the 16S rRNA and ITS region, we characterized 39 rhizosphere samples of V. floribundum that included individuals from the four genotypic clusters previously reported for this species and incorporated samples from three differentiated soil regions in the Ecuadorian Highlands. Our results showed that Proteobacteria and Acidobacteria were the most abundant bacterial phyla found in the analyzed rhizosphere samples and that fungal communities were not dominated by any specific taxa. Mixed linear models revealed that the soil region was the main predictor for bacterial alpha diversity, whereas plant genotype was the most significant factor for fungal diversity. Going deeper, two edaphic factors, phosphorous and lead, were sufficient to explain the bacterial alpha diversity. This study highlights how bacterial and fungal microbiomes are driven by distinct environmental factors. Bacterial communities depend more on the soil and its mineral content, while plant genetics tampers the fungal communities' assembly in the rhizosphere. Our work, albeit preliminary, illustrates plant-microbe associations and the drivers of their variation in the Ecuadorian Andes.

I12 - The microbiome of the halophyte *Atriplex nummularia* (old man saltbush) in northeastern Brazil

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Atriplex nummularia, popularly known as old man saltbush, is one of the main species used for phytoremediation of salt affected soils. However, little is known about its endophytic microbiome and how this community is affected by salt content in soil. To characterize the bacterial community associated to this plant, we performed 16S rRNA gene sequencing of DNA extracted from leaves, roots and rhizospheric soil of 30 different A. nummularia bushes from the Northeast of Brazil. The plants were collected in plantations in the cities of Caruaru (CA), Ibimirim (IB) and Serra Talhada (ST), located in the state of Pernambuco. We did alfa diversity, beta diversity, network, indicator species and core analysis to describe and detect differences among plant niches (leaf, root and rhizospheric soil) and areas (CA, IB and ST). OTU richness and Shannon index were higher in soil, with no differences among plant niches (root and leaf). No differences among areas were detected for alpha diversity and among the most abundant bacterial phyla and classes. In beta diversity, all niches were different among themselves, while CA area was different from IB and ST. Leaf and root communities showed a high similarity in community assemblage. Networks showed higher clustering in endophytic niches when compared to soil. Leaf and root network both showed two highly negatively connected OTUs (Leuconostoc and Paenibacillus for leaf; Ohtaekwangia and Candidatus Phytoplasma for root). These results describe the microbiome of A. nummularia in northeastern Brazil and show a high level of selection of the endophytic community by the plant, since communities from a same niche were alike regardless of the sampled area. Also, this knowledge helps selecting potential plant growing promoting bacteria (PGPB) for halophyte plants involved in phytoremediation initiatives and also expand what is known about plant-microorganisms' interactions in extreme environments.

I13- Estudios de microbioma de raíz de *Deschampsia antarctica* para el diseño de estrategias de fitorremediación de hidrocarburos en suelos antárticos

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Los hidrocarburos del petróleo son los contaminantes más frecuentemente reportados en todo el mundo por su uso generalizado y masivo como combustibles y materia prima. La Antártida no es la excepción. Las estaciones científicas, el transporte y las actividades turísticas, dependen de la energía generada a partir de ellos, incrementando el riesgo de contaminación. Por las estrictas normas ambientales que regulan la actividad en ése continente, surge la necesidad de aplicar métodos de remediación amigables con el ambiente y aceptados por la comunidad internacional. En el caso de los suelos, la fitorremediación asistida por microorganismos es la estrategia de fitorremediación referida con mayor frecuencia para remediar hidrocarburos. En la base argentina Carlini se ha registrado la presencia de ejemplares de D. antarctica en suelos crónicamente contaminados con gasoil. Su tolerancia convierte a esta especie y su microbioma asociado en candidatos para integrar un sistema de fitorremediación de suelos antárticos. El objetivo de este trabajo fue conocer y comparar la composición de las comunidades microbianas presentes en raíces de plantas creciendo en suelos contaminados y prístinos. Para ello se recurrió al metabarcoding del gen rRNA16S, incluyendo 12 muestras rizosféricas y 12 de la endosfera radicular. Se identificaron 17949 variantes de secuencia de amplicones (ASVs) en los microbiomas rizosféricos y 6848 en los endofíticos. El Análisis de componentes principales (PCA) reveló que los microorganismos relacionados con el suelo contaminado difirieron significativamente de los suelos prístinos. Adicionalmente, el análisis discriminante lineal evidenció las familias que podrían explicar estas diferencias, identificándose un total de 34 familias en la rizosfera y 8 familias en endosfera radicular. Conocer la composición de las comunidades microbianas nos permitirá comprender su dinámica y orientar la búsqueda de cepas de interés, optimizando así el diseño de un método de fitorremediación de hidrocarburos asistida por microorganismos eficaz en suelos antárticos.

I14 - Assessing major patterns and the core bacteriome of endophytic communities in plant species from globally distinct locations

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Endophytic bacterial community has been linked to the maintenance of plant nutrition and development. Their presence is also related to plant health and immune system response, since endophytes occupy the same ecological niches as phytopathogen they have been largely proposed as biocontrol agents. Due to all these characteristics, bacterial endophytes are promising targets for different types of bioproducts, and can potentially play a major role in a more sustainable agriculture. Besides that, we still have much to learn about endophytic diversity. For instance, global study aiming the comparison of the endophytic bacteriome from multiple plant genera has never been done. To fill this gap, this work aims to identify patterns of diversity and composition of endophytic bacteriome from different plant species using high throughput 16S rRNA gene sequencing data from independent and publicly available studies. For this, literature searches were made in public repositories. Available data were downloaded and the analysis was performed using bioinformatics tools. We compared 25 plant species from 14 different studies. Results indicated that even with a great variation in the composition of bacterial genera, and the great divergence in the abundances observed, a bacterial core was still present. The data shows that the main factor related to bacteriome composition variation is the plant species. Also, the number of bacterial genera per plant species varies from around 200 to 1500. The core found was shown to be composed of bacteria present in commercial consortia and by genera common to some environments. In addition, correlation networks indicated the great complexity of ecological relationships existing in the analyzed communities. Herewith, it is possible to conclude that the endophytic community has a high degree of diversity and may contain patterns potentially associated with the plant organism, the composition of the soil and products aimed at commercially available plant growth.

I15 - Microbiome-metabolome relations in the halophyte *Salicornia ramosissima*

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The plant microbiome influences important plant traits, such as growth, abiotic stress tolerance, resistance to disease and nutritional value. Still, at present, our understanding of the effects of the microbiome on plant metabolites remains limited. Secondary metabolites from halophyte plants have great potential as nutraceuticals and natural bioactive substances.

Understanding the relation between the plant metabolome and microbiome can support the perspective of improving the metabolite profile and increasing the commercial value of cultivated plants by targeted manipulation of plant associated microbial community. This study was focused on the endophytic microbiome of the halophyte Salicornia ramosissima and its metabolite profile. Bacterial communities and plant metabolites were investigated in plants collected in a natural saltmarsh and an intensive crop field within the same estuarine system (Ria de Aveiro, Portugal). Endophytic bacterial communities were characterized by 16S rRNA gene sequencing using the Illumina Miseq platform, and the metabolite profile was analyzed by GC-MS of n-hexane extracts of plant material. Bacterial richness was higher in the crop culture site, but bacterial diversity was similar in both sites. Wild plants accumulated significantly higher amounts of Na, K, Mg, and carbohydrates, while crop plants have significantly higher amounts of unsaturated fatty acids. In addition, wild plants were enriched in steroids and terpenoids, such as ethyl iso-allocholate, a steroid derivative that has interesting antitumoral applications. The prediction of microbial metagenome indicated that some KEGG pathways related to pathogenicity were enhanced in the crop endosphere and pathways related to nitrogen metabolism were enhanced in wild plants. This study provides clues for a better understanding of the interdependence between plant metabolism and endophyte symbionts and reinforces the perspectives on microbiome engineering as a tool to modulate the metabolite profile of the plant.

I16 - Caracterización de rizobacterias promotoras de crecimiento vegetal aisladas de *Solanum elaeagnifolium* desarrollándose en suelos contaminados con metales pesados

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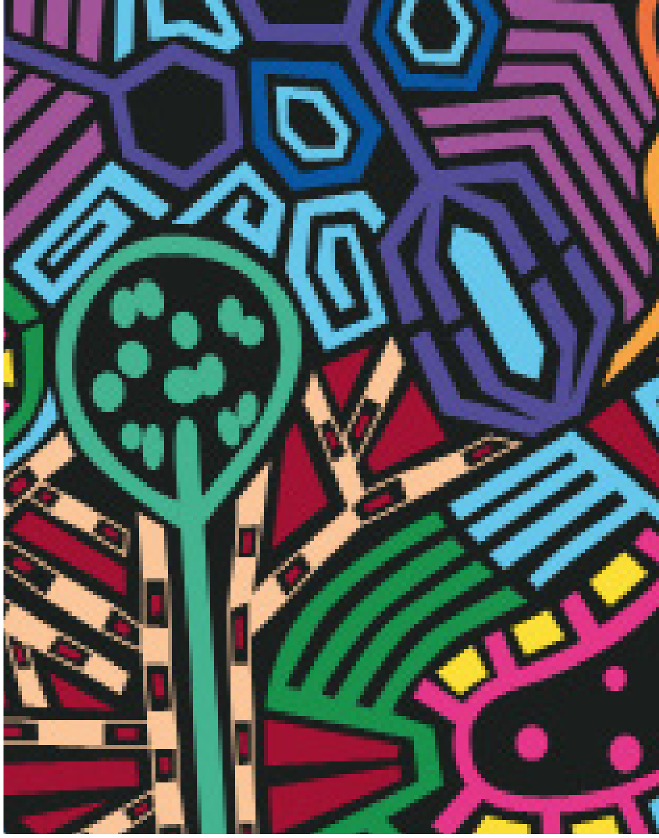
La rizósfera es la porción de suelo que se encuentra influenciada por la actividad de las raíces. En esta se llevan a cabo relaciones simbióticas mutualistas entre las plantas y los microorganismos. Las rizobacterias promotoras del crecimiento vegetal tienen la capacidad de disminuir el estrés en las plantas ocasionado por metales pesados presentes en el suelo. El objetivo de este estudio fue aislar PGPR presentes en la rizósfera de las plantas de Solanum elaeagnifolium que se desarrollan en los antiguos jales de mina del pueblo de Peñoles en el municipio de San Pedro del Gallo, Durango, México. Las rizobacterias se aislaron utilizando el medio de cultivo Luria Bertani enriquecido con 50 ppm de plomo, zinc, cadmio, cobre y arsénico. Se realizaron confrontaciones in vitro con Arabidopsis thaliana para determinar la capacidad que tienen las rizobacterias de promover el crecimiento vegetal, posteriormente se caracterizó su capacidad de producción de sideroforos y solubilizacion de fosfatos, también se identificaron molecularmente mediante la amplificación por PCR del gen 16S rRNA. De la rizósfera se aislaron 54 cepas bacterianas, de las cuales 11 fueron tolerantes a plomo, 9 a zinc, 3 a cadmio, 9 a cobre y 16 a arsénico. En total se lograron obtener 7 cepas rizobacterianas con características de promoción de crecimiento. Los parámetros que se tomaron en cuenta, fue longitud de raíz, raíces secundarias y peso fresco. La identificacion molecular resultó en las siguientes especies bacterianas; Bacillus subtilis, B. cereus, B. tequilensis, Aeromonas dhakensis y Brevibacterium frigoritolerans.

POSTER SESSIONS



J

SOIL MICROBIAL ECOLOGY

J1 - Aerobic methanotrophic bacteria in saline-alkaline soil of the former lake Texcoco, Mexico

Valentín Pérez-Hernández[1] *, Mario Hernández-Guzmán[2], Joaquín A. Montes-Molina[1], Luc Dendooven[2]

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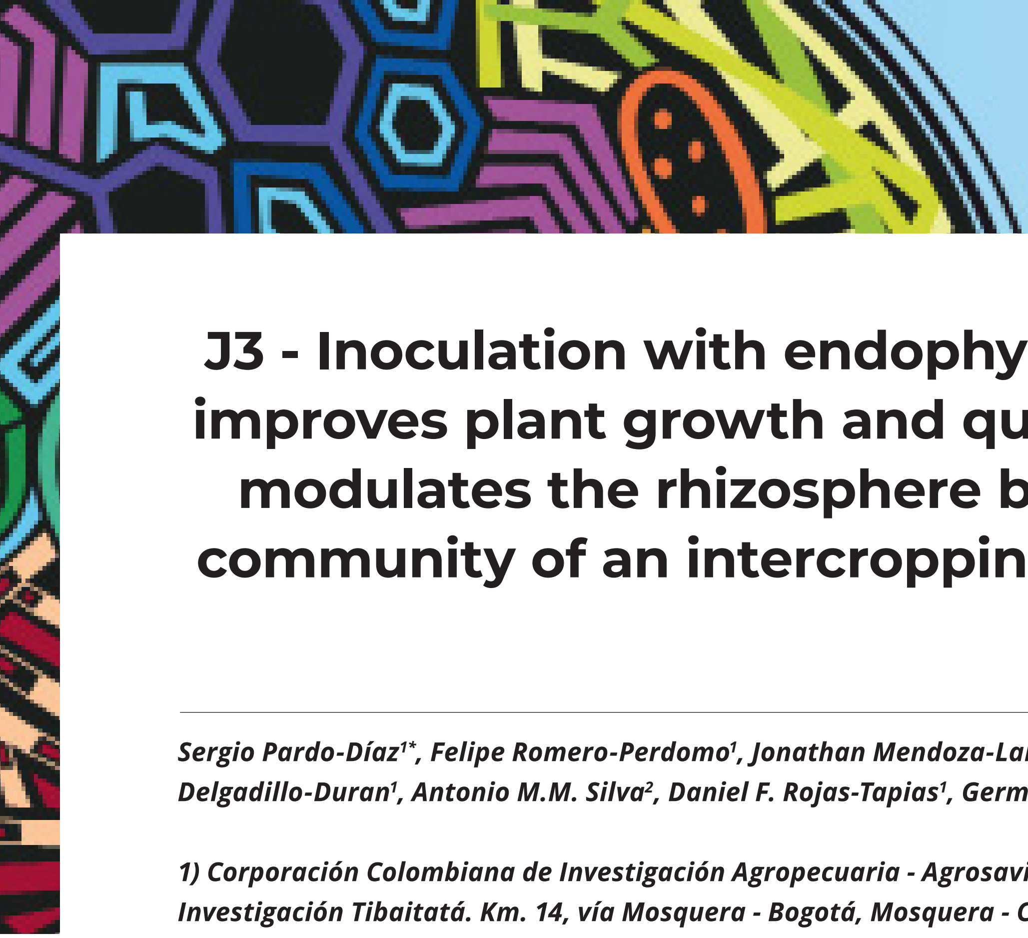
Methane is a greenhouse gas that absorbs more energy than CO2, slowing the rate of energy spread to the space, causing global warming. Methanotrophic bacteria carry out the oxidation of methane to methanol and finally to carbon dioxide. These bacteria regulate the amount of methane in the environment, therefore it is important to identify them in saline soils. Three saline-alkaline soils from the former lake Texcoco with different pH and electrolytic conductivity and two control soil (non-saline) were used to study the functional gene pmoA using pyrosequencing to identify the methanotrophic bacteria present in this environment. Raw sequences were analyzed with the pipeline “Quantitative insights into microbial ecology” (QIIME) v1.9, using a published database that include only methanotrophic bacteria, and the R software was used to perform statistical analysis. Sequences in Texcoco soil were mainly assigned to Nitrosococcus-rel (methanotroph type I), gp23 group and MOB-like cluster. The control (non-saline) soil presented a higher number of assigned groups than Texcoco soil, e.g., methanotroph type I: JR2, JR3, Methylocaldum USC-g and methanotroph type II: Methylosinus, Methylocystis, and USC-a. Aerobic methanotroph diversity were significantly affected by soil pH and EC. The diversity of methanotroph in soil has a possible effect on methane oxidation rate as it was observed that the oxidation rate decreases with increased of soil pH and EC in Texcoco. Despite being subjected to high soil pH and EC, methanotrophic bacteria were able to adapt to adverse conditions and perform the methane oxidation in Texcoco soil.



J3 - Inoculation with endophytic PGPB improves plant growth and quality, and modulates the rhizosphere bacterial community of an intercropping system

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Intercropping of ryegrass and red clover is an alternative to mitigate the adverse effects of intensive livestock production on pasture degradation by increasing the yield and quality of forage. However, limitations in forage nutrition, associated with soil fertilization, restrict its use. The implementation of biofertilization technologies has been widely used to improve the nutritional properties of the soil and, therefore, has the potential to ensure the success of this multicultural system. To determine the impact of bioaugmentation on forage, we evaluated inoculation of two plant growth-promoting bacteria (PGPB) under reduced use of nitrogen. For this, we carried out greenhouse experiments using ryegrass (Lolium perenne L.) and red clover (Trifolium pratense L.) in intercropping. A completely randomized design with a factorial arrangement composed of nitrogen fertilization doses (0, 50, 75 and 100% urea) and inoculation of PGPB (Herbaspirillum sp. AP21, Azospirillum brasilense D7, Herbaspirillum sp. AP21 + Azospirillum brasilense D7, and uninoculated,) was used. . Forage growth and quality, and diversity of the microbial community using bacterial amplicon sequence variants (ASVs) were determinated. Overall, inoculation with AP21 had a greater effect than D7 on plant growth. We further noted that the inoculation with Herbaspirillum sp. AP21 together with 50% of the required nitrogen rate increased the shoot dry weight, the crude protein and the shoot nitrogen content, and decreased the amount of neutral detergent fiber compared to the uninoculated control. Inoculation with PGPB changed the structure of the rhizosphere bacterial community (PERMANOVA: $p<0.001$) that was associated with growth and forage quality. We conclude that the inoculation with AP21 has the potential to improve the growth of the ryegrass-red clover system, decreasing its nitrogen fertilization requirements.

J4 - The effect of agricultural practices on the soil microbiome in Colombian Caribbean tropical dry forest

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In Colombia, agriculture, cattle, and forestall resources exploitation are some proximate causes of fragmentation and biodiversity loss of Tropical Dry Forests, directly impacting forest cover and soil. Despite the interest in forest conservation, its ecological factors involved are unclear. Even though the importance of edaphic microorganisms regulating soil biochemical cycling is well-known, a better understanding of how microbial communities respond to land-use changes is crucially needed. Then, our main concern is to estimate the effect of agricultural use of forest on the soil microbial biodiversity. Through a metagenomic approach, we compared the composition and diversity of bacteria (v4-v5 16s rRNA) and fungi (ITS2) communities in bulk soils from an ecological succession (Primary forest, Secondary forest, and Agricultural area) in Luruaco, Atlántico, Colombia. Differences in the taxonomic distribution of bacteria and fungi were found. Secondary forest following primary forest soils revealed higher bacteria and fungi alpha-diversity. Likewise, for most common indexes, agricultural soil and secondary forest had the most significant differences. Furthermore, the Bray Curtis dissimilarity index (PCoA) grouped samples into specific clusters, showing clear differences in the community structure. The agricultural area and the secondary forest exhibited higher differences (Paired Adonis Test), confirming different microbial community profile. Several saprophytic, mycorrhizal, and lichen-forming fungi (Eurotiomycetes, Agaricomycetes and Dothideomycetes) were found enriched in our forest samples. Other bacterial genera involved in nitrogen and carbon cycling (Solirubrobacter, Mycobacterium and Bryobacter) were overrepresented, indicating their importance for forest soil restoration. However, further research is necessary to understand the environmental factors involved in microbial profiles shifts. Our results suggest how forest transformation influences the soil microbiome and how these can mediate the dry forest dynamics. This information will support forest recovery strategies to protect their diversity and ecosystem services by using microorganisms.

J5 - Greenhouse gases fluxes associated with the compositional and functional dynamics of bacterial communities in response to rain on pasture soils

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Greenhouse gases (GHGs), such as CO2, CH4 and N2O, are significantly emitted through changes in land use to establishment and maintenance of livestock activity. Soil microorganisms produce and oxidize GHGs, and their activities are influenced by different factors, including soil moisture content and degradation. The dynamic involving GHG fluxes and soil microorganisms, however, is poorly understood. In this context, the present work aimed to understand how GHG fluxes are related to soil moisture, and how it affects the soil bacteriome and the transcription of some genes related to C and N cycles. For this, a controlled simulated rain event was performed in a degraded and in a non-degraded pasture, and soil attributes were monitored for 16 days. The rain promoted different responses in each area. A higher CH4 emission was found in the non-degraded area, while the N2O flux increased in degraded and decrease in non-degraded area after the rain simulation. The transcripts evaluation was performed only for non-degraded area, due to higher RNA concentration, important for application of the RT-qPCR technique. A significant relationship was found between soil moisture and the expression of the nosZ gene. For nifH, nirS, mcrA and pmoA genes, an increase in the number of transcripts was observed days after the rain simulation, which may indicate a delayed response to this stimulus. Analyzing the sequencing of the region encoding the 16S rRNA, it was observed that the alpha diversity of the bacterial community was similar between the areas and between the first and last day of monitoring, while the structure of the bacterial communities was highly altered by pasture degradation. The results reinforce the importance of adopting managements that preserve soil microbial communities and favor soil carbon stock.

J6 - Fungal root endophytes of tropical pioneer plants from a premontane forest in Colombia

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It is well-known that leaf fungal endophytes are hyperdiverse in tropical ecosystems; however, little is known about the root endophytes inhabiting tropical tree species. Based on the diversity of hosts and microclimates, a high species diversity of root endophytic fungi associated with tropical tree species is also expected. The interactions between root endophytes and their host as well as with other microorganisms are considered as important as those of relationships established by mycorrhizal fungi. We used culturing and molecular identification to characterize the community and functional traits of root fungal endophytes associated with three pioneer plant species (Bambusa sp., Cecropia sp. and Araliaceae sp.) in an early successional tropical forest in the Cundinamarca, Colombia. For each fungal species isolated, we measured growth rate, hyphal diameter, and culture coloration. Growth rate assays were performed using Potato Dextrose Agar media. Three replicates per isolate were grown at 25 °C for 23 days and photographed to monitor their diameter. Pigmentation and cytoplasmic contents were described under a light microscope. A total of 41 fungal isolates, representing 26 species, were obtained from the roots of the three plant hosts. For Bambusa sp. The most abundant genera were Penicillium and Fusarium, and for Cecropia sp. and Araliaceae was Diaporthe. We found different growth patterns among species, and their hyphal characteristics also varied in terms of diameter and coloration. Ecological substitution is driven by plant pioneer species, which have high colonization capacity but a low capacity to compete. It has been suggested that biotic interactions with pathogens and herbivores can alter successional patterns. Therefore understanding the functional ecology of root-associated fungi and their biotic interactions with pioneer tree species is crucial to understand succession in tropical montane forests.

J7 - How ectomycorrhizal communities vary from natural to urban ecosystems: *Quercus humboldtii* as an study case in the tropical Andes

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Urban landscapes are becoming more important due to the accelerated population growth and increasing urbanization and serve as home to diverse plant and fungal communities. However, studies focusing on the diversity and structure of biological communities are uncommon in this habitat. In Colombia, Quercus humboldtii Bonpl. (Fagaceae) is a conspicuous ectomycorrhizal species present in tropical montane forests. Studies based on fruiting body collections had shown that it hosts a high diversity of ectomycorrhizal fungi in its roots. Quercus humboldtii is commonly used as an urban tree in Bogotá but the ectomycorrhizal communities of this species have not yet been studied in urban ecosystems. We studied how the ectomycorrhizal fungal communities associated with this tree change between natural and urban ecosystems. Roots of 24 trees were sampled in two sites, Chicaque Natural Reserve (natural) and three neighborhoods of Bogotá city (urban). Using Ilumina sequencing, the ITS1 region of all root associated fungi was amplified and analyzed using both OTUs and ASVs bioinformatic pipelines. We found 949 OTUs in Bogotá and 514 OTUs in Chicaque. We didn't find significant differences in the species richness between Bogotá and Chicaque sites based on Fisher's alpha or species-accumulation curves. In Chicaque communities the most abundant genera were Russula and Lactarius, while Scleroderma, Hydnangium, and Trechispora were highly abundant in Bogotá. An NMDS analysis showed that samples from the natural site had a significantly different community composition compared with urban trees. Our results highlight the importance of oak trees in Bogotá as reservoirs of ectomycorrhizal fungal diversity. However, propagation, gardening, and maintenance techniques that are usually applied to urban trees can alter fungal communities or introduce exotic species. It is important to study more about the responses of urban root-associated fungi to biotic or abiotic factors and the influence of these factors in structuring these communities.

J8 - Random forest predicts microbial communities and functionality associated to composition and soil depth in temperate European forests

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Depending on their tree species composition, forests recruit different soil microbial communities, likewise the vertical nutrient gradient along soil profiles also impacts these communities and their activities. In soils of forest ecosystems, bacteria and fungi coexist, because their substrate preferences and nutritional requirements differ, but as they also interact the mechanisms behind soil microbe community assemblies are complex and challenging to decipher. Machine learning algorithms are useful to classify organism communities at high taxonomic levels such as those of the bacterial and fungal kingdoms. By using soil bacterial and fungal amplicon sequencing with random-forest models, we aimed to analyses diversity indices of bacteria and fungi in relation with tree forest composition (deciduous or evergreen trees and their mixtures) and soil depth (10cm, 10-20cm and 20-30cm soil depths). Microbial taxa showed higher changes in relative abundance across soil depths than in relation to forest composition. The microbial Shannon diversity was specially affected by soil depth and by the proportion of evergreen trees. Our RF model validated further that bacterial communities are primarily shaped by soil depth, in contrast to fungal communities, which are rather influenced by the forest composition. Random-forest classifier showed higher accuracy to predict taxonomic composition than bacterial metabolic pathways and fungal functional guilds. Deciduous forest were characterized by bacteria linked to nutrient-rich conditions and saprotrophic fungi. In contrast, evergreen forests harbored soil bacteria and fungi tolerant to harsh soil conditions, like low pH. Random-forest predict higher levels of key processes such as photosynthesis, nitrogen cycling, and production of a broad diversity of metabolites, especially in top soils, indicated an enhanced rate of soil functioning in mixed forests than in pure deciduous or evergreen ones, which highlights the importance of tree mixtures for forest soil functioning

J9 - Levaduras y actinobacterias rizosféricas tolerantes a salinidad y sequía de la estepa Patagónica

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Los microorganismos del suelo están relacionados al mejoramiento de ambientes sometidos a sequía y salinidad, y también son utilizados para mejorar la producción vegetal en ambientes adversos, como los observados en la estepa Patagónica argentina. Los suelos con alta salinidad o baja disponibilidad de agua, presentan microorganismos adaptados que toleran dichas condiciones de estrés. El objetivo fue realizar la prospección de levaduras y actinobacterias nativas de dos sitios de la estepa Patagónica: uno con alta salinidad y otro con baja disponibilidad de agua. El diseño de muestreo fue balanceado y las comunidades vegetales fueron similares en ambos sitios. Los microorganismos se aislaron de la rizósfera utilizando medios selectivos y específicos. Se evaluó su crecimiento a distintas concentraciones de NaCl (2,5,7.5,10,12.5 y 15%) y en medio con glucosa al 50%. Se obtuvo un total de 32 aislamientos de levaduras y 60 de actinobacterias. Ambos grupos fueron más abundantes en el sitio de alta salinidad que en el sitio de baja disponibilidad de agua. 18 aislamientos de levaduras toleraron hasta 10% de NaCl y 7 toleraron 50% de glucosa. Para actinobacterias, 2 aislamientos toleraron hasta 15% de NaCl y 5 toleraron 50% de glucosa. Se obtuvo un gran número de levaduras con tolerancia a ambas condiciones de estrés y un número reducido de actinobacterias, pero con mayor tolerancia a salinidad. Este trabajo permitió seleccionar levaduras y actinobacterias tolerantes a salinidad y baja disponibilidad de agua, que se utilizarán en futuros estudios de promoción de crecimiento vegetal en zonas de condiciones adversas de la Patagonia. De esta forma, se busca estudiar el aporte de estos microorganismos a la fertilidad y recuperación de suelos en procesos de degradación de la región, y también, beneficiar la economía productiva de zonas rurales, fomentando una agricultura sustentable.

J10 - Comparative genomics of environmental isolates of *Nocardia* and *Streptomyces* from contrasting environments

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Natural products from Actinobacteria represent an extraordinary source of chemical diversity with a wide range of biomedical applications. The physiological role of the natural products in host strains is difficult to understand experimentally under laboratory conditions. On the other hand, the occurrence of BGCs is strongly related to the ecological context as production confers adaptive advantages. In this work, we present isolation of actinobacteria from the sediment of two contrasting environments: a highly oligotrophic sediment at the Cuatro Cienegas Basin and the rainforest of Calakmul. Groups of Streptomyces of four different species and Nocardia were analyzed. We performed a functional genomics analysis in order to identify environmental clues related to their biosynthetic potential. The genomes were obtained by sequencing on MiSeq of Illumina system and the BGCs content was elucidated with antiSMASH platform. Phylogenetic and genome-mining analysis shows differences in BGCs presence between samples from different environments. Also, the novelty of BGCs was explored showing that oligotrophic environments are a good source to find new chemical diversity of specialized metabolites. This study shows a strong correlation of the biosynthetic potential and novelty of isolates according to the environmental origin.

J11 - Antagonistic effect of *Bacillus* sp. isolated from agricultural soils against phytopathogenic-fungi

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Diseases in plants generate losses of up to 40% of world agricultural production, mainly generated by phytopathogenic-fungi. Bacteria representing the genus Bacillus are bacteria that generally inhabit the soil and are well known for producing many compounds of biotechnological importance, such as antibiotics, biopolymers, insecticidal compounds, antifungals, among others. Bacillus is recognized for being antagonists of phytopathogenic fungi. However, the antagonistic effect in native strains of Bacillus against phytopathogenic fungi in Venezuela is not widely studied. Here we show the antagonistic effect of bacteria of the genus Bacillus isolated from agricultural soils against important phytopathogenic fungi that affect plantations in Venezuela (Moniliophthora sp., Moniliophthora sp. V_647, Fusarium oxysporum, Phytophthora sp.). We isolated 63 strains of Bacillus from Manilkara zapota, Psidium guajava, Allium cepa, Musa balbisiana, crops of great economic importance. The strains were isolated by thermal shock and identified by amplifying the 16s RNA gene. Agar diffusion assays were performed to measure the inhibitory effect. Finally, the crude extracts were used to evaluate the effect of the metabolites. Our results demonstrate the antagonistic effect of native strains isolated from agricultural soils against important phytopathogens that affect Venezuelan plantations. Only 19 strains showed an inhibitory effect greater than 50% in all phytopathogenic fungi. The metabolites produced by the strains LPV-013, LPV-028, LPV-037 and LPV-045 demonstrated an inhibitory effect more significant than 70%. Bacillus strains have been described as producing an inhibitory effect due to direct competition for niches, competition for nutrients, and the production of low-molecular-weight fungicidal compounds and extracellular hydrolytic enzymes that could explain the antagonistic effect observed in this study. Therefore, we propose using native Bacillus strains as potential controllers of agricultural diseases, with the perspective of creating antifungal formulations free of chemical pesticides that do not alter the physical, chemical, and biological characteristics of agricultural soils.

J12 - Using isothermal microcalorimetry to measure cadmium-tolerant activity in soil microbial communities of cacao-growing farms in Colombia

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In Colombia, cacao is the second largest crop in importance due to its economic and social inclusion to vulnerable populations. However the presence of cadmium in the cacao-growing soils has become one of the biggest challenges to sustain both production and chocolate quality. Therefore, several approaches have converged into mitigation strategies to diagnostic cadmium in soils and prevent its fluxes until its accumulation in the cacao beans. Interestingly, the flux regulation of cadmium in cacao soils, is in part mediated, by the microbial diversity related to this system able to deal with the heavy metal, where the activity of cadmium tolerant bacteria (CdtB), is from a major interest due to its metabolic pathways to interact with Cd (i.e., due to its bioweathering capacity). This study introduces the use of the tool of isothermal microcalorimetry, measuring the heat released during cadmium exposition for 90 hours, to assess the bacterial community convergence into CdtB active populations. In this study, we selected 5 cacao farms were studied taking soil samples and comparing the Cd distribution with bacteria diversity and activity. As positive controls autochthonous soil samples from a region with higher Cd Concentration in Santander district were used. The calorimetric thermograms shown higher metabolic activities between first 10h and then at 50 hours, indicating and increase on cadmium metabolization mediated by both fast and slow-growing populations. The metabolic fluxes and the maximum heat-flow produced were small overall, and reflect the metabolic activity associated with bacteria or archaea (to be confirmed by Illumina MiSeq Platform), where the average heat-flow does not exceed 300 mW and of 60.8 Joules of heat. In this study, we found that farms with natural higher cadmium concentrations in soil had higher bacterial activity when we intentionally added cadmium at 1 mg/kg, which suggests that CdtB populations were enriched on these soils.

J13 - Diversidad y taxonomía de comunidades bacterianas asociadas a suelo de dos manglares en la Bahía de Panamá

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Los manglares constituyen ecosistemas únicos y diversos, localizados a lo largo de las costas intermareales de latitudes tropicales y subtropicales, altamente productivos, y que sirven de apoyo para comunidades más complejas. Esta investigación tuvo como objetivo identificar la composición taxonómica de comunidades bacterianas en suelo de dos manglares de la Bahía de Panamá y generar información sobre la dinámica temporal de las mismas en función de cambio estacional. Los dos manglares muestreados fueron 1) manglar en desembocadura de río Juan Díaz caracterizado por el desarrollo urbanístico a sus alrededores y alta contaminación por desechos sólidos que son arrastrados por el río Juan Díaz y el oleaje que llega a estos manglares; y 2) el manglar en desembocadura de río Bayano caracterizado por con bajo nivel de contaminación. Se implementó la secuenciación por síntesis (Illumina) de amplicones de la región V4 del gen para ARNr 16S (250nt en finales pareados) y programas de análisis Qiime2 y RStudio (paquetes phyloseq y qiime2R) para identificar las bacterias presentes muestras de suelo de 10cm de profundidad. En total se identificaron 20,691 variantes de secuencias de amplicones (ASVz) en 59 muestras; siendo el Manglar de Bayano significativamente más diverso que el manglar de Juan Díaz con significativo de p value = 0.002, a pesar de contar con muchas menos muestras. La abundancia relativa de los taxones bacterianos varió dependiendo del lugar y época del año muestreada (épocas seca y lluviosa), encontrándose incremento de taxones como Actinobacteria, Bacteroidota, Chloroflexi, y Desulfobacterota asociados con el cambio de estación seca a lluviosa en el Manglar de Juan Díaz. La diversidad y composición taxonómica encontrada es similar con la reportada en otros estudios en donde se reporta el género Sulfurovum sp. como dominante y que se caracterizan por ser oxidantes de azufre.

J14 - Influence of plant genetic diversity on rhizosphere fungal communities associated with *Nothofagus alpina* established under a native forest and an exotic plantation

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Fungi are one of the most important soil microorganisms and can be used as bioindicators for monitoring ecological changes and the effects of human activities on ecosystems. Nothofagus alpina is an ecologically and economically important species of South American temperate forests currently included in domestication and conservation programs. Provenance trials installed in different environments of Patagonia are ideal for studying how tree genetics might influence the associated microbiota. Despite afforestation with fast-growing exotic Pinus species is an important economic activity in Patagonia, nowadays there is an increasing interest in the establishment of Nothofagus plantations and for using Pinus plantations for assisted Nothofagus migration. The main objective of this work was to explore the structure of different fungal communities in the rhizosphere of N. alpina with different genetic diversity (high, intermediate, low) implanted under a native Nothofagus forest and a Pinus plantation. Fingerprinting based on TGGE revealed differences in the structure of fungal communities between specimens established under the native forest and the exotic plantation, but also regarding genetic diversity. Basidiomycetes dominated in the native forest, and Ascomycetes in the plantation. In the native forest, N. alpina specimens with intermediate genetic diversity were associated with the highest richness of Basidiomycetes and total fungi. Besides, individual tree genetic parameters significantly correlated with Ascomycetes richness. Soil physicochemical characteristics and the dominant forestry species seemed to be the main factors determining these significant differences between the native forest and the plantation, since they provide different quantity and quality of litter inputs and are associated with different ectomycorrhizal fungi. Beyond highlighting the potential of applying soil fungi as bioindicators, our study contributes to understanding the relationship between host genetics and rhizosphere fungi. This information is relevant for conservation and restoration programs, but also for taking management decisions on sustainable forestry and domestication of native species.

J15 – Efecto de la agricultura por irrigación en las comunidades microbianas y las funciones de un suelo semiárido de la Patagonia

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La expansión de la frontera agrícola es una continua demanda en los sistemas de producción de alimentos a nivel mundial. La agricultura irrigada posibilita y aumenta la productividad de los cultivos en zonas áridas y semiáridas, evitando la deforestación en bosques nativos. En este trabajo, hemos analizado la transformación de los montes semiáridos en la rivera del Rio Negro (NorPatagonia) hacia la agricultura intensiva con riego. Este emprendimiento de productores particulares utiliza practicas conservativas incluyendo una alta rotación de cultivos, el uso de cultivos de cobertura y la siembra directa con el fin de mantener la estructura del suelo. Con el objetivo de comparar el suelo en ambos sistemas, hemos analizado tanto las comunidades bacterianas y fúngicas por medio de métodos de secuenciación de ADN, como las actividades enzimáticas del suelo involucradas en los ciclos biogeoquímicos (carbono, nitrógeno, fosforo y azufre) y el estado de agregación del mismo. Luego de 5 años de manejo, la agricultura con riego aumento significativamente la materia orgánica acumulada, la actividad enzimática y la formación de los macro-agregados a expensa de la abundancia de los micro-agregados. A su vez, las comunidades microbianas mostraron diferencias significativas entre en los sitios con agricultura y los montes prístinos. La alfa-diversidad basada en la riqueza mostro un aumento en las comunidades bacterianas en los sitios agrícolas y una disminución en las comunidades fúngicas, en particular en el filo Basidiomycota. Indicadores seleccionados por medio del método LEfSe asocio a los taxa Acidothermus, Conexibacter y Thermoleophilum con los montes prístinos y los Asticcacaulis, Aquicella y Acromobacter con la agricultura intensiva. El filo Ascomycota cambió la composición de su comunidad con los taxa Aspergillus y Alternaria reducidos y taxa Stagonospora y Metarhizium aumentados en su densidad por la agricultura irrigada. Las propiedades físico-químicas alteradas por la agricultura modificaron la estructura de las comunidades microbianas del suelo, fomentando aquellos microorganismos que se asocian con la mayor captura de C (Acidobacteria, Chloroflexi y Betaproteobacterias) y los macro-agregados (Actinobacteria, Alfaproteobacteria y Firmicutes) del suelo.

J16 - Microbiome transitions from soil to the rhizosphere of common bean *(Phaseolus vulgaris)*

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Nitrogen fixation by symbiotic associations between diverse Rhizobium species and leguminous plants are an essential ecological process and key for sustainable agriculture. Although the nodule has been the main target in many studies, the rhizosphere remains poorly characterized. In this work, we aim to understand the bacterial species composition of the rhizosphere of the common bean (Phaseolus vulgaris), Specifically, we want to know, the transition in the microbiome from uncultivated soil to rhizosphere, in agriculture plots with and without cultivation history. To do this, we sampled two neighboring soils with and without previous history of bean cultivation. Samples were obtained before sowing the bean seeds and 48 days after planting (flowering stage). DNA was extracted from the soil samples and randomly sequenced with Hiseq 4000. After the quality filter (Trim-Galore), we obtained an average of 80 million pair-end reads of about 150 pb per sample (17 samples in total). The reads were analyzed with the Kraken2-Braken software to make taxonomic and abundance inferences. The rhizosphere samples collected post-planting, both in native or cultivated soil, showed that species of the Proteobacteria are the most abundant (about 97% of the classified sequence reads), followed by Actinobacteria (2%). Within Proteobacteria, species of Pseudomonas, Rhizobium, and Pantoea are dominant in the samples. In contrast, the phylum Actinobacteria is the most abundant (52%), and Proteobacteria constituted 40% in the soils before sowing. We observed a transition in the diversity and abundance of the species found before and after sowing, independently if the field was previously cultivated or not.

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J17 - Actividad antifúngica de aceites de frutos de palmas *Oenocarpus bataua*, *Cocos nucifera*, *Elaeis oleifera*, *Maurita flexuosa* y *Acrocomia aculeata* frente a *Fusarium solani*

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Fusarium solani causa infecciones dirigidas a humanos y plantas. Se distribuyen en suelo, aire y agua; donde se dispersan por extensión micelial o por medio de conidios, siendo las vías de infección. Las infecciones por Fusarium solani en plantas afectan la calidad, rendimiento y producción de cultivos, ocasionando grandes pérdidas monetarias. Se tiene documentada la actividad antifúngica de diferentes extractos de plantas sobre Fusarium solani, sin embargo, la mayoría de estos estudios se han desarrollado con plantas endémicas de Asia, Europa y África. Colombia ocupa el primer lugar en América del Sur y el tercero a nivel mundial por poseer mayor riqueza de la familia Arecaceae, con alrededor de 220 especies y 43 géneros, entre los productos que se obtienen a partir de las palmas se encuentran los aceites de los frutos de las especies Oenocarpus bataua, Cocos nucifera, Elaeis oleífera, Mauritia flexuosa y Acrocomia aculeata con actividad antibacterial, antiviral entre otras. Determinar la actividad antifúngica de aceites de frutos de las palmas Oenocarpus batuta, Cocos nucifera, Elaeis oleífera, Mauritia flexuosa,y Acrocomia aculeata frente a Fusarium solani. Se evalúo la inhibición del crecimiento micelial por medio de dilución en agar. Se recolectaron los conidios y se mezclaron con los respectivos aceites, se sirvieron en cajas de Petri. Los aceites Elaeis oleífera, Mauritia flexuosa (crecimiento micelial) y Oenocarpus batua (germinación de conidios) presentaron actividad antifúngica frente a Fusarium solani. El funguicida produjo el 100% de inhibición de crecimiento micelial, sin embargo, presentó una baja efectividad en la inhibición de conidios. Los aceites anteriormente nombrados pueden llegar a ser una alternativa en el control correctivo y preventivo de Fusarium solani. El funguicida carbendazim es altamente tóxico para el crecimiento micelial pero no para la germinación de conidios de Fusarium solani. Los aceites Elaeis oleífera, Mauritia flexuosa y Oenocarpus batua son de interés para el control futuro de las infecciones ocasionadas por Fusarium solani.

J18 - Impacto del cultivo previo al arroz irrigado sobre la comunidad de bacterias y archaeas metanogenicas vinculadas a la fermentación de ácidos orgánicos

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El cultivo de arroz es una de las principales fuentes antropogenicas de metano, un potente gas de efecto invernadero. El metano se produce por la degradacion anaerobia de la materia organica, en la que participan diversos grupos de microorganismos del suelo durante la etapa inundada del cultivo. Los exudados de las raíces de la planta consti tuyen una fuente importante del metano producido, y al momento de maxima emisión, se componen principalmente por ácidos orgánicos como málico, tartárico y succínico. En Uruguay, el sistema tradicional de cultivo implica cuatro anos de pasturas para ganadería seguidos de dos anos de arroz irrigado. Recientemente ha cobrado importancia la intensificacion del cultivo, aumentando la frecuencia de arroz o intercalando otros cultivos como soja. La hipotesis del trabajo es que el uso de diferentes cultivos previo al arroz irrigado (arroz, pasturas o soja) afecta la estructura y la actividad de bacterias y archaeas responsables de producir metano a partir de dos de los principales acidos orgánicos exudados por la planta de arroz. Para probar esta hipotesis se realizaron incubaciones de suelo en micro- cosmos con tartrato y succinato, cuantificacion de productos de fermentación y metano producido, secuenciacion masiva del gen 16S ARNr de Archaea y Bacteria, T-RFLP y cuantificacion de un gen funcional de la metanogénesis. Los resultados obtenidos confirman la hipotesis. Suelos con diferente cultivo previo presentaron diferencias en la estructura de la comunidad de bacterias y archaeas. En los suelos con arroz irrigado como cultivo previo se observo mayor densidad de archaeas metanogenicas, se consumieron más rápido los intermediarios de degradación de los acidos, y su comunidad metanogénica fue la más similar a la del suelo antes de incubar. Estos resultados indican que podría ser mas amigable con el medio ambiente utilizar soja en lugar de arroz para intensificar sistema de cultivo tradicional.

J19 - Los hongos micorrícicos arbusculares aumentan la fertilidad del suelo en agroecosistemas: resultados desde una aproximación meta-analítica

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El aumento de la fertilidad del suelo en los agroecosistemas es un objetivo fundamental para mantener una producción agrícola sostenible. Existe numerosa evidencia científica que muestra que los hongos micorrícicos arbusculares (HMA) aumentan el crecimiento y el rendimiento de los cultivos; sin embargo, todavía es necesario un análisis exhaustivo y cuantitativo de sus efectos sobre distintas propiedades del suelo que determinan su fertilidad. Utilizando un enfoque meta-analítico, analizamos cuantitativamente el papel de los HMA en la estructura y fertilidad del suelo bajo distintos tipos de cultivos en todo el mundo. Basándonos en 169 registros provenientes de 49 estudios publicados sobre agroecosistemas bajo distintas condiciones ambientales y contenido inicial de materia orgánica del suelo, encontramos un claro efecto positivo de los HMA en las propiedades del suelo seleccionadas. Los HMA tuvieron un efecto importante en la estructura del suelo al mejorar los agregados estables al agua, su diámetro promedio y los macroagregados en un 51%, 27% y 15%, respectivamente. También evidenciamos, por primera vez, un aumento en el carbono orgánico total (16%) y en su fracción particulada (46%) en sistemas asociados a HMA; mientras que no hubo efecto sobre la fracción asociada a minerales. La inclusión de diversas variables bióticas y abióticas en el modelo meta-analítico mostró que la textura del suelo, la profundidad de muestreo y el tipo funcional del cultivo dominante tuvieron la mayor influencia en modular el efecto general de los HMA sobre las variables del suelo. El contenido inicial de materia orgánica del suelo y el tipo de inoculación de los HMA también aparecen como moduladores significativos para algunas de las variables medidas. Nuestro trabajo demuestra que los HMA representan un componente necesario de ser considerado a la hora de restaurar los servicios ecosistémicos del suelo, en pos de una visión más ecosistémica de la producción agrícola.

J21 - Characterization of a high cadmium accumulation soil bacterium isolated in *Theobroma cacao* crops with geogenic cadmium levels

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The presence of geogenic cadmium (Cd) contaminated environment, especially in soil, has raised serious health hazards through the food chain. Theobroma cacao L. crops in several neotropical regions produce food and nutrient sources consumed worldwide. Cacao crops are able to bioaccumulated Cd in roots and translocate it to the beans, imposing a serious limitation regarding quality and safety. Bacteria have been applied for bioremediation of cadmium-contaminated environment by biosorption or bioaccumulation mechanisms; this process is considered as a potential eco-friendly alternative and may be a solution in natural Cd contaminated soils to avoid Cd translocation to cacao plant. Here, ten bacterial strains previously isolated in soils of cacao crops with geogenic Cd levels, which showed the highest tolerance against Cd measured by inductive coupled plasma spectrometry with optical emission (ICP-OES), were selected to determine bioaccumulation mechanism of Cd by Transmission electron microscopy (TEM) and Fourier transform infrared spectroscopy (FT-IR). After determining growth variables, we explored the effect of three strains in a greenhouse bioassay that employed CCN51 cacao genotype seeds grown in soil with different concentrations of Cd. Our TEM results showed deformation in cell morphology for all bacteria strains and identified six strains with biosorption interactions and four strains with intracellular Cd accumulation. FT-IR spectra suggested that amide, carbonyl, hydroxyl, ethyl, and phosphate groups on bacteria were the main binding sites for Cd; in the pot experiments, the Cd concentration is distributed in all parts of the cacao plant, but certain decreased the accumulation of Cd in cacao roots in presence of Klebsiella sp. (18-4B). This strain exhibits promising application for use to avoid translocation of Cd to cacao plants.

J22 - Impacto de la aplicación de un consorcio bacteriano sobre estructura de la comunidad bacteriana del cultivo de maíz (*Zea mays* L.)

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En la agricultura orgánica es común la aplicación de microorganismos en los cultivos para estimular el crecimiento vegetal, aumentar la producción y disminuir el uso fertilizante como N inorgánico. Sin embargo, es importante evidenciar que hay sobrevivencia y proliferación de estos microorganismos alóctonos que son aplicados en el suelo y correlacionarlos con el crecimiento vegetal. El objetivo de este estudio fue evaluar el efecto de la aplicación de un consorcio bacteriano no comercial como biofertilizante del maíz (Zea mays L) en un experimento en invernadero. Se realizó un experimento en columnas con suelo sin cultivar y en otras se hizo la siembra de maíz, se aplicó el biofertilizante sin esterilizar, estéril, y un control sin biofertilizante. Se evaluó el crecimiento vegetal y las comunidades bacterianas en el suelo después de 44, 89 y 130 días. No se encontró un efecto significativo en el crecimiento del maíz por el uso del biofertilizante. La comunidad del consorcio aplicado en el suelo fue dominada por el género Lactobacillus (11.9 % abundancia relativa). El efecto de la aplicación del biofertilizante estéril en las comunidades bacterianas del suelo mostraron un pequeño cambio en la abundancia relativa en un número limitado de taxa de bacterias como Delftia, Halomonas, Lactobacillus y Stenotrophomonas, sin alterar significativamente la estructura de la comunidad. Se encontró que el cultivo de maíz afectó significativamente la estructura de la comunidad bacteriana lo cual mostró variaciones grandes y significativas en el tiempo en el suelo cultivado y sin cultivar. Es importante recordar que este experimento se realizó en invernadero, por lo cual resultaría interesante poder probar el impacto de este biofertilizante con experimentos en campo. Como conclusión las bacterias aplicadas como biofertilizante tuvieron un efecto limitado sobre la abundancia relativa de estos grupos en suelos sin cultivar o suelos cultivados con maíz.

J24 - Soil microbial community is influenced by rice straw incorporation strategy, altering carbon-cycling function

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Rice is a staple food in the world, consequently more than 750 Mton are produced worldwide for 2019. With 1.5 tons of rice straw produced on average per ton of rice, the management of this residue is a challenge to farmers. It is well known that microbial communities play major roles in soil organic matter cycling. Therefore, this study explores the changes on the composition and function of microbial communities associated with four rice straw (RS) management strategies in an experimental field: 1) RS as mulch with addition of microorganisms; 2) RS incorporated with addition of microorganisms; 3) RS as mulch without microorganisms, and 4) Burning of RS and ashes incorporation. Samples collected from bulk soil at four different sampling times (initial, degradation, flowering, and harvest) were evaluated by shotgun metagenomics and enzyme activities (cellulase, □-1.4 glucosidase, □-xylosidase, and □-galactosidase). Statistical analyses were performed with STAMP® and R®. The data revealed differences in alpha diversity across time but not between treatments. The most abundant bacteria belongs to Bacillus (1), Ca. Solibacter (1), uncutured bacterium (2), Acidobacteriales (2), Firmicutes (1), Proteobacteria (1) and Actinobacteria (2) phylum, with specific changes through different sampling times. These phyla are recognized by their capabilities to degrade labile and recalcitrant compounds. The shotgun analysis revealed the presence of 262 CAZy families mostly associated with glycosyl hydrolases. Carbon enzymes showed higher activity in □-xylosidase, and □-galactosidase in comparison to cellulose. In addition, statistical differences were identified at degradation time in □-1.4 glucosidase, and at flowering time in celullose and □-xylosidase activity. These results showed that bacterial community structure and function is influenced by treatment and time. These results can guide farmers with the rice straw disposal strategy selecting the best alternative according their possibilities.

J25 - Solubilización y mineralización de fósforo por cepas del género *Bacillus*
Phosphorous solubilization and mineralization by *Bacillus* genera

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La necesidad de incrementar los rendimientos agrícolas y la reducción progresiva del uso de fertilizantes y pesticidas con efectos nocivos, es posible mediante el empleo de biofertilizantes, algunos de los cuales se basan en la utilización de Bacterias Promotoras del Crecimiento Vegetal (PGPB). El género Bacillus posee grandes potencialidades para la estimulación el crecimiento vegetal, además de su gran diversidad metabólica y funcional, lo que propicia su amplio uso en la agricultura. El objetivo del presente trabajo fue evaluar la capacidad solubilizadora y mineralizadora de fósforo de cepas del género Bacillus aisladas de cultivos de interés económico. Para ello se determinó la capacidad solubilizadora de fosfatos de las cepas mediante la siembra en medio NBRIP sólido con tres fuentes de fosfato inorgánico: Ca3 (PO4)2, FePO4 y AlPO4. Los índices de solubilización fueron calculados a diferentes tiempos. Todas las cepas solubilizaron fósforo desde las 24 horas de incubación, lo que permitió su clasificación en solubilizadoras tempranas y cuatro de ellas resultaron clasificadas como solubilizadoras intermedias para todas las fuentes de fósforo. Se seleccionaron varias cepas que se corroboró esta capacidad en medio líquido, demostrando una elevada correlación con el pH, lo que demuestra la incidencia de la producción de ácidos en la solubilización. Se evaluó la capacidad mineralizadora de fósforo mediante la producción de enzimas fosfatasas en medio sólido y líquido. Todas las cepas produjeron fosfatasas ácidas y alcalinas, exceptuando las cepas RP11 para alcalinas y RCQ7 para ambas enzimas. En interacción con plantas de tomate a nivel de invernadero se demostró la capacidad promotora del crecimiento vegetal con diferentes fuentes de fósforo inorgánico en el suelo, probablemente por el aumento la biodisponibilidad de fósforo para las plantas. mediante su solubilización y mineralización; ofreciendo perspectivas para potenciales aplicaciones como biofertilizantes.

J26 - Soil microbial communities' responses to deforestation and reforestation processes in the Eastern Amazon

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Land-use change affects soil microbial communities and their ecological functions. Previous studies from our research group have revealed that the forest-to-pasture conversion in the Amazon region impacted the taxonomic and functional profiles of soil archaeal and bacterial communities and, consequently, soil biogeochemical cycles and greenhouse gas emissions. The attributes of the microbial communities are also influenced by edaphic and climatic factors, such as soil moisture and temperature. In this study, we continue this work by investigating microbial communities' responses to both deforestation and reforestation processes in the Tapajós National Forest (PA) and adjacencies in the Brazilian Eastern Amazon. We collected soil and gas samples from a primary forest, a secondary forest (with 40 years of passive regeneration), and a pasture site during wet and dry seasons (July and November 2019, respectively). Following DNA extractions, the 16S rRNA genes of Archaea and Bacteria were evaluated by quantitative real-time PCR. The study sites exhibited positive (emission) N2O fluxes in both samplings, mainly from the pasture sites. Season influenced CH4 results, which presented both positive and negative (consumption) fluxes. Regardless of the season, most sampling points of the pasture site emitted CH4, while only in the primary forest it was observed to occur methane consumption. Interestingly, the secondary forest displayed an intermediate profile, consuming CH4 in most of the sampling points. The number of bacteria has not changed according to land-uses and seasons, but the archaeal abundance was higher in the primary forest. Overall, our preliminary data demonstrate that secondary forests can be an effective strategy for forest recovery and greenhouse gas mitigation.

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J27 - The conversion burnt-to-green harvest in sugarcane promotes microbial functional diversity and soil organic matter resilience

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Currently, sugarcane is a major global crop produced in over 130 countries, being Brazil the largest producer. In Brazil, different sugarcane harvest systems are commonly applied, such as manual handling with burnt sugarcane (burnt harvest) and mechanical harvesting (green harvest). In this work, we evaluated the effect of sugarcane burning on microbial communities' taxonomy and function in soils under burnt and green harvest, through metagenome and GeoChip. Based on RDA analysis, the microbial taxonomical structure was different according to the harvest system, with organic matter, aluminum, phosphorus, and potential acidity presenting a significant correlation with the microbial community. The burnt system showed a decrease of diversity, with nine phyla being depleted compared to the green harvest system, for example, Planctomycetes, Verrucomicrobia, Cyanobacteria, Thaumarchaeota, among others. Regarding the functional profile, the structure was also different between the two harvest systems, with a decrease in functional diversity in the burnt soils. Genes related to N assimilation, denitrification, and dissimilatory N reduction were significantly higher in green harvest, while assimilatory N reduction, denitrification, and N fixation were higher in burnt harvest system. Regarding the carbon cycle, the amylase functional gene was different in labile carbon (starch and hemicellulose) degradation between the two sugarcane systems, being higher in burnt harvest soil. On the other hand, the gene related to recalcitrant carbon degradation encoding manganese peroxidase was higher in green harvest soil. Also, genes involved in carbon fixation presented differences between the two systems, where the tktA gene was higher in green harvest, while the genes FBPase, TIM, and FTHFS, were higher in burnt harvesting. The genes related to the phosphorus cycle presented no differences between the two systems. Taken together, our data revealed that burnt harvest management affects microbial community composition and functions, with a potentially negative effect on soil processes and health. Acknowledgements: FAPESP and CNPq.

J28 - Chilean blind spots in soil biodiversity and ecosystem function research

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Soil harbor up to a quarter of the world's biodiversity, contributing to many ecosystem functions. It is of great importance to identify distribution patterns of soil organisms and their ecosystem functions to support their conservation and policy building. This has been recently analyzed at macroecological scales, but analyses at national/local scales are scarce. Here we identify and analyze the blind spots in soil taxa and ecosystem functioning data in continental Chile, through a Web of Science articles (1945-2020) search, and focusing on ten soil taxonomic groups and four ecosystem functions (nutrient cycling, decomposition, water infiltration, soil respiration). A total of 741 sampling sites were obtained from 239 articles. In 49.25% of the sites soil biodiversity was studied, while this percentage was 32.65% for ecosystem functions; in 18.10% of the sites both soil biodiversity and ecosystem functions were investigated at the same time, a surprisingly high percentage compared to global studies. By far, Bacteria/Fungi and nutrient cycling were the most investigated taxa and function, respectively. There is a significant number of soil taxa (Acari, Collembola, Nematoda, Formicoidea, Protista, Rotifera) represented by just a few sites concentrated in specific Chilean regions. Places like the central zone, the Atacama desert, and the Valdivian temperate forests present a proliferation of studies on soil Fungi, Bacteria, and nutrient cycling, reflecting historical interests of established research groups. Based on this research, we are identifying the causes of the data blind spots and invite the Chilean soil ecology community to propose ideas on how to fill them.

J29 - Global diversity of desert soil prokaryotic communities

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Deserts are dominant ecosystems as they cover a fifth of the Earth's surface and have polyextreme environments as they are water-deficient with extreme daily temperature fluctuations, low amount of nutrients, high ultraviolet radiation and strong winds. Despite these adverse conditions, they harbor diverse microbial communities which have an important functional role in desert biogeochemical cycling. The purpose of this study was to characterize and compare the diversity of the prokaryotic communities of nine deserts in South and North America (Atacama, Mojave), Africa (Namibia, Namaqualand, Richtersveldt), Asia (Tarim Basin, Mu Us), middle east (Negev) and Antarctica and to identify a desert core soil microbiome. Desert prokaryotic communities were found to be highly diverse, Antarctica and Atacama presented the lowest richness, and the Australia desert the highest. NMDS analysis at the phylum level showed that Antarctica edaphic prokaryotic communities were significantly different from the communities of all the other deserts. Furthermore, it showed that the soil communities from the Richtersveldt, Namaqualand, Namibia, Australia and Mojave deserts were highly similar, as were the communities of the Mu Us and Atacama deserts and Tarim Basin desert has a great dissimilarity with the other deserts. Antarctica edaphic communities were dominated by members of the phylum Proteobacteria (80%), whereas in Actinobacteria (30-70%) predominated in all of the other deserts. Thaumarchaeota and Euryarchaeota were found specially in the hot soils such as but with low relative abundance (between 0,2 and 0,8%). A desert core microbiome was very diverse and composed of Actinobacteria, Proteobacteria, Bacteroidetes, Acidobacteria, Firmicutes, Parcubacteria and Saccharibacteria phyla.

In conclusion, these results are a precedent for other studies of the structure and composition of the prokaryotic communities of other deserts and corroborate the analyzes of other deserts, allowing to show that the composition and structure of the microbial communities are biogeographic patterns of desert soils.

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J31 - Continuous land use and fallow periods generate differential effects on the rhizospheric microbiome and greenbean production (*Phaseolus vulgaris* L)

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Currently, the microbiological component of the soil has taken a great interest in agricultural productivity due to the importance for the growth of healthy and productive crops. This component can be affected by different agronomic practices. The present study compared a cropping field with a long tradition of intensive agriculture with a fallow field, seeking to establish the effect of these practices on the rhizosphere microbiome and productivity of a green beans in three different farms. Green beans were planted in each of the six crop fields and rhizosphere soil samples were taken in the flowering stage of the crop. From these samples, the microbial community was determined by culture-dependent (plate count for different functional groups) and culture-independent (denaturing gradient gel electrophoresis) techniques. Besides, microbial functionality was also evaluated through enzymatic activities such as cellulase, nitrogenase, acid, and alkaline phosphatase. The results show that, for the three farms, the fallow soil showed significantly higher counts ($P < 0.05$) for the phosphate solubilizers and total heterotrophic bacteria. Regarding the four enzymes evaluated, the fallow soils presented a higher activity (statistically significant, $p < 0.05$) compared to the agricultural soil for each of the three farms. The bacterial community, in the same way, showed a different response for farms 1 and 2 under the two management practices. On the other hand, the crop productivity was significantly higher ($p < 0.05$) in fallow soils compared to agricultural soils. Finally, green beans seeds were planted in normal soil and sterilized soil, where the role of the soil microbiome on plant growth parameters was evaluated. This work shows that the continuous use of soils leads to a deterioration of the biological functions and a subsequent reduction of crop yield, which can be recovered when the soil is left at fallow for prolonged periods of time.

J32 - Effect of Samarco´s mine tailing on enzyme activities at Rio Doce estuarine top-and sub-soils in rice crop soils

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On November 5th, 2015, the a Samarco Mining dam collapsed in the southeastern region of Brazil. This disaster deposited around 50 million m3 of waste along rivers course all way to the Rio Doce delta. Among the affected areas, the estuarine region is one of the most worrisome, because the anoxic condition increases the bioavailability of trace metals (Mn, Zn, Pb) associated with the crystalline iron forms in the mine tailing. Enzyme activities are greatly influenced by soil properties and could be significant indicators of heavy metal toxicity in soil for bioavailability in sediments. In this work, we determined the joint effects of metals on soil enzyme activities. Two years after the disaster, we took core samples of six sites from Rio Doce estuarine area with intense mine tailing deposition and measure the activity arylsulfatase, b-glucosidase, acid phosphatase and correlated with metal fractions analysis (available and oxides). Our results suggest that the deposition of mine tailing increase the activity of microorganism, increasing the availably of metal. Concerning the subsoil, the general trend of enzyme activities demonstrated a gradual decrease with depth. Arysulfatase is the enzyme that have higher correlation with metal concentration in oxides fraction Zn, Cd, Mn (0.78, P

J35 - Diversidade de leveduras cultiváveis associadas a sedimentos de floresta de mangue no nordeste do Brasil

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Os manguezais são ecossistemas costeiros de transição, situados entre ambientes terrestres e marinhos em regiões tropicais e subtropicais, possuindo características físico-químicas e microbiológicas singulares com alta relevância econômica e ecológica, como proteção da costa e são habitat para diversos organismos. Embora diversos estudos tenham demonstrado uma alta diversidade de micro-organismos em manguezais, a maioria dos estudos focam em procariotos, deixando uma lacuna sobre as comunidades de fungos, principalmente as leveduras, associadas a sedimento de manguezais. Sendo assim, o presente estudo teve como objetivo verificar a diversidade e a composição de leveduras cultiváveis associadas a sedimentos de um manguezal, localizado no nordeste do Brasil. Foram identificados 42 isolados de leveduras, obtidas de três pontos de coletas distintos no mangue ao longo do rio Santo Antônio, Alagoas, por meio do sequenciamento da região D1/D2 do gene 26S. A maioria das espécies possuem pouco registro de ocorrência nas amostras. As duas espécies mais frequentes foram Saturnispora sylvae (9,1%) espécie prevalente em ambientes ecótonos aquáticos devido a disponibilidade de nutrientes, e Candida pseudolambica (18,2%) espécie cosmopolita, isolada frequentemente de solo e de bivalves que vivem em manguezais. As leveduras podem desempenhar papéis essenciais no ecossistema habitado. A identificação da comunidade de leveduras torna-se importante, pois a presença ou ausência de algumas espécies nos ecossistemas está diretamente relacionada às mudanças no ambiente. A espécie Kluyveromyces aestuarii, por exemplo, é uma espécie recorrente em manguezais e sua ausência pode indicar alterações ambientais de origem natural ou antropogênica. O presente estudo fornece uma importante contribuição para um melhor entendimento da diversidade de comunidades de leveduras presentes nos sedimentos de manguezais, evidenciando a importância de novos estudos ecológicos e taxonômicos deste grupo. Além disso, podemos encontrar novos bioindicadores de qualidade ambiental e novos fungos para aplicações biotecnológicas.

J37 - The rhizosphere microbiome of wild tomato in the Andean mountains

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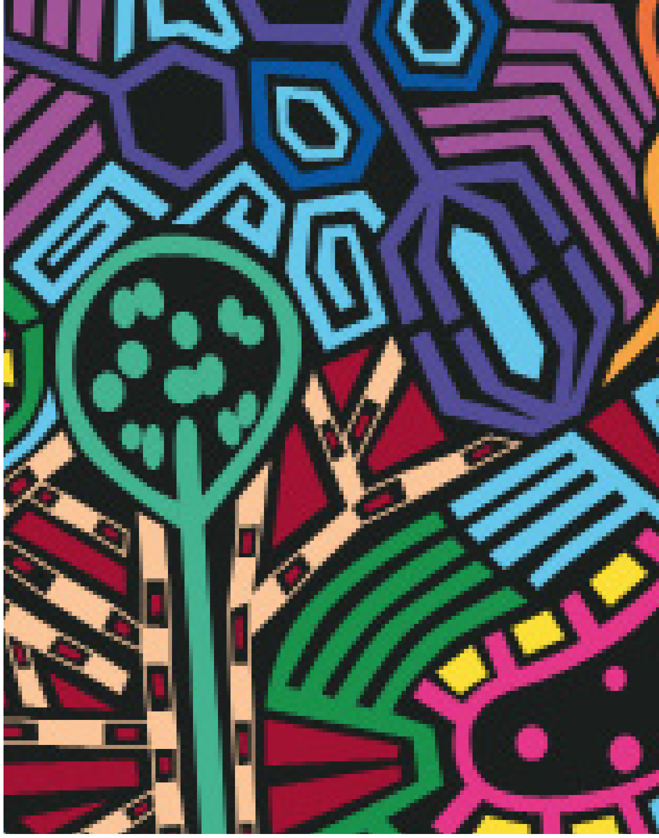
Domestication and breeding have substantially changed the genetic and phenotypic traits of plant species. How domestication affected the taxonomic and functional diversity of microorganisms living on and inside plant tissues is largely unknown for most species. To investigate if domestication of plants impacted the association with specific microbial taxa and beneficial microbial traits, we took a BackToRoots approach to first determine the taxonomic and functional composition of wild tomato plants growing in the arid lowlands of the Andes depression region between southern Ecuador and northern Peru, the center of origin of tomato. We specifically focused on taxonomic profiling of bacteria and fungi associated with tomato roots in three areas in the Low Andes. Three sites in Loja province (South of Ecuador) from 1400 to 200 masl (meters above sea level) were selected for sampling wild tomatoes. The sites resulted to be significantly different based on their environmental parameters which were clustered in a Principal Component Analysis-PCA (PERMANOVA sites: r2 = 0.18048, p = 0.0112). The beta diversity analysis showed that for all three sites, the rhizosphere microbiome was significantly different from that of the bulk soils both in bacteria (PERMANOVA soil type: r2 = 0.09567, p = 0.0001) and fungi (PERMANOVA soil type: r2 = 0.08384, p = 0.0001). On the other hand, the latitude, percent organic matter and magnesium content of the soils were determinative factors in rhizobacterial and fungal community assembly ($p < 0.05$). The differential abundance analysis on the microbial composition revealed that wild tomato rhizosphere is dominated by Enterobacter, Lactococcus, Lechevalieria, unidentified fungi, Acrocalymma, Aspergillus and Fusarium. To further reveal the functional diversity of the rhizosphere microbiome of wild tomatoes, we have initiated a metagenomic analysis. These and culture-based analyses will be conducted to resolve if the rhizosphere of wild tomato harbors yet unclassified microbial genera and microbial traits that were lost during domestication.

POSTER SESSIONS



K

MICROBIAL ECOLOGY OF AQUATIC ENVIRONMENTS

K2 - Cyanobacterial characterization in microbialites of Cenote Azul and Bacalar Lagoon, Mexico

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Microbialites are organo-sedimentary structures formed by microbial activity which trap and precipitate minerals. Previous studies have shown that cyanobacteria are one of the most relevant microorganisms in the formation of microbialites. Bacalar Lagoon (BL) and Cenote Azul (a sinkhole within BL) in Quintana Roo, Mexico exhibit the largest occurrence of modern microbialites. Although there are already studies on the ecology and microbial diversity of these microbialites, a detailed characterization of cyanobacteria associated to microbialites is still needed. Hence the objective of this work was to characterize the cyanobacterial component of microbialites in BL and CA. For this we used a polyphasic approach, with 16S amplicon sequencing (iTag) and shotgun metagenomics, then molecular data was validated with microscopic observations from field samples, cultures and descriptions from previous works. BL and CA microbialites showed differential cyanobacterial composition attributed to different concentrations of light and nutrients. Both sites exhibited completely unknown taxa of Cyanobacteria, an unknown Chroococcales composed the 70% of relative abundance through all depths in CA, while BL was dominated by Nostocales.

K3 - Molecular ecology of the North Atlantic phytoplankton spring Bloom

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Every spring the North Atlantic hosts one of the most important biological pulses on earth: the phytoplankton bloom. This massive accumulation of phytoplankton biomass is the climax of an annual cycle driven by the seasonality of physical, chemical and biological features in the ocean. The timing and geographical distribution of the spring bloom as well as the resulting biomass accumulation have largely been studied using the global capacity of satellite imaging. However, fine-scale variability in the taxonomic composition, spatial distribution, seasonal shifts, and ecological interactions with heterotrophic bacterioplankton has remained largely uncharacterized. Molecular techniques, as high-throughput amplicon sequencing, provide a unique framework to characterize microbial communities in a single experiment with highly-defined phylogenetic resolution. As part of The North Atlantic Aerosols and Marine Ecosystems Study (NAAMES), we generated 16S rRNA gene amplicon profiles of phyto- and bacterio- plankton communities to investigate the seasonal changes in the studied area. The results from this research have provided a better definition of the ecological regions in the North Atlantic, a precise characterization of the phytoplankton bloom annual progression and its influence on the bacterioplankton communities. Furthermore, this dataset provides accurate microbiological context to analyze concurrent measurements such as flow cytometry phytoplankton cell counts, biovolumes, and vitamin B1 concentrations, among others. These integrative analyses have led to overarching environmental observations as B1-auxotrophic bacterioplankton responding to high vitamin concentrations in the accumulation phase of a bloom, but also to unexpected findings as the dominance of small phytoplankton during the climax transition of the bloom.

K4 - Antibiotic resistant bacteria isolated from volcanic lake water in Ecuador

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Research carried out in recent years in aquatic ecosystems that are extreme for life, such as glaciers, volcanic lakes and hot springs, have revealed a diversity of microorganisms with natural resistance to antibiotics that have survived and developed in these environments. They have adapted to the prevailing extreme conditions, constituting a natural reservoir of resistance to antibiotics called environmental resistomes, which have been little studied. Therefore, the objective of this work was to know the profiles of resistance to antibiotics of bacterial strains isolated from two volcanic lakes in Ecuador. A total of 32 water samples were collected from the volcanic lakes Cuicocha and Quilotoa in Ecuador. The isolation of the bacterial colonies was carried out by the membrane filtration technique, using Millipore filters of 0.45 µm pore, a sample volume of 100 mL and R2A agar. The isolated and purified strains were identified following the MacFaddin schemes, complemented with the biochemical tests of the Microgen galleries. The antibiotic resistance profile was determined by the plaque diffusion method. Seven strains of the genus Aeromonas were identified (the majority multi-resistant to the antibiotics ampicillin, amoxicillin/clavulanic acid and cephalothin), 8 strains of the genus Bacillus (resistant to the antibiotics clindamycin, erythromycin, gentamicin and oxacillin), 5 strains of the genus Pseudomonas (resistant to the antibiotics amikacin, ampicillin, chloramphenicol, gentamicin, imipenem and trimethoprim/sulfamethoxazole) and 4 strains of the genus Staphylococcus (resistant to oxacillin). The results indicate the presence of a diversity of bacterial resistomes in the water of the volcanic lakes analyzed and indicate the need for frequent and seasonal studies to better understand these findings.

K5 - Diving into the unknown: identification of antimicrobial resistance hotspots in a tropical urban estuary

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Antimicrobial resistance is widely studied under the clinical perspective. However, there is a knowledge gap regarding this issue in environmental settings. This study aimed to evaluate the presence of potentially pathogenic and antimicrobial-resistant bacteria in the Guanabara Bay (GB), a heavily polluted estuary and a tourist attraction in Rio de Janeiro, Brazil. In June 2020, six water samples were collected in three sites along a pollution gradient in the GB. Bacterial isolation was carried out by three different approaches: culture of undiluted water aliquots on Thiosulfate Citrate Bile Salts Sucrose (TCBS) agar (1) and culture of undiluted (2) and filtered (3) water aliquots on TCBS agar supplemented with ceftriaxone (2 μg/mL). Isolates were identified by mass spectrometry. The most frequently isolated genera were Aeromonas and Vibrio. Susceptibility to aminoglycosides, beta-lactams, including third-generation cephalosporins and carbapenems, fluoroquinolones, tetracyclines, and sulfonamides was assessed by the disk diffusion method. Resistance to all classes was detected, especially beta-lactams, being 21.6% of the isolates multidrug-resistant. Production of extended-spectrum beta-lactamases (ESBL) was verified and, among the tested isolates, 66.6% were positive, out of which two strains were putative AmpC producers and one was a putative carbapenemase producer. From these, beta-lactam resistance genes blaCTX-M-1,2, blaCTX-M-14, and blaTEM were detected in 7.1%, 28.5%, and 42.8% of the tested strains, respectively. Resistant bacteria and ESBL-positive isolates were more often isolated in impacted sites in the GB, which were marked by higher coliform counts and higher nutrient concentrations owing to the discharge of untreated sewage. Here, we report the presence of clinically relevant traits in environmental bacteria, including potential pathogens, suggesting risks to public health. Results constitute a basic understanding of resistant microorganisms in these waters and indicate a hotspot of antimicrobial resistance, highlighting the pertinence of risk-assessment research for better comprehension of this issue in aquatic environments.

K6 - Caracterización de las comunidades microbianas del río Rímac utilizando 16S rRNA metabarcoding

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El río Rímac es la principal fuente de agua de la ciudad de Lima. Desde la vertiente de los Andes dónde nace hasta su desembocadura en el océano Pacífico, distintos eventos ambientales afectan a este río, que influyen en su biota. Hasta el momento no se han caracterizado las poblaciones microbianas presentes en el Rímac. Con el objetivo de caracterizarlas, se recolectaron 13 muestras de agua, y sus réplicas, a lo largo del río, clasificando estas muestras de acuerdo a las sub-cuencas identificadas por la Autoridad Nacional del Agua del Perú. Se extrajo el ADN total y se secuenció un fragmento del 16S rRNA utilizando tecnología Illumina MiSeq. Los reads de cada muestra fueron analizados utilizando el paquete DADA2 en R v.3.6.3, especializado en análisis de variante de secuencia del amplicón. Por último, se utilizó Piphillin para realizar una predicción funcional basada en la frecuencia de las secuencias de 16S rRNA comparadas con genomas anotados de la base KEGG. Reportamos que las comunidades bacterianas más cercanas al entorno urbano eran menos diversas. Un análisis de escalado multi-dimensional (MDS) agrupó a las comunidades microbianas de acuerdo a su ubicación geográfica. Clases bacterianas tales como Alfaproteobacteria, Bacteroidia y Campylobacteria fueron los taxa más frecuentes en las comunidades cercanas a la urbe. Los géneros Flavobacterium e Hypnocyclicus fueron más predominantes en los puntos cercanos a la sub-cuenca andina. Se logró identificar también al patógeno emergente Arcobacter cryaerophilus (de la familia Campylobacteraceae) asociado por la literatura a contaminación fecal y normalmente no identificable mediante métodos microbiológicos tradicionales. Nuestro trabajo permitió observar el cambio en la composición de las comunidades microbianas del río Rímac revelando una marcada diferenciación entre comunidades por ubicación geográfica además de resaltar la utilidad del metabarcoding del 16S rRNA en una posible vigilancia de patógenos de interés.

K7 - Characterization of plastisphere associated with plastic polymers during biofilm succession in the coastal Southwest Atlantic of Brazil

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Annually millions of tons of plastics are release into the oceans, causing an increasing accumulation of this waste, becoming one of the main environmental problems of the last several decades. Once in the oceans, plastic is quickly colonized by a complex microbial community called "Plastisphere". Although recent studies have made efforts to characterize the biofilm associated with these plastic matrices, however factors affecting the development and composition of these microbial communities are still poorly understood. In our experimental study, we evaluated the diversity and the composition of the microbial community associated with the 3 different polymers, High Density Polyethylene (HDPE), Low Density Polyethylene (LDPE) and Polybutylene Terephthalate Adipate (PBAT) deployed at 1,5 m depth of Southwest Atlantic coastal waters of Ubatuba, São Paulo for 36 days, through 16s RNA sequence analysis. Sampling was performed in duplicate, every 15 days (Week 1; 3 and 5), in addition to seawater samples. Alpha diversity indices demonstrated that there is an increase in bacterial diversity associated with plastisphere (Kruskal-Wallis; $p < 0.05$) over the weeks, and beta diversity, using the Bray-Curttis dissimilarity index, demonstrated that the time and type of polymer have an effect on the structure of microbial communities (PERMANOVA; $p < 0.05$). The phyla Bacteroidota, Chloroflexi, Myxococcota and Verrucomicrobiota have a significant increase (ANOVA; $p < 0.05$) in their abundance over the weeks, while the phylum Cyanobacteria decreases (ANOVA; $p < 0.05$). The partial results of the study demonstrate that time is a factor that influences the biofilm modulation associated with plastic, in which has been observed to increase the abundance of some phyla over time, and that may indicate a selection of microorganisms adapted to the polymers tested.

K8 - Diversity of culturable methane-oxidizing bacteria from deep sediments of the Southwest Atlantic Ocean

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Methane is one of the main gases produced in marine sediments, having biotic or abiotic origin. This important greenhouse gas is mitigated in the sediment and water column thanks to the activity of methanotrophic bacteria (MOB), capable to use methane as sole source of carbon and energy. This work was carried out in the Santos Basin, which is a sedimentary basin located in the Southeast-South region of Brazil, representing the largest producer of oil and natural gas in the country. The objective of our study was to characterize the diversity of microorganisms in microbial consortia from sediment samples. The samples were collected in 10 sample points, through a box-corer and inoculated in culture medium NMS + 3.5% NaCl with headspaces filled with methane: air (1: 1) in aerobic cultures and methane: argon (1: 1) in anaerobic cultures, at 20 °C, for 8 months. The genomic DNA was extracted from the cultures and the 16S rRNA gene was sequenced using the Illumina Miseq platform. Gas chromatography for the methane detection was performed with the consortia where methanotrophs were detected. The analysis of alpha diversity revealed no difference in species richness, but beta diversity revealed that samples grown with different headspaces are dissimilar, that is, there is a difference in the structure of microbial communities according to the treatment. The Phylum Proteobacteria was dominant in the taxonomic analysis, with emphasis on the Gammaproteobacteria class. Three methanotrophic genera were identified in four microbial consortia whose methane consumption was confirmed by gas chromatography, namely Methylomicrobium, Methylomonas and Methylovulum. The functional inference from the 16S rRNA highlighted that microbial communities among the consortia are involved in the cycles of carbon, nitrogen and sulfur. These preliminary results represent the record of the cultivable deep-sea methanotrophic microbiome in the Santos Basin.

K9 - Síntesis de halometanos en la cuenca del sur de California: ¿Qué papel juegan las distintas variables bióticas y abióticas en este sistema?

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Los halometanos son gases biogénicos que transportan a la atmósfera diversos halógenos reactivos (ej. cloro, bromo y yodo) que destruyen el ozono estratosférico. Una fracción de estos compuestos proviene del océano y son producidos por macroalgas, microalgas, cianobacterias y bacterias. Un estudio reciente muestra que, la síntesis de halometanos está directamente relacionada con las tasas de crecimiento de bacterias heterotróficas marinas en cultivos. Sin embargo, existen pocos estudios que identifiquen los parámetros ambientales relacionados con la síntesis de estos compuestos en el medio natural. Con el objetivo de validar qué variables ambientales explican la síntesis de halometanos en la superficie del océano, a través del preconcentrador Medusa GC-MS (espectrometría de masas por cromatografía de gases) se determinaron las concentraciones de diversos halometanos en más de 2000 muestras de aire medidas a lo largo del año 2015 en la estación del Scripps Pier, en La Jolla, California. Estos datos se compararon directamente con otros parámetros físicos, químicos y biológicos los cuales se obtuvieron in situ, de boyas y sensores. El yoduro de metilo (CH3I) presentó correlaciones positivas con la producción bacteriana, temperatura, mientras que el bromuro de metilo (CH3Br), bromoformo (CHBr3) y dibromo metano (CH2Br2) presentaron correlaciones positivas solamente con la temperatura. Por otro lado, el cloruro de metilo (CH3Cl), cloroformo (CHCl3) y dicloro metano (CH2Cl2) presentaron correlaciones negativas con la producción bacteriana, clorofila-a, temperatura, y abundancia de grupos de fitoplancton. Estos datos confirman la importancia de las bacterias heterotróficas principalmente en la síntesis de CH3I. Además, la capacidad de observar la dinámica temporal de estos compuestos a tan alta resolución permite identificar franjas temporales de síntesis o consumo neto a lo largo del año que a su vez pueden ser atribuidas a ciertos grupos de bacterias presentes en el agua identificadas a través del gen 16S.

K10 - A multi-omics approach to assess the chemical ecology of *Pseudonocardia* spp. from marine sediments

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Actinobacteria is a phylogenetically diverse bacterial phylum widely distributed across both terrestrial and aquatic ecosystems. In particular, the genus Pseudonocardia and their specialised metabolites have been extensively studied in terms of their antagonistic interaction with other microorganisms and their mutualistic interactions with insects. However, the chemical ecology of marine-origin Pseudonocardia remains understudied. In this study, metabolomics and genome mining tools were used to assess the role of the specialised metabolites on interactions between members of the Pseudonocardia genus isolated from different marine environments. First, using challenges bioassays, antagonist interaction between nine Pseudonocardia spp. isolated from marine sediments and two non-marine species was examined and correlated to the strains' phylogeny and their metabolomics profile. Then, in a focused experiment, the correlation between three Pseudonocardia spp. isolated from two different locations in the deep Southern Ocean, as well as three other phylogenetically closely related species were analysed. To this end, a metabologenomic approach which included the analysis of Biosynthetic Gene Clusters (BGCs) using BiG-SCAPE and a mass spectrometry-based metabolomics using GNPS was applied. To understand the spatial dynamics, matrix-assisted laser desorption/ionization (MALDI)-mass spectrometry imaging (MSI) was used to examine in situ species chemical interactions between the Southern Ocean strains and their closest relatives. The results showed that phylogeny has a primary role in the antagonist inter-species interactions, as well as in the specialised metabolite profile. However, it was also suggested that polyketide synthase and non-ribosomal peptide synthetase BGCs are important for local environmental adaptation. These results provide an important insight into the role of the specialised metabolism in the inter-species microbial interaction of Pseudonocardia strains from marine environments.

K11 - Bacteria and seston in tropical reservoirs from different latitudes present similar carbon to nutrients ratio

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Planktonic bacteria are key elements in nutrient cycling and energy flow in the microbial trophic web in aquatic ecosystems. Thus, their chemical composition and requirements are critical drivers for these functions. In the oceans and continental aquatic ecosystems in temperate regions, bacterial biomass is relatively nutrients-rich (close to the Redfield C:N:P ratio 106:16:1), but in low latitudes environments they seem to vary widely. Latitudinal gradients exert strong influence in light and temperature variability and may be an important driver of seston and bacterial stoichiometric regulation. This work aims to evaluate the latitude effect on the ratio of nutrients (C, N and P) present in bacterial biomass. Seston and bacteria from reservoirs situated at two different locations in the tropical zone (low and medium latitude) were retained in glass fiber. The N and P amounts were determined in the seston, in the bacteria and in all filtered fractions. The concentrations of N varied between 0,14 to 18,27 (seston) and 0,07 to 3,61 (bacteria) mM/L, P ranged from 0.0002 to 4.6072 (seston) and 0.0004 to 0.7555 (bacteria). The C data from the filters is being processed. To perform the stoichiometric ratios, the chlorophyll-a content was considered a proxy for the C amount in the seston. Chlorophyll-a ranged from 0.91 to 1125.21 ug/L. The C:N:P ratios for seston as the C:N ratios for bacteria were higher than Redfield's , on average 305:15:1 and 1887:151:1 (seston) and 40:1 and 16:1 (bacteria) low and medium latitude, respectively. The Wilcoxson test found that there was no significant difference in the C:N:P ratios between low and medium latitude environments neither for bacteria nor seston fractions. We will discuss the potential stoichiometric ratios regulators in bacteria and seston in tropical reservoirs.

K12 - Microbial signature in urban wetlands of Llanquihue and Puerto Montt, Chile

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Urban wetlands are those located in cities and their surroundings, constituting a natural, social and ecological heritage, which are constantly threatened by anthropogenic pressure, such as real estate development and unsustainable resource management. They are key pieces to keep biodiversity, both flora and fauna in urban areas. It is estimated that in Chile there are more than 40 thousand wetlands, with a total area of 4.5 million hectares. According to data from the national inventory of wetlands from the Ministry of the Environment, in the Los Lagos region there is a record of 6,929 wetlands, of which 340 are in the Puerto Montt, 192 in Puerto Varas and 42 in Llanquihue. In recent years, various works have studied the microbiology of wetlands using massive nucleic acid sequencing techniques. Iliev (2019), studied the microbial structure of the Maritsa River through massive sequencing, finding differences in its composition according to the studied location. Usharani (2019), described those bacteria and fungi associated with wetlands help to treat wastewater, being able to eliminate pollutants such as sulfate, phosphorus and nitrogen. In Chile, Eissler (2019), described the microbial composition in different locations of the wetland of the Salar del Huasco, finding differences in each of the studied sites. In this work, we have used amplicon sequencing for the 16S regions of bacteria and archaea, using V3 to V4 hypervariable region, to describe the microbiology of urban wetlands in the cities of Llanquihue and Puerto Montt. Our results show differences between the wetlands studied. At phylum level, the main bacteria found in wetlands belong to Proteobacteria, Firmicutes, Bacteroidota, Actinobacteriota and Verrucomicrobiota, while main archeas found belong to Halobacterota, Crenarchaeota and Euryarchaeota. This study proposes the use of sequencing methodologies for the environmental monitoring of microorganisms in order to take care of these important ecological niches.

K13 - Efecto de la disponibilidad de nutrientes sobre el bacterioplancton fotótrofo con proteorodopsinas en un sistema productivo costero

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Las proteorodopsinas son proteínas transmembranales que capturan luz para generar energía bioquímica, la cual puede ser utilizada para crecimiento y supervivencia en bacterias marinas. Mediante la cuantificación de retinal, como proxy de este fotosistema, las mayores concentraciones de proteorodopsina se han observado generalmente en ambientes oligotróficos donde las concentraciones de clorofila-a y nutrientes inorgánicos son bajas. Sin embargo, en un estudio reciente en la zona de surgencia de la cuenca del Sur de California se observó que las máximas concentraciones de proteorodopsina coincidieron con concentraciones de clorofila-a durante las proliferaciones algales de primavera. Para comprender mejor la dinámica de comunidades fotótrofas, en este estudio investigamos las relaciones ecológicas entre la disponibilidad de nutrientes, el crecimiento del fitoplancton y microorganismos con proteorodopsinas, y la estructura de las comunidades microbianas asociadas al desarrollo de proliferaciones algales en un ambiente controlado. Con ese objetivo se realizó un experimento de incubación de mesocosmos durante 20 días con agua de mar colectada en la cuenca del Sur de California, induciendo el crecimiento fitoplanctónico con la adición de nutrientes inorgánicos. Se cuantificó la clorofila-a, proteorodopsina, abundancia bacteriana y se secuenciaron amplicones de la región V4-V5 del gen 16S del ARNr. Las máximas concentraciones de clorofila-a se presentaron entre los 8 y 12 días después del inicio del experimento, mientras que los niveles más altos de proteorodopsina y abundancias bacterianas se presentaron entre los 14 y 20 días. Bacterias en los órdenes Flavobacteriales y Rhodobacterales dominaron la estructura de las comunidades bacterianas, sugiriendo la utilización de proteorodopsinas en miembros de estos grupos. Estos datos sugieren que, a diferencia de lo observado en sistemas oligotróficos, en sistemas productivos la asimilación activa de nutrientes y materia orgánica por parte del bacterioplancton está acoplada a la obtención de energía solar mediante proteorodopsinas.

K14 - Disentangling the main metabolic pathway found on Brazilian soda lakes

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The microorganisms communicate with each other using different chemical signal molecules. These molecules are critical for synchronizing the activities as nutrient uptake, and for that directly impacting the environmental functioning. This work aims to describe the main metabolic pathway found on Brazilian soda lakes. Applying flux balance analyses (FBA) on metagenomic data, we evaluated the main metabolic pathways found on Brazilian soda lakes to predict how these organisms support the higher productivity observed in this alkaline environment. Three different watercolor soda lakes (crystalline, black and green color) were evaluated on three sampling times (dry-wet-dry periods). The relative abundance of total bacterial varied through the time, but the most prevalent phyla were Actinobacteria, Bacteriodetes, Cyanobacteria and Planctomycetes. The green color lake has this color due to the occurrence of Cyanobacteria bloom and this lake was enriched with amino acids and nitrogen compounds as urea and nitrite. The compounds predicted on evaluated lakes variety through the sampling time. Considering the CAZy (carbohydrate-active) enzymes, the green-water lake was enriched in almost all evaluated categories, except to redox enzyme categories enriched in the black-water lake. The green lake seems to show a more dynamic production of compounds, specially associated with nitrogen metabolism. This observation could be a result of Cyanobacteria activity. These results shed light on the complexity of metabolic interactions detected on Brazilian soda lakes and they still under evaluation.

K15 - Análisis de la redundancia funcional de la comunidad bacteriana de una planta de tratamiento a lo largo de un ciclo anual, usando la herramienta de predicción funcional PICRUST2

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La comunidad bacteriana que conforma los lodos activados, utiliza su potencial metabólico para transformar la materia orgánica del afluente y convertirla en biomasa bacteriana y CO2, entre otros. Este proceso es fundamental para la remoción de materia orgánica del agua residual y regular la eficiencia de las plantas de tratamiento. Es bien sabido que la composición taxonómica de la comunidad bacteriana de los lodos activados cambia a lo largo del tiempo, en respuesta a las fluctuaciones del agua residual y a cambios en la operación del sistema. No obstante, es menos claro cómo estos cambios taxonómicos se ven reflejados en la variabilidad del metabolismo de la comunidad, con las consecuencias potenciales sobre la eficiencia del proceso. Previamente, identificamos cuatro grupos de bacterias especialistas dentro de una planta de tratamiento de la ciudad de Medellín-Colombia, cuyos comportamientos sugieren preferencias por condiciones contrastantes, relacionadas con los patrones estacionales de precipitación y cambios en la edad de lodos dentro del sistema. Por lo tanto, aquí evaluamos qué diferencias hay en el potencial metabólico entre estas poblaciones especialistas y qué niveles de redundancia funcional encontramos en el proceso, a lo largo de un ciclo anual. Para ello, estimamos el potencial funcional de cada grupo, utilizando la herramienta de predicción funcional PICRUST2, con base en los inventarios taxonómicos de 66 muestras tomadas a lo largo del año 2018, utilizando la secuenciación de amplicones con ILLUMINA MiSeq y su procesamiento con Qiime2. Los resultados obtenidos permitieron evidenciar una alta redundancia funcional entre los grupos. No obstante, pudimos detectar cambios significativos en la abundancia de múltiples rutas metabólicas compartidas, que podrían explicar las fluctuaciones en el desempeño del proceso de tratamiento. De manera interesante, nuestros datos sugieren que estos niveles de redundancia pueden mantenerse gracias a las altas tasas de inmigración de bacterias provenientes del afluente.

K16 - Discriminación de diferentes grupos de especialistas bacterianos en una planta de tratamiento de lodos activados, mediante el uso de análisis de redes de interacción

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El sistema de tratamiento de aguas residuales con lodos activados es un proceso biológico constituido, en su mayoría, por una comunidad bacteriana que contiene miles de especies y un alto número de relaciones. Esta complejidad intrínseca se agudiza debido al carácter altamente dinámico del sistema que, a su vez, depende de parámetros de diseño y de las fluctuaciones cuantitativas y cualitativas en el flujo de agua residual que ingresa al sistema. Por lo tanto, el estudio de esta comunidad de lodos activados representa un gran desafío para la ecología microbiana, que implica: i) entender los factores que regulan la dinámica de la comunidad bacteriana de estos sistemas y ii) discriminar poblaciones que respondan de manera diferencial a las fluctuaciones cuantitativas y cualitativas de los flujos del afluente, mediante la reducción y/o manejo de la complejidad intrínseca de estas comunidades. Este trabajo integró el análisis de redes y el método de Valor Indicador (IndVal) para establecer si es posible diferenciar grupos de especialistas bacterianos relacionados con condiciones variables de operación, con datos obtenidos de una planta de tratamiento de aguas residuales de la ciudad de Medellín a lo largo de un ciclo anual. Este análisis se basó en los inventarios de la comunidad bacteriana de los lodos activados durante el año 2018, usando secuenciación de amplicones del rRNA con ILLUMINA MiSeq y el procesamiento de las secuencias con Qiime 2. Este ejercicio permitió discriminar los ASVs de nuestro estudio, en cuatro grupos de especialistas con comportamientos temporales característicos, relacionados con las fluctuaciones estacionales de la precipitación y con cambios en la edad de lodos de la planta de tratamiento. Nuestros resultados sugieren que estos cuatro grupos de especialistas recogen, de manera simplificada, las fluctuaciones de la mayor parte de la comunidad bacteriana de los lodos activados durante un ciclo anual.

K17 - Análisis comparativo de la comunidad bacteriana asociada a dos linajes de la diatomea invasora, *Didymosphenia geminata*, utilizando QIIME y DADA2

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Las invasiones biológicas pueden generar pérdidas significativas en la biodiversidad del ecosistema receptor. Particulamente, las invasiones por microorganismos son más complejas de detectar, por ende, difíciles de prevenir. Al transportarse, estos invasores llevan consigo a una microbiota acompañante la cual alberga un conjunto de comunidades microbianas que han sido poco exploradas. Las interacciones funcionales entre hospedero - huésped y con el ambiente invadido, pueden jugar un rol importante en el éxito invasor. Comprender cómo se estructura la comunidad microbiana que se asocia a un ecosistema es el primer paso para determinar las diversas interacciones entre organismos y el ambiente. El objetivo de este estudio fue establecer la comunidad bacteriana asociada a la diatomea invasora Didymosphenia geminata y realizar un análisis comparativo de la microbiota bacteriana en dos linajes genéticos con clara diferencia en distribución geográfica (linaje americano y europeo) de la microalga. Se evaluó la hipótesis de que los microbiomas bacterianos del linaje americano y europeo de D. geminata comparten una microbiota bacteriana central, debido a que existe una estrecha interacción entre los microorganismos y la diatomea. Usando la técnica de metabarcoding a partir de DNA ambiental (eDNA) extraído de la mata de exopolisacaridos de la microalga, se realizó un análisis de biodiversidad bacteriana utilizando el gen 16S como marcador genético. Para los análisis taxonómicos y de diversidad microbiana, se escogieron y compararon las plataformas bioinformáticas QIIME y DADA2. Como resultado, se determinó que existe una microbiota bacteriana central compartida entre ambos linajes de la diatomea, independiente de su punto geográfico y que, adicionalmente, cada linaje posee una comunidad de bacterias propias.

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K18 - Bacterial community composition in shallow lakes from *Nothofagus pumilio* forest (Patagonia, Argentina)

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In Patagonia, the deciduous tree Nothofagus pumilio constitutes an important source of organic matter for both, lakes and rivers. In this study, we aimed to analyze bacteria community composition and diversity in four nearby environments (<50 m of altitude range) located at 1500 m a.s.l. in a N. pumilio forest. We also characterized the dissolved organic matter (DOM) and determined carbon consumption in laboratory experiments. Sampling was performed in autumn, spring and summer, in the Challhuaco Mountain. We observed differences in DOM composition, that was dominated by humic-like compounds (Lake Verde) or protein-like molecules (Lake Sol). The highest OTU richness (S) and diversity (H) were observed in environments located at lower altitude (Lake Mallín, S=1298, H=5.67). OTUs Ordination analysis (NMDS) showed a clear segregation in three groups: Lake Verde, Lake Sol, and the lower altitude environments constituting a homogeneous group. Considering the main bacterial classes, we observed a clear dominance of Actinobacteria, Flavobacteria, and Betaproteobacteria. Carbon consumption rates were higher in Lake Mallín (0.35 d-1) than in the environments located at higher altitude (0.003 d-1). Our results showed that even at a small geographic scale there are important differences in bacterial community composition and C-consumption rates very likely associated with variations in DOM quality.

K19 - Efecto de la luz en el metabolismo de la bacteria con rodopsina *Stakelama pacifica* BTS27C

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Las bacterias marinas son capaces de usar la luz solar como fuente de energía capturándola a través de fotosistemas basados en clorofila o en rodopsinas. La rodopsinas microbianas están presentes en más del 80% del bacterioplancton, haciendo este el metabolismo más común en la superficie del océano. Sin embargo, los mecanismos específicos por los cuales estas bacterias se benefician de la energía solar están poco caracterizados y requieren ser cultivadas para su estudio. Se ha reportado que ciertas bacterias marinas utilizan la luz para optimizar la toma de sustratos, mientras que otras utilizan esta energía para sobrevivir durante periodos de inanición. Este trabajo tiene como objetivo clasificar la rodopsina presente en Stakelama pacifica BTS27C, aislada de la Bahia Todos Santos, Baja California, México. Así mismo, evaluar la respuesta del metabolismo de este organismo en condiciones de luz y oscuridad con el fin de comprender las funciones fisiológicas y ecológicas de la luz.

La caracterización fotofisiológica de esta cepa mediante el estudio de su genoma es relevante debido a la presencia de un gen de bacteriorodopsina con residuos de aminoacidos caracteristicos de absorción en luz verde (L105) y con gran similitud a rodopsinas sensoriales. Para evaluar la respuesta fototrófica de esta bacteria se hicieron incubaciones a temperatura ambiente en presencia y ausencia de luz natural. El resultado más distintivo fue la mayor abundancia de biomasa en el cultivo expuesto a luz creciendo en un medio rico en nutrientes. El estudio del metaboloma de BTS27C mediante análisis genómico, cromatografía de líquidos-espectrometría de masas en Tándem (LC-MS2) y quimioinfórmatica revela cambios en la abundancia de metabolitos (rango de150 a 1350 Da) en respuesta a la ausencia de luz. Particularmente, se observó que las condiciones de luz afectaron el metabolismo de derivados del ácido cólico y de algunas clases de lípidos.

K20 - Ecotipos de la cianobacteria *Raphidiopsis raciborskii*: más allá del individuo

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El creciente aumento en la distribución global de Raphidiopsis raciborskii, cianobacteria formadora de floraciones, en lagos tropicales, subtropicales y templados genera gran preocupación debido a su capacidad de producir toxinas. Se ha propuesto que su actual presencia en distintas latitudes se debe al desarrollo evolutivo de ecotipos con diferente nicho y con distintas respuestas a los cambios ambientales. En consecuencia, es esperable que aislamientos de distintas partes del mundo presenten preferencias ecológicas y toxicidad diferentes, lo que ha permitido determinar patrones biogeográficos de la especia. Recientemente se ha propuesto que un aspecto importante para explicar el éxito de las cianobacterias es la presencia de una comunidad de bacterias heterótrofas asociadas a su mucílago (microbiota). Dicha microbiota es fuente relevante de funciones metabólicas, generando que ambas partes (cianobacteria y microbiota) sean mutuamente dependientes para sobrevivir. En este sentido, es esperable que ecotipos de lugares contrastantes del planeta presenten diferencias a nivel ecológico y en su microbiota. En este estudio analizamos las características morfológicas, tasas de crecimiento y la microbiota mediante la secuenciación del ARNr 16S de dos aislamientos de R. raciborskii pertenecientes a ecotipos diferentes, provenientes de extremos latitudinales: uno tóxico (Cuenca del Plata, América del Sur) y uno no tóxico (América del Norte). Se encontró que, si bien bajo idénticas condiciones de luz y temperatura ambos muestran tasas de crecimiento similares, sus diferencias se evidencian en la morfología y la estructura comunitaria de las microbiotas. Esto sugiere que las diferencias entre ecotipos de R. raciborskii no solo se debe a características individuales, sino también a las características funcionales que resulten de la interacción con la microbiota e implica que para entender y predecir la aparición y dominancia de estos organismos es necesario estudiarlos como holobiontes y no como especies aisladas.

K21 - Caracterización fenotípica de microalgas y cianobacterias del perifiton de los ríos aportantes del embalse altoandino Succus, Cordillera Real del Ecuador

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El conocimiento de la abundancia y la composición de microalgas y cianobacterias perifíticas resulta fundamental para los ecosistemas acuáticos porque son consideradas bioindicadores de la eutrofización de las aguas y ayudan en el diagnóstico de sistemas lénticos. El embalse Succus forma parte del sistema de humedales de páramos hídricos del Parque Nacional Cayambe-Coca en la Cordillera Real del Ecuador, que provee de agua potable al Distrito Metropolitano de Quito. Con el objetivo de caracterizar fenotípicamente microalgas y cianobacterias del perifiton de los ríos aportantes de este embalse para establecer una línea de base para el estudio de la composición de la comunidad microbiana fotosintética y la determinación biológica del estado trófico y la calidad de agua para consumo humano, se realizaron dos muestreos en los tributarios 1 y 2 en los meses de febrero y abril de 2021. Se tomaron muestras de sedimento, raspados de rocas, plantas nativas del lugar y agua. Las muestras se examinaron bajo un microscopio óptico invertido. Se utilizaron claves taxonómicas para la clasificación de cada forma distintiva a nivel de género y, en ocasiones específicas, hasta especie. Hasta el momento, se identificaron 33 taxones distribuidos en cinco divisiones. Se encontraron 18 géneros considerados como potenciales bioindicadores del estado del ecosistema, con los que se concluyó que el estado trófico del embalse se encuentra en transición entre la oligotrofía y la mesotrofía. Se identificaron taxones que deberían priorizarse en el monitoreo bimensual de la Empresa Pública Metropolitana de Agua Potable y Saneamiento del Distrito Metropolitano de Quito, pues su seguimiento puede determinar cambios considerables en la comunidad microbiana que, potencialmente, alterarían la calidad del agua. Además, destacó la importancia de un monitoreo constante de estas comunidades fotosintéticas, la presencia/ausencia de determinados taxones cuando exista eutrofización y/o cambios climáticos proyectados en el contexto del calentamiento global.

K23 - Temporal dynamics of *Legionella* (Proteobacteria, *Legionellaceae*) in a Pampean shallow lake

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Species belonging to Legionella genus are of great interest regarding public health since many of them are pathogenic for humans, causing a variety of pulmonary diseases: ranging from Pontiac fever (with symptoms similar to influenza) to a severe pneumonia, called Legionellosis, with Legionella pneumophila being responsible of 95% of these cases. This bacterium is ubiquitous in nature and frequently found in a variety of environments, including recreational waters. One of the main contagion routes is by aerosols from contaminated waters. The main purpose of this work was to assess the temporal dynamics of Legionella species on a monthly basis throughout 2016 in El Carpincho shallow lake, located near the city of Junín (Buenos Aires, Argentina) and the factors causing it. To achieve this, environmental variables were obtained in situ and quantitative Polymerase Chain Reaction was performed using primers and specific probes for Legionella, as well as a standard concentration curve for quantification of the samples. Principal components analysis revealed that the first 3 axes accounted for about 85% of the variance (PC1: 52%, PC2: 20%, PC3: 13%). Samples mainly ordinate along the first axis, principally defined by temperature (r= 0.93), dissolved organic carbon (DOC, r= 0.82), pH (r= 0.89), ammonium (r= -0.76) and Legionella abundances (r= -0.68). Summer samples ordinated towards higher temperatures, DOC and pH values, whereas winter samples towards higher Legionella abundances and ammonium concentrations. Overall, this information, together with bivariate correlations, suggests Legionella variation is associated mostly to these variables. In conclusion, the analysis of pathogenic bacteria allows us to report on the presence as well as the quantity of microorganisms potentially harmful to human health and to design strategies for protection in recreational waters used for multiple purposes.

K24 - Patrones de distribución de metabolismos fotoheterotróficos en comunidades microbianas del mar Mediterráneo

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Las comunidades microbianas marinas controlan la biogeoquímica del océano mediante sus procesos metabólicos. La fotoheterotrofía a través de proteorodopsinas es el mecanismo de utilización de luz más abundante en la superficie del océano y permite a las bacterias generar energía celular transformando luz solar en gradientes electroquímicos. Por lo tanto, estudiar cómo la abundancia de ciertos grupos microbianos explica la distribución de proteorodopsinas en el mar puede ayudar a comprender la importancia de la fototrofía bacteriana en distintos ambientes y su impacto en los ciclos biogeoquímicos. A partir de muestras colectadas en diferentes regiones oceanográficas del mar Mediterráneo y océano Atlántico, se analizaron los niveles de proteorodopsina y otras variables fisicoquímicas y biológicas. En particular, el análisis de la estructura de las comunidades microbianas mediante secuenciación del gen ARNr-16S y ARNr-18S nos permitió observar cambios en la disponibilidad de nutrientes y productividad primaria relacionados con el tipo de fototrofía dominante en cada región. Se realizó un análisis de correlaciones que fue visualizado en Cytoscape. Los grupos de bacterias fotoheterotróficas conocidas (e.g., SAR11, Bacteroidetes) se encontraron en distintas proporciones a lo largo del Mediterráneo dependiendo de factores ambientales como la disponibilidad de nutrientes inorgánicos y el nivel de productividad primaria. Por un lado, no se encontraron correlaciones entre los niveles de proteorodopsina y bacterias del grupo SAR11 en ninguna de las regiones estudiadas. Sin embargo, en las regiones más productivas del oeste del Mediterráneo, sí fue posible observar relaciones entre grupos copiotróficos de vida libre (e.g., Bacteroidetes) y los niveles de proteorodopsina en la comunidad. Estos datos preliminares muestran que existe una estrecha relación entre la productividad primaria del sistema y la fotoheterotrofía. Conocer mejor dicha relación permitirá establecer modelos ecológicos para determinar el impacto de la fotoheterotrofía en el mar y su relevancia a escala global.

K25 - Fluorescent dissolved organic matter produced by freshwater phytoplankton axenic cultures

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Dissolved organic matter (DOM) is a heterogeneous mixture of molecules with different weights and reactivity that vary spatio-temporally across aquatic ecosystems, and is key element of biogeochemical cycles. Phytoplankton are the major producers of labile DOM, regulating its quantity and composition. The bioavailable DOM pools are important for the carbon flow through food webs, standing up as an important, but poorly explored fraction within DOM pool. The study of the optical properties of the fluorescent DOM (FDOM) is a rapid and unexpansive method that provides information on DOM origin and reactivity. Here, we characterized the DOM produced by phytoplankton using fluorescence spectrometry and parallel factor analysis (PARAFAC) in 123 samples from 45 different species of freshwater phytoplankton grown in axenic cultures. Despite the increasing use of this method in aquatic ecology, little is known about the FDOM produced by freshwater phytoplankton. We hypothesized that related species would produce similar compounds, and this could be detected by signals in FDOM signatures. We were able to identify three fluorophore components that were cross-validated using the OpenFluor database. The predominant component was characterized as autochthonous protein origin, and the other two components were identified as non-processed terrestrial (allochthonous origin) and processed by microbial activity, respectively. The freshness and humification indexes varied according to the age of the culture, indicating that degradation can occur under the absence of microorganisms or UV radiation, but probably through oxidation. Besides providing a solid database of FDOM produced by freshwater phytoplankton, we show that the FDOM composition is extremely variable among species and within replicated cultures of the same species. Therefore, the FDOM produced by freshwater phytoplankton and detected by optical methods does not seem related to phytoplankton phylogenetic structure.

K26 - Predicción de la abundancia de células tóxicas de colonias de *Microcystis* spp. mediante *remote sensing*

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Las propiedades ópticas de las comunidades de fitoplancton varían de acuerdo a determinados rasgos funcionales de los organismos dominantes, siendo la morfología uno de los más relevantes. Recientemente, hemos demostrado que la morfología de las colonias del complejo Microcystis aeruginosa (CMA) constituye un indicador de la capacidad de producir toxinas. Esta relación morfología-toxicidad puede ser utilizada para generar sistemas de monitoreo remoto basados en fotografías digitales, midiendo la energía lumínica reflejada en las bandas roja (turbidez), verde (clorofila-a) y azul (agua) del espectro. En Uruguay, el CMA es el grupo de cianobacterias que forma floraciones tóxicas superficiales en embalses, ríos y estuarios siendo fundamental desarrollar métodos rápidos de monitoreo para este grupo. Este estudio plantea determinar si la relación existente entre la morfología y la toxicidad del CMA se puede capturar in situ a través de las propiedades ópticas inherentes del cuerpo de agua, empleando las cámaras fotográficas de los teléfonos inteligentes y una aplicación que las analiza para obtener la reflectancia en las bandas del azul, rojo y verde (Hydrocolor). Para ello, se realizaron muestreos en diversos ecosistemas (embalse de Salto Grande, río Uruguay, Río de la Plata, río Negro), donde se obtuvieron valores de reflectancia, muestras de agua para determinar la abundancia de células tóxicas del CMA (qPCR de genes mcy involucrados en la síntesis de microcistinas) y valores de diversas variables abióticas (ej. temperatura, salinidad, viento). La aplicación de distintos modelos estadísticos mostró que el cociente entre las reflectancias del rojo/verde, así como la conductividad del agua explican un 30 y 33% de la varianza observada de la abundancia de CMA en embalses y estuario, respectivamente. Por otro lado, las variables explicativas al modelar todos los sistemas en conjunto fueron la temperatura y el cociente rojo/verde con una varianza explicada de la abundancia de CMA de 45%.

K27 - Relación entre la abundancia del bacterioplancton y la presencia de trucha arco iris, experimentación *in situ*

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Actualmente se conoce la importancia del bacterioplancton en varios ciclos biogeoquímicos, procesos de mineralización y estabilidad de la red trófica acuática, sin embargo, estudios sobre los componentes bióticos que pueden influir sobre estas comunidades aún son deficientes en la ecología microbiana acuática, especialmente en cuerpos de agua tropicales. Por tanto, el presente estudio permitió inferir cómo se comporta la abundancia del bacterioplancton en presencia del pez Oncorhynchus mykiss, en un experimento de mesocosmos in situ en la laguna Cristalina ubicada en el departamento de Boyacá, Colombia. Se establecieron ensayos, con peces y sin peces; de los cuales se tomaron muestras de agua en el tiempo 0 (inicio) y a los 20 días después; las muestras se tomaron por triplicado y fueron procesadas en laboratorio utilizando la técnica de epifluorescencia con el colorante naranja de acridina, para los recuentos de células microbianas. Posteriormente se determinó la abundancia bacteriana para cada caso, las cuales mostraron una disminución con el tiempo, sin embargo, en el ensayo con presencia de peces se observa una mayor reducción de la abundancia en comparación con el control. Como la reducción se presentó en ambos casos, el motivo de esto puede ser ajeno a la presencia o incidencia de O. mykiss, como por ejemplo a factores ambientales. También se analizaron las formas bacterianas más frecuentes entre los ensayos, encontrándose en una mayor y menor proporción células cilíndricas y células circulares respectivamente. Cabe mencionar que aún falta analizar la abundancia bacteriana durante el tiempo del experimento, es decir, durante el transcurso de los 20 días, puesto que en varias investigaciones se ha evidenciado que la presencia de peces puede favorecer el crecimiento bacteriano y de productores primarios, gracias al efecto bottom-up en la red trófica y a la tasa de excreción de nutrientes proveniente de los peces.

K28 - Bacterias epífitas y endófitas aisladas de macroalgas marinas de la especie *Ulva lactuca*

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Las macroalgas marinas son un hábitat propicio para bacterias epífitas y endófitas con diversas capacidades metabólicas. En esta interacción, el intercambio de nutrientes cumple un papel relevante. Debido a la falta de información en cuanto a las bacterias asociadas a macroalgas marinas localizadas en el Caribe colombiano, en este estudio se aislaron bacterias endófitas y epífitas de macroalgas de la especie Ulva lactuca, con el fin de comparar la diversidad de grupos bacterianos que se establecen en la superficie, con aquellos que habitan al interior de la macroalga. Las macroalgas fueron colectadas en la Punta de la Loma (Santa Marta-Colombia) y transportadas en refrigeración hasta el laboratorio de Microbiología Ambiental de la Universidad Jorge Tadeo Lozano. Para el aislamiento de bacterias endófitas se empleó un tratamiento con etanol para remover epífitos, posteriormente las macroalgas tratadas fueron sometidas a un proceso de homogenización, a partir del cual se realizaron los aislamientos. Para la obtención de bacterias epífitas se emplearon metodologías previamente estandarizadas, tales como agitación constante de las macroalgas en solución salina estéril con el fin de desprender las bacterias asociadas a la superficie, además de frotis con hisopos estériles sobre los talos macroalgales. Las muestras fueron incubadas en medio nutritivo con cloruro de sodio ($NaCl$) (1 % p/v) a 28°C. Posteriormente, las diferentes colonias obtenidas fueron reinoculadas hasta lograr asilamientos puros, los cuales fueron caracterizados morfológicamente mediante tinciones Gram. Como resultado se aislaron 85 bacterias, 37 epífitas y 48 endófitas. Adicionalmente, se trabajó la identificación mediante análisis del gen ARNr 16S. Los resultados obtenidos en este estudio, aportan al conocimiento acerca de los grupos que componen la comunidad de bacterias epífitas y endófitas de U. lactuca y brindan información base para el estudio de la interacción entre bacterias y macroalgas marinas.

K29 - Selección de genotipos tóxicos de *Microcystis* en ecosistemas eutróficos: temperatura, turbidez y conductividad como variables más relevantes

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Las especies del género Microcystis son las más frecuentes en formar floraciones tóxicas en sistemas dulceacuícolas de todo el mundo. La diversidad intraespecífica (ej. a nivel de genotipos) de Microcystis sería un factor importante para la adaptación de estos organismos al ambiente local. En estudios previos desarrollamos una metodología basada en qPCR y análisis de melting de alta resolución (HRMA) del gen mcyJ (síntesis de microcistinas) para estudiar la diversidad de genotipos tóxicos de Microcystis en un gradiente subtropical embalse-río-estuario de Uruguay, donde la concentración de nutrientes es siempre suficiente para sostener el desarrollo de cianobacterias. Se determinó en dicho gradiente que la temperatura, conductividad y turbidez son las variables que seleccionan a diferentes genotipos tóxicos de Microcystis, existiendo genotipos adaptados a distintas combinaciones y exhibiendo distinto perfil de microcistinas (por ej. genotipos que proliferan a baja temperatura y alta conductividad). Con el objetivo de evualuar si la influencia de dichas variables en la selección es un mecanismo general en sistemas eutróficos, se aplicó la misma metodología en un sistema embalse-río tropical (Colombia). Se emplearon muestras tomadas de tres sitios del embalse Porce II, el cual presenta floraciones de Microcystis. Se obtuvieron las curvas de melting para cada muestra y a partir de ellas se extrajeron los coeficientes (variable de respuesta) que luego fueron analizados mediante árboles de clasificación y regresión (CART) para evaluar qué variables ambientales (variables explicativas) segregan a las diferentes poblaciones. El análisis de CART mostró a la temperatura, turbidez y conductividad como las variables más relevantes en explicar la presencia de los distintos genotipos tóxicos. Estos resultados confirman los hallazgos previos y sugieren que una vez establecidas las condiciones eutróficas en un sistema acuático, la combinación de actividad metabólica (temperatura), disponibilidad de luz (turbidez) y presión osmótica (conductividad) es la principal fuerza selectiva de poblaciones tóxicas.

K30 - Long-term composition of 16S-based bacterial communities associated with algal bloom events in northern Chile

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Introduction: There is an increasing interest in harmful algal blooms (HAB) affecting seawater desalination plants. These plants are located in northern Chile to supply drinking and municipal water. Localized HAB can affect the plant operation leading to temporary shutdown and they are related to changes in the HAB holobiome diversity. Objective: To understand changes in microbial diversity in a HAB Bloom in a coastal scenario. Methodology: we use high-throughput DNA sequence analyses to study the diversity of alga-associated bacteria (attached and free living) focused on an event of Akashiwa sanguinea bloom in December 2019 on the coast of Antofagasta, Chile, where desalination plants are located. We considered weekly data from Nov. 2019 to Jan. 2020 in two locations. We computed alpha and beta diversity indices for previous HAB event (PRE) and during the event (HAB), including Principal Coordinate Analysis (PCoA), and Venn Diagram. Results: we found that attached Cyanobacteria relative abundance changes during the HAB bloom and Epsilonproteobacteria increases in abundance. Free bacteria have minor changes in relative abundance with an increase in Epsilonproteobacteria. Conclusions: based on our analysis, we detected higher changes in the relative abundances of attached bacteria during PRE and HAB, compared with free-living bacteria. We also found bacterial taxa which are shared during long term in analyzed samples. Higher studies are required to understand the changes and influence of holobiome in the development of HAB in northern Chile and their impact on seawater desalination plants.

K31 - Microbial communities network structure across strong environmental gradients: How do they compare to macroorganisms?

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The way strong environmental gradients shape multispecific assemblages has allowed us to examine a suite of ecological and evolutionary hypotheses about structure, regulation, and community responses to fluctuating environments. But whether the highly diverse co-occurring, free-living microorganisms are shaped in similar ways as macroscopic organisms, across the same gradients, has yet to be addressed in most ecosystems. The ‘everything is everywhere’ hypothesis suggests they are not, at least not to the same extent. Here we characterize the structure of intertidal microbial biofilm communities and compare the intensity of zonation at the ‘species’ level, changes in taxonomic diversity and composition at the community level, and network attributes, with those observed in co-occurring macroalgae and invertebrates. At the level of species and OTUs, for dominant macro and microorganisms, respectively, microbes showed less variability across the tidal gradient than macroorganisms. At the community-level, however, microbes and macro-organisms showed similarly strong patterns of tidal zonation, the proportion of ‘environmental specialists’ in different tidal zones was remarkably similar, taxonomic richness and diversity followed similar trends, and network analyses showed similar connectivity and transitivity. A high proportion of positive co-occurrences within all tidal zones were observed among habitat specialist taxa of micro-and macro-organisms. Thus, our results partially support the idea that microbes are less affected by environmental variability than macroscopic counterparts. At the species-level, the most common microbe species exhibit less variation across tides than most common macroscopic organisms, suggesting the former perceive a more homogeneous environment and/or are more resistant to the associated stress. At the community-level, most indicators of community and network structure across the gradient are similar between microbes and macro-organisms, suggesting that despite orders of magnitude differences in richness and size, these two systems respond to stress gradients, giving rise to zonation patterns.

K32 - Floraciones de *Microcystis* spp. en el Río de la Plata: temperatura como determinante del tamaño y la toxicidad

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Las floraciones de cianobacterias tóxicas, producto de la eutrofización antrópica y la modificación hidrológica, son un problema ambiental y de salud pública en ecosistemas de todo el mundo. En particular, en la Cuenca del Plata se desarrollan floraciones de cianobacterias coloniales del género Microcystis, cuyas especies son capaces de producir microcistinas, un metabolito tóxico para humanos y animales. En trabajos previos propusimos que la toxicidad de Microcystis spp. (producción de microcistina) está relacionada a la morfología de las colonias (tamaño) y refleja la etapa más activa de crecimiento de la comunidad. Por tanto, conocer qué condiciones ambientales favorecen la proliferación de los tamaños de colonia más tóxicos en cada ecosistema resulta relevante para la predicción del riesgo. Con el objetivo de dilucidar eso, en este trabajo se evaluó la relación entre la morfología (tamaño de las colonias), la proporción de células tóxicas y las condiciones ambientales (temperatura, turbidez, conductividad). Para ello, se tomaron muestras de agua en zonas del Río de la Plata donde frecuentemente se desarrollan floraciones de Microcystis y se tamizaron por tamaño (fracciones: <20µm, 20-60µm, 60-150µm y >150µm), cuantificándose por qPCR el número de copias del gen mcyJ en las distintas fracciones. En todas las muestras evaluadas se detectó el gen mcyJ, indicando que todas las comunidades de Microcystis analizadas eran potencialmente tóxicas. Asimismo, se observó una correlación positiva entre la abundancia total de células tóxicas y la temperatura del agua, por encima de 26,5°C la abundancia se mantuvo constante. En todos los casos, las fracciones coloniales >150µm y <20µm tuvieron un número significativamente mayor de células tóxicas. Sin embargo, solo las <20µm presentaron un comportamiento similar al de la comunidad total en relación a la temperatura, sugiriendo que era la fracción dominante y probablemente más activa de la comunidad durante la floración.

K33 - Rol ecológico de la formación de biopelículas por el patógeno de salmónidos *Piscirickettsia salmonis*

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Piscirickettsia salmonis es un patógeno primario intracelular causante de la piscirickettsiosis, una enfermedad de alto impacto sobre el cultivo de salmónidos en Chile. Una estrategia para su supervivencia en ambientes marinos podría ser la formación de biopelículas como reservorios ambientales. El objetivo de este trabajo fue realizar una caracterización profunda de la formación in vitro de biopelículas por 2 aislados representativos de P. salmonis mediante técnicas microscópicas, a fin de clarificar su papel ecológico en la persistencia ambiental. Primeramente, se evalúo in vitro la respuesta citotóxica de la línea de salmón SHK-1 a la bacteria, observando diferencias entre las cepas de P. salmonis examinadas, aunque no necesariamente entre estado de crecimiento (biopelícula vs. planctónico). La formación de la biopelícula mostró una fase retardada de longitud variable y asociada a importantes fluctuaciones en la viabilidad celular. Todos los aislados formaron biopelículas maduras a partir de las 288 h de incubación. Estudios in vitro mostraron que algunas biopelículas de P. salmonis fueron susceptibles a la acción antibacteriana del moco de la piel de ejemplares de salmón del Atlántico durante su formación temprana, mientras otras fueron más tolerantes. No hubo asociación entre la capacidad de P. salmonis para formar biopelículas y la producción endógena de N-acil homoserina lactonas. La formación de biopelículas en agua de mar viables y tolerantes al moco de piel indican buena capacidad de persistencia y diseminación de P. salmonis. Futuros estudios de campo ayudarán a validar este resultado.

K34 - Descifrando las relaciones intra- e interdominio en biopelículas costeras

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Las biopelículas en el ambiente marino están conformadas por una gran cantidad de especies, pertenecientes a todos los linajes actuales de organismos (i.e. Eucariontes, Bacterias, Archeas, Virus). Las biopelículas se considera un estilo de vida muy exitoso que, al promover las interacciones entre los microorganismos, permite que surjan una serie de ventajas. Estas comunidades se pueden formar sobre todo tipo de superficies, incluyendo infraestructuras antropogénicas. De este modo, algunas biopelículas pueden influenciar sobre la corrosión de superficies metálicas, pudiendo aumentar en grandes cantidades los costos de mantención. Sin embargo, hasta muy recientemente ha sido estudiado de forma exclusiva el componente bacteriano de esta comunidad, obviando el eucariota. El carácter complejo del sistema implica que para una mejor compresión del fenómeno se requiere el estudio de todos los componentes en conjunto. En este trabajo se realiza el análisis de los resultados de secuenciación masiva de biopelículas marinas formadas sobre placas de acero inoxidable durante los primeros 30 días de colonización con un alto número de réplicas. El estudio se centra en la evolución de las interacciones entre distintas especies durante la sucesión primaria, y en como los componentes Eukarya y Bacteria/Archaea aportan al ensamblaje de la comunidad mediante teoría de redes. Los resultados mostraron una mayor cantidad de especies e interacciones Bacteria/Archaea a lo largo de todo el análisis. Por otro lado, el componente Eukarya determinó la estructura modular de la comunidad, especialmente en los tiempos iniciales, lo cual sugiere que asumen un rol importante y hasta el momento poco estudiado. La estructura modular se maximizó en el tiempo final mostrando la formación de múltiples clústers que podrían corresponder a los característicos gremios tróficos de las biopelículas. Finalmente, los componentes Eukarya y Bacteria/Archaea inicialmente mostraron un bajo número de interacciones interdominio que aumentaron con el tiempo. Este estudio por lo tanto muestra la importancia del dominio Eukarya y de las interacciones interdominio en biopelículas marinas asentadas sobre acero inoxidable.

K35 - Cyanobacteria mediated nitrogen transformations in tropical soda lakes

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Nitrogen is an essential element for life with direct impact on local and global food webs and its distribution depends on ecosystem stability. The ecology of the nitrogen cycle in soda lakes remains underexplored. Applying molecular techniques (metagenomics and genomics) associated with isotopic and chemistry analysis we evaluated the nitrogen cycle steps performed by microorganisms in Brazilian soda lakes. Three different types of lakes previous classified according to chemistry patterns as eutrophic turbid (ET), oligotrophic turbid (OT) and clear vegetated oligotrophic (CVO) were analyzed. In the ET lake, high levels of nitrogen in water was found (TN, NH4+ and organic nitrogen) concomitant with a high abundance of members of Nostocales order (Cyanobacteria). Furthermore, the flux balance analysis demonstrated significant positive values of L-glutamate, urea and nitrite when compared to other two lakes. These data were corroborated by a strong presence of biological nitrogen fixation (BNF) observed by the isotopic analysis (15N = 0.54 ‰) and positive N2O flux (0.41 mg m2 dia-1). The isotopic signature of BNF was marked by abundant heterocyst-forming cyanobacterium (Anabaenopsis elenkinii), which reinforces the importance of these organisms for nutritional dynamics in ET lakes. Otherwise, OT and CVO lakes showed low abundance of Cyanobacteria (bellow < 2%) and prevalence of nitrogen in sediment (NH4+, NO2-, NO3- e TN) instead of diluted in the water. Moreover, in OT and CVO lakes the sediment showed to act as a nitrogen and carbon source. These results reinforce the uniqueness of metabolic pathways on Brazilian soda lakes and highlight the enhancement of nitrogen input mediated by Cyanobacteria phylum.

K36 - Prokaryotic microbiota and biomineral microstructure in coralline algae reveal new ecological and conservation frontiers

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Marine coralline algae are worldwide carbonate builders and important components of marine systems considered to be founder species and biodiversity hotspots. Coralline algae habitats currently face major threats related to warmer temperature, increasing atmospheric CO2 and to the degradation of their natural habitat. Similarly to corals, the vulnerability of coralline algae seems related to their still understudied, symbiotic relationships with microbes. Further, the interplay of the algal microbiota with the mineral bioconstructions, as well as their ecological properties remain poorly understood. Neogoniolithon trichotomum is one of the main species of coralline algae in tidal pools of the Gulf of California, Mexico. In this study, we performed a multi-disciplinary assessment of these coralline Rhodophyta using XRD, SEM microscopy, synchrotron infrared imaging and metabarcoding to survey their prokaryotic microbiota in summer and winter. The results show a specific microbiota for N. trichotomum whose seasonal dynamics is correlated to temperature and nutrient availability (particularly to nitrate and silicate). Both, the discovery of abundant halophilic bacteria in the summer microbiota and the presence of dissolution-resistant minerals: high-magnesium (18-19 mol % Mg) calcite and dolomitic minerals make coralline algae interesting models to study marine systems resilience in an increasing CO2 world.

K37 - Impacto de la contaminación sobre la actividad proteolítica en las aguas de los ríos Almendares y San Juan

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Las reacciones enzimáticas de las comunidades microbianas son rápidas y adecuadas a los cambios de la composición de la materia orgánica y los factores ambientales, por tanto, pueden ser utilizadas como descriptores de las respuestas biológicas en los sistemas dulceacuícolas. El objetivo de este trabajo fue evaluar la calidad de agua de los ríos Almendares y San Juan y determinar la actividad enzimática proteolítica en las aguas de estos ecosistemas. Se realizaron muestreos durante los meses de Febrero, Abril, y Junio de los años 2016 y 2017, y se determinaron las variables temperatura, pH, concentraciones de nutrientes inorgánicos, Demanda Química de Oxígeno, oxígeno disuelto, sólidos totales disueltos, concentraciones de Escherichia coli y enterococos. Se calculó el índice de calidad de agua a partir de los indicadores físico-químicos y microbiológicos y se determinó la actividad proteolítica. El río Almendares presentó altos valores de contaminación química ([NH4+-N] = 17, 62 mg.L-1, [PO43—P] = 25,64 mg.L-1) y microbiológica ([E. coli] = 1 x106 UFC.100 mL-1), por lo tanto, índices de calidad de las aguas entre muy pobre e inutilizables para el consumo, lo que imposibilita su uso para la recreación. En cambio, el río San Juan presentó bajos valores de contaminantes ([NH4+-N] = 0,22 mg.L-1, [PO43—P] = 0,014 mg.L-1, [E. coli] = 2 x101 UFC.100 mL-1), por lo que la calidad de sus aguas se clasifica entre excelente y buena. Las mayores actividades proteolíticas se detectaron en el río San Juan respecto al río Almendares. Además, se obtuvieron las mayores actividades proteolíticas en el año 2016 respecto al 2017 en ambos ríos. La actividad enzimática proteolítica disminuye en ecosistemas contaminados en comparación con ecosistemas menos impactados y muestra una variación anual.

K38 - Detección de genes de nitrito y óxido nitroso reductasa en bacterias desnitrificantes del humedal Santa María del Lago

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La desnitrificación es la reducción secuencial de nitrato (NO_3^-) a gas dinitrógeno (N_2). Este proceso remueve más de la mitad del nitrógeno inorgánico fijado en cuerpos de agua, mediado por procesos microbianos. Dichos procesos, son catalizados por sistemas enzimáticos que son codificados por genes funcionales específicos. En este trabajo se realizó la detección de genes que codifican para reductasa de óxido nitroso (nosZ) y reductasa de nitrito (nirS), relacionados con la reducción de productos tóxicos como el óxido nitroso y nitrito respectivamente. Dicha identificación fue realizada en bacterias desnitrificantes aisladas previamente del humedal Santa María del Lago usando amplificación por PCR de ambos genes funcionales. Esta investigación, demostró, la presencia de genes nosZ y nirS en los 27 morfotipos desnitrificantes. Se observó una dominancia del gen nirS con presencia en 37% de los aislamientos, congruente a lo reportado en otros ecosistemas eutróficos. En comparación, nosZ sólo se observó en el 32%, sugiriendo que en el humedal se está dando un proceso de desnitrificación parcial o incompleta, que conlleva a una posible emisión de óxido nitroso el cual es un gas tóxico de efecto invernadero. Solo tres aislamientos presentaron ambos genes estableciendo una desnitrificación completa en el humedal. Además, los resultados demostraron que la presencia de estos genes se guía por factores ambientales en los sedimentos del humedal como lo son MOT, COT, altas concentraciones de NO_3 y pH (6.4-6.8) entre los más importantes. La investigación, representa una base para estudios ecológicos sobre las comunidades desnitrificantes en sedimentos del humedal encargadas de regular los niveles de nitratos, nitritos y de óxido nitroso en este ecosistema acuático urbano de Bogotá. Actualmente, se trabaja en la evaluación de la presencia de genes involucrados en la desnitrificación y su relación con la reducción de óxido nitroso en aislados bacterianos de sedimentos del humedal Santa María del Lago.

K40 - Identification of secretion systems in bacterial strains isolated from Antarctic sponges

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Antarctic sponges host a bacterial symbiont community highly complex in diversity and function. Secretion Systems are commonly associated with virulence and pathogenesis. However, they play a main role in the establishment of mutualistic lifestyles too. Although little is known about the genetic organization of Secretion Systems in sponge holobionts, evidence shows that Secretion Systems type 3, 4 and 6 are complete in bacterial symbionts isolated from sponges. The hypothesis of this work is that bacterial members of Antarctic sponge microbiomes present a diverse functional repertoire associated with Secretion Systems. To test this hypothesis, we identify Secretion Systems in bacterial genomes from Antarctic sponges and determine their genetic organization and genomic architecture. Using MacSyFinder, we explored 9 different bacterial strains isolated from the Antarctic sponges Dendrilla antartica and Iophon sp. and found bioinformatic evidence of the presence of Secretion Systems type 1, 2, 4, 6 and 9 in a complete state. Genome analysis shows clusterization of some of these secretion systems, providing partial evidence of function, as all known complete operons from Secretion Systems are active. Exploring the diversity and function of Secretion Systems is crucial to understand the mechanisms that allow a symbiotic life between bacteria and their sponge host.

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K41 - Assessment of oil degrading multi-domain microbial consortium immobilized in calcium alginate applied in adaptable mesocosms

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Lately coral reefs have been affected by several anthropogenic factors. Oil contamination can be highlighted as one of the main factors considered toxic and persistent pollutants in the environment. Thus, a series of works have pointed to bioremediation as an effective tool for decontamination of impacted environments. One of the strategies that seek to increase the effectiveness of this technique is microbial immobilization. It involves the attachment of microorganisms in support, enabling greater stability and better handling of the microorganisms at the contaminated site. To assess the efficiency of the biodegradation by a multi-domain consortium (composed of six bacterial and three fungal strains) immobilized in calcium alginate, an experiment occurred in adaptable mesocosm with the fire coral Millepora alcicornis. The consortium members were isolated from two species of Brazilian endemic corals and the seawater surrounding the corals. To test this inoculant, a factorial experiment was carried out, using oil, alginate, and intercropping combined in eight different treatments. We accessed the profile of the microbial community associated with the M. alcicornis through the sequencing of the 16S region of the bacterial ribosomal RNA. The bioinformatics analyzes were performed using the Mothur software, utilizing the Greengenes database. -diversity results demonstrated that the factors oil and alginate promoted the variation of microbial communities of the M. alcicornis throughout the experiment. The relative abundance of the M. alcicornis associated OTUs demonstrated at the phylum level, Proteobacteria was dominant in all treatments; Bacteroidetes showed greater abundance in treatments without oil, while Firmicutes showed dominance in treatments with oil. The results generated in this work allowed a better understanding of how calcium alginate can be used as a microbial support in oil spills bioremediation processes.

K42 - *De novo* transcriptome comparison of *Minidiscus* spp. from the English Channel and Antarctica coastal waters

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Minidiscus spp. are the smallest known centric diatoms of the phytoplankton and comprise 11 species. Members of this group have been poorly described due to their tiny size and the lack of unique pigments, making it difficult to study using classic approaches such as flow cytometry, or pigment-based methods. With the use of 'omic' methods, it has been described that they are globally distributed and are among the 20 most abundant genera in the global oceans. Nevertheless, there are still many questions associated with their functionalities that allow its great success globally. Here, we present transcriptomes from species belonging to the genera Minidiscus isolated from the English Channel (Minidiscus spinulatus, Minidiscus variabilis and Minidiscus comicus) and the Western Antarctic Peninsula (Minidiscus sp. RCC4582, RCC4584 and RCC4590). These results include the first transcriptomes for species of the genus Minidiscus. The transcriptomes were carried out in Illumina HiSeq generating ~25 M of high quality reads for each strain, which were assembled using Trinity. An average of 57,500 contigs were obtained, indicating an adequate sequencing depth for the complexity of these organisms. The evaluation of the integrity was carried out by comparison to single-copy orthologs through BUSCO. Results indicate high completeness of the transcriptomes, with between 16 and 19% of the total BUSCO genes missing. Comparative analysis revealed a clear clusterization according to the environment from which the strains belong. Differential expression analyses of strains from these two contrasting environments show the flexibility of Minidiscus, revealing differentiation in the mechanism to cope with low temperatures.

K43 - Diversity and distribution of ammonia-oxidizing archaea in Santos Basin

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Microorganisms play a central role in the marine biogeochemical cycles. The ammonia-oxidizing archaea, a chemolithoautotrophic group comprising several taxa from the class Nitrososphaeria, can carry out the first step of nitrification while fixing inorganic carbon, thus a key player in the nitrogen and carbon cycles. Most Nitrososphaeria species are uncultivated, and only few have been isolated. Recent studies have indicated the importance of these organisms to the marine environment, but our knowledge is still very limited, and scarce information is available for the South Atlantic Ocean. Here we studied ammonia-oxidizing archaea in the Santos Basin (South West Atlantic) using molecular and culturing approaches. To evaluate the diversity and distribution of this group a compositional dataset of the V4 region of the 16S rRNA was used. The dataset corresponds to DNA was extracted from 94 sediment and 175 water samples from neritic and oceanic zones of the basin. In addition, enrichment cultures were performed with water samples collected from an estuarine area. In the 16S rRNA gene sequencing, the Class Nitrososphaeria accounted for up to 60 and 20% of the communities in water and sediment samples, respectively. In water samples, Candidatus Nitrosopelagicus was the most common assigned genus. However, in samples from the deep sea, unclassified genera prevailed. In the marine sediment, the genus Candidatus Nitrosopumilus was dominant in both coastal and oceanic samples. In the enrichment cultures, the ammonia-oxidizing archaea and bacteria from the families Nitrosopumilaceae and Nitrosomonadaceae, respectively, were obtained. However, Nitrosopumilaceae was predominant, representing 63% of the community. Nitrite-oxidizing bacteria from the genus Nitrospira was also in the culture, accounting for 2% of the community. The results are the first step in the characterization of this key group in the Santos Basin.

K45 - Diversidad microbiana aislada de sedimentos y esponjas presentes en cenotes de la península de Yucatán con potencial biotecnológico

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Introducción: los cenotes son ambientes de formación kárstica, lo cual los dota de características distintivas poco frecuentes en el planeta y permiten la presencia de bacterias que podrían ser distintas a las comúnmente reportadas en otros sedimentos de cuerpos acuosos. Esta diversidad puede convertirse en una fuente novedosa de productos naturales de interés biotecnológico. Hasta la fecha solo hay un trabajo reportado sobre comunidades microbianas cultivables provenientes de cenotes y sus actividades antimicrobianas, lo cual nos muestra la importancia de realizar estudios más profundos en este tipo de ambientes. Una caracterísitica importante de algunos cenotes presentes en zonas costeras, es la intrusión salina debido a la cercanía con el mar. Dentro de este ambiente hemos encontrado esponjas que igualmente pueden albergar una gran diversidad de microorganismos con potencial biotecnológico. Objetivo: Buscar metabolitos secundarios de interés biotecnológico a partir de bacterias cultivables presentes en sedimentos y esponjas procedentes de cenotes de la península de Yucatán. Métodos: Caracterización fenotípica: Siembra en medios selectivos en placa. Descripción de morfología colonial y microscópica. Caracterización genotípica: Extracción de DNA con kit comercial, cuantificación de DNA y electroforesis. Amplificación (PCR) y secuenciación (Sanger) de genes 16S rRNA. Resultados y discusión: La mayoría de las bacterias cultivadas de ambos ambientes pertenecen al grupo Gram positivas (62.5% sedimentos; 61.3% esponjas). Las colonias seleccionadas presentaban alguna característica fenotípica como pigmentación o actividad inhibitoria contra bacterias de la misma muestra observada por la presencia de halos de clarificación alrededor de las colonias. Se presentarán los resultados de la identificación taxonómica de bacterias cultivadas utilizando las secuencias del gen 16S rRNA amplificadas por PCR. Conclusiones: Las diferentes bacterias cultivables presentes en sedimentos de cenotes y esponjas tienen interacciones con el resto de la comunidad microbiana presente en estos ambientes y pueden convertirse en una fuente importante de productos naturales.

K46 - Microplastics associated to bacterial communities from surface seawater of the Northern Chilean Patagonia

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The accumulation of microplastics in the world's ocean and coastlines is an important environmental pollution problem. In this study, we determined the plastisphere using metagenomic data of microplastics collected at Detif and Lelbun, Chiloé, Los Lagos Region and Chaihuin, Los ríos Region, from Northern Chilean Patagonia. To analyze microplastics we used Fourier-transform infrared spectroscopy (FT-IR). Later, these microplastics particles were analyzed with scanning electron microscopy (SEM) and next-generation sequencing to characterize the microplastics attached to microbial communities. The structure and composition of plastisphere communities varied among the locations. Microbial communities' diversity of microplastics was higher than those present in seawater. Sequencing analysis revealed that plastisphere microbial communities on polystyrene microplastics have the most abundance of Proteobacteria and Bacteroidetes phylum. In general, microbial communities showed different abundance patterns in the microplastics. Our results showed the diverse and heterogeneous microbial assemblages that occur on microplastics helping to know the plastisphere ecology.

K47 - Relación del ensamblaje fitoperifitico con tres sustratos naturales en un tramo del Río Dulce – Sasaima, Cundinamarca

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Las perturbaciones como la heterogeneidad espacial y temporal presentes a lo largo de los ríos definen la distribución y la estructura de las comunidades como el fitoperifiton que se desarrollan adheridas a un sustrato sumergido. De igual forma, la colonización de las especies de algas depende del tipo de sustrato disponible que proporcione la superficie y las condiciones adecuadas para su desarrollo y supervivencia. El objetivo de este trabajo fue determinar la relación entre los diferentes sustratos naturales y los ensamblajes de la comunidad de fitoperifiton en un tramo del Río Dulce – Sasaima, Cundinamarca, donde se realizaron dos muestreos durante octubre y febrero en un tramo de 50 metros tomando muestras de agua para análisis de fisicoquímicos y muestras de algas en tres sustratos diferentes (roca, madera, hojarasca) a partir de las que se determinó la composición y la diversidad (Shannon). Se registraron 42 morfotipos de algas distribuidas en 20 géneros de 19 familias, siendo la hojarasca el sustrato con mayor riqueza con un total de 33 morfotipos, seguido por madera con 30 y por ultimo rocas como el de menor riqueza con 26 morfotipos. En cuanto, a la diversidad aunque los valores se mantuvieron en el rango normal para los tres sustratos, se observó una disminución en febrero con respecto a octubre debido al efecto del aumento del caudal generando desprendimiento y desplazamiento de organismos y cambios en las concentraciones de nutrientes que llevan a la pérdida de especies; además, se evidenciaron diferencias en la diversidad en los sustratos, presentando la hojarasca los valores más altos, H = 3,07 durante octubre y H = 2,96 en febrero, mientras las rocas mostraron valores más bajos durante ambos meses, dado que las especies se desarrollan mejor en sustratos que les proporcionen mayor estabilidad ante la acción de la corriente.

K48 - Protists sorting optimization from a wide salinity range polyextreme aquatic system, Salar de Huasco (Atacama Desert), suitable for genome sequencing

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Protists are unicellular eukaryotic organisms with a wide size, taxonomic and functional diversity. These microorganisms are key and have important implications in primary production, assimilation, reincorporation of dissolved organic matter and the recycling of nutrients in the trophic chain. In this wide protist diversity are heterotrophs, which play an important ecological role as bacterial grazers and nutrient remineralizers in aquatic ecosystems; autotrophs, which are the main carbon fixers in these aquatic systems; and mixotrophs. However, protists have been understudied, especially in high-altitude aquatic saline systems. Therefore, for a better understanding of their microbial and functional diversity, particularly in polyextreme environments, we are optimizing a cell sorting method from frozen samples coming from Salar de Huasco located in the Chilean Altiplano. Samples of different salinities were sorting using a BD FACSJazz cytometer. Sea water samples from the coast of Antofagasta have been used to optimize the technique. Microbial communities have been selected depending on their size and fluorescence (Pigment fluorescence and SybrGreen) trying different preservation methods: direct samples without any fixative and flash frozen in liquid nitrogen samples previously fixed with glutaraldehyde, GlyTE (glycerol-TE) or DMSO. We use glutaraldehyde as a control, since it is favourable both to separate well-defined frozen communities with the flow cytometer, as well as for confocal microscope visualization, however, less optimal for high throughput sequencing than DMSO or GlyTE. Using DMSO we have obtained differentiated communities with the flow cytometer, but cell degradation observed with the confocal microscope, very evident in autotrophs. In contrast, using GlyTE we have less defined communities, however better performance in the confocal microscope. The optimization of this method is especially useful to study protists communities coming from frozen samples, with particular physical-chemical conditions such high salinity concentrations (□50psu), suitable of being processed for genome sequencing and visualized with a confocal microscopy.

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K50 - A ^{31}P-NMR-based method for the detection of phosphonate compounds in aquatic samples

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Phosphonates are interesting molecules since they contain a chemically stable carbon-phosphorous (C-P) bond. Phosphonates are widely distributed amongst the most primitive lifeforms such as bacteria, constituting a significant component of the total dissolved organic phosphorous reservoir. Thus, phosphonates play an important role in global biogeochemical P cycling and in the extend connections to carbon and nitrogen dynamics in aquatic ecosystems. The knowledge regarding the enzymology of C-P bond generation in bacteria is still limited, especially in bacteria inhabiting scarcely explored niches such as sinkholes. In line with this, our aim is to employ genome mining tools to discover the presence of phosphonate synthetic genes in isolated actinomycetes strains obtained from sinkholes located in the Yucatan's peninsula. Therefore, in order to further verify the functionality of the encoded information we need to establish precise and suitable analytic approaches for the analysis of the synthetized phosphonates. Spectroscopic methods such as 31P-NMR provide a powerful spectroscopic tool to undoubtedly detect phosphor-containing compounds. Moreover, as 31P is highly abundant in nature, an external supplementation source of the NMR active isotope is not required, highlighting the advantages of using this approach. Herein, we report a suitable 31P-NMR-based method customized for the direct detection of molecules harboring a phosphonate (C-P bond).

K51 - Evaluación de la actividad lacasa en bacterias epifitas de macroalgas de la especie *Ulva lactuca* localizadas en Santa Marta (Caribe Colombiano)

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Los compuestos fenólicos son frecuentes como residuos en la industria textil, de papel y curtiembres. Esto genera serios problemas ambientales al ser contaminantes recalcitrantes. Su biodegradación enzimática mediada por lacasas surge como una alternativa ecológica y eficiente, en comparación con tratamientos fisicoquímicos convencionales. Las enzimas de origen marino presentan características de interés en diversos procesos biotecnológicos, debido a que muchas son activas a pH alcalino y condiciones de salinidad y temperatura variables. En este sentido las macroalgas marinas están siendo reconocidas como reservorios de enzimas y compuestos bioactivos, debido a que sus superficies son susceptibles a la colonización de microorganismos benéficos, en una interacción en la cual, los microrganismos aprovechan los nutrientes producidos por los exudados macroalgales, mientras que, intervienen en procesos morfofisiológicos y de defensa de la macroalga. En este estudio se realizó el tamizaje funcional de la actividad lacasa, en bacterias aisladas de la superficie de macroalgas de la especie U. lactuca, colectadas en La punta de la loma, Santa Marta (Caribe-Colombiano). Dentro de los aislamientos obtenidos, uno, identificado como Achromobacter denitrificans exhibió actividad lacasa frente a tres sustratos fenólicos en placa: guayacol, acido tánico y 2,6-dimetoxifenol. La confirmación de la presencia de la enzima se verificó mediante la secuenciación del genoma completo con la plataforma Ilumina. Con las secuencias obtenidas se realizó un análisis de calidad, seguido de los procesos de ensamblaje y anotación, haciendo uso de diferentes programas bioinformáticos. Los resultados indican la presencia de genes codificantes para lacasas en el genoma de A. denitrificans, demostrando el potencial de bacterias epifitas de U. lactuca en la producción de enzimas, las cuales podrían presentar propiedades funcionales de interés en procesos como la biodegradación de compuestos fenólicos bajo condiciones más versátiles y eficientes, en comparación con las lacasas convencionales producidas por hongos terrestres.

K53 - Presencia de rodopsinas en bacterias cultivables: características genómicas, patrones taxonómicos y distribuciones ambientales

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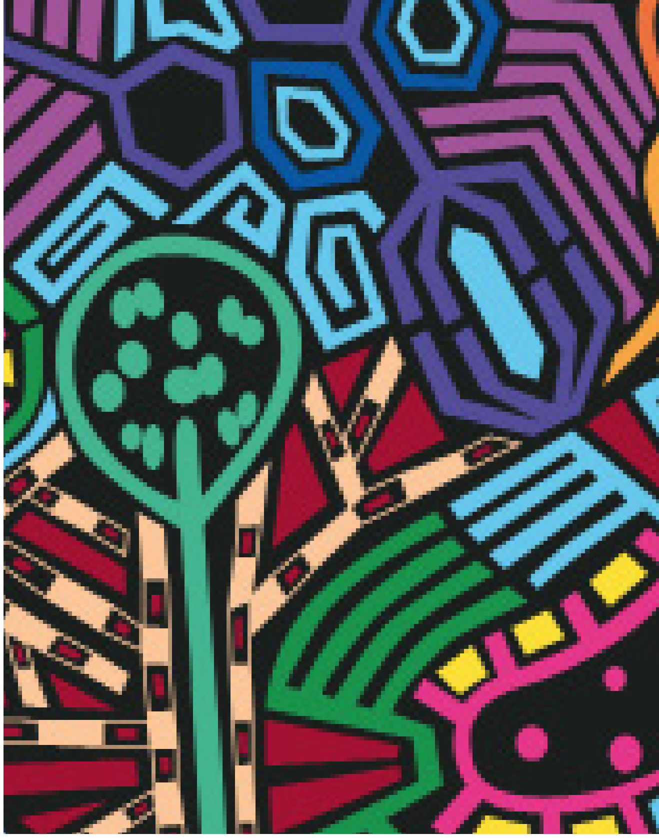
Las rodopsinas son fotosistemas muy abundantes en distintos ambientes acuáticos con el potencial de capturar gran cantidad de energía solar en la superficie del agua. Más del 75% de los genomas del bacterioplancton contiene genes para sintetizar rodopsinas, convirtiéndose en el fotosistema más abundante en el mar. Sin embargo, se conoce poco sobre las diferentes estrategias metabólicas y fisiológicas de los distintos organismos con rodopsinas, por lo que su impacto ecológico en los distintos ambientes no es claro. Para ampliar la diversidad conocida de cepas con rodopsinas que pueden ser analizadas y caracterizadas fisiológicamente en el laboratorio, en este trabajo se detectó la presencia de genes de rodopsina en genomas de bacterias cultivadas aisladas de ambientes acuáticos, depositados en la base de datos del Sistema Integrado de Genomas Microbianos (IMG). De los 3056 genomas bacterianos estudiados, 235 (7.69%) contienen la función de rodopsina. Los phyla Proteobacteria, Bacteroidetes y Actinobacteria se identificaron como los de mayor incidencia en cuanto a la presencia de dichos genes, las proteorodopsinas fueron el tipo de rodopsina más abundante y se han aislado en su mayoría de ambientes marinos. Así mismo, los genomas con genes de rodopsina son significativamente más pequeños que los genomas que no cuentan con dicha función. Esta observación es consistente con estrategias de vida de bajo costo energético, donde los organismos conservan únicamente aquellos genes que contribuyen a las funciones necesarias para sobrevivir y para los cuales la fototrofía a través de rodopsinas podría jugar un papel fundamental (e.g., bacterias del grupo SAR11). En conjunto, este trabajo amplía significativamente nuestro conocimiento de bacterias de distintos grupos taxonómicos y ambientes acuáticos que podrán ser caracterizados fisiológicamente en estudios futuros, además de establecer tendencias genómicas, taxonómicas y ambientales de dichos genomas.

POSTER SESSIONS



L

HUMAN MICROBIOME AND HEALTH

L1 - Dysbiosis and structural disruption of the respiratory microbiota in COVID-19 patients with severe and fatal outcomes

Alejandra Hernández-Terán[1*], Fidencio Mejía-Nepomuceno[1], María Teresa Herrera[2], Omar Barreto[3], Emma García[3], Manuel Castillejos[4], Celia Boukadida[5], Margarita Matias-Florentino[5], Alma Rincón-Rubio[5] Santiago Avila-Rios[5], Mario Mújica-Sánchez[6], Ricardo Serna-Muñoz[1], Eduardo Becerril-Vargas[6], Cristobal Guadarrama-Pérez[7], Víctor Hugo Ahumada-Topete[4], Sebastián Rodríguez[1], José Arturo Martínez-Orozco[6], Jorge Salas-Hernández[8], Rogelio Pérez-Padilla[1], Joel Armando Vázquez-Pérez[1*].

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COVID-19 outbreak has caused over 3 million deaths worldwide. Understanding disease pathology and the factors that drive severe and fatal clinical outcomes is of special relevance.

Studying the role of the respiratory microbiota in COVID-19 is particularly important since it´s known that the respiratory microbiota interacts with the host immune system, contributing to clinical outcomes in respiratory diseases. As part of a surveillance program at the Instituto Nacional de Enfermedades Respiratorias Ismael Cosío Villegas (INER), we collected respiratory samples and its demographic, health-related, and clinical data. By using 16S rRNA sequencing we characterized the respiratory microbiota of patients with mild, severe, or fatal COVID-19, and compared with healthy controls and patients with non-COVID-19-pneumonia. Overall, 58.2% of the patients presented at least one comorbidity and 78.9% received antibiotic treatment before hospitalization. Regarding the characterization of the microbiota, we found low microbial diversity and higher levels of dysbiosis in COVID-19 patients (regardless of severity level). Also, we detected higher abundance of opportunistic pathogens (e.g. Prevotella spp, Neisseria spp, Megasphaera spp) in severe and fatal COVID-19 patients, and found Rothia dentocariosa highly associated with fatal patients, which is a group that has been recently proposed as a biomarker for severe COVID-19. Finally, we found differences in diversity structure among COVID-19 patients, finding particular low complexity in the microbial networks associate to severe and fatal disease. Our data suggest that comorbidities and antibiotic uptake could be affecting the respiratory microbiota before SARS-CoV-2 infection, potentially compromising the immunological response of the host against disease and promoting secondary bacterial infections. For instance, the presence of dysbiosis coupled with low microbial structural complexity in the respiratory microbiota of COVID-19 patients, could have consequences for the host and microbial community level. Altogether, our findings identify the respiratory microbiota as a potential factor associated with COVID-19 severity.

L2 - The effects of *Physalis peruviana* L. consumption on the gut microbiota of healthy men

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Fruits rich in bioactive compounds are promising to manage cardiometabolic risk. Golden berry (Physalis peruviana L.) is rich in antioxidants and dietary fiber, and has been proposed to control glycaemia in individuals with impaired glucose metabolism. However, its impact on the human gut microbiota has never been tested. Yet, gut microbiota is one crucial factor associated with cardiometabolic risk. In this nutritional intervention, in which 18 healthy adult men (27-49 years old) consumed 150 g/day of golden berry for 19 days, we evaluated the effects of fruit intake on the diversity, composition and functional potential of the gut microbiota before (day 0), at the end (day 19) and one month after the end (day 49) of the intervention through 16S rRNA gene sequencing. We found that intake of golden berry did not affect the gut microbiota of all individuals in the same way, but shifted it in a personalized manner. The gut microbiota of some individuals responded more markedly than others. At baseline (day 0), responders had lower microbial alpha diversity than non-responders, a microbiota depleted in Bifidobacterium bifidum and with lower capacity to degrade fiber and produce short-chain fatty acids. The intervention homogenized the alpha diversity of all individuals, shifted OTU abundance patterns and modified the predicted metabolic capacity of the gut community, increasing the abundance of pathways involved in carbohydrate and amino acid degradation, as well as propionate production. One month after the end of the intervention (day 49), the gut microbiota tended to return to the baseline levels, although some changes remained. While there was a personalized response to golden berry consumption, we identified consistent patterns in the gut microbiota that help understand the response to golden berry consumption and its possible role in cardiometabolic regulation.

L3 - Comparison of the variation of gut bacterial diversity marker genes in public genomes: a case study of the class *Clostridia*

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Characterization of microbial communities is commonly performed using the 16S ribosomal RNA marker gene. However, recent advances in sequencing technologies have exposed several limitations of this marker to distinguish prokaryotes at finer taxonomic levels. It has been proposed that the use of alternative, more variable marker genes counteracts 16S rRNA disadvantages, while maintaining a cost-effective and highly informative methodology. We evaluated the suitability of DNA kinase1 (dnak1) and gyrase subunit B (gyrB) genes as genetic markers for the study of community diversity of the class Clostridia. We first built a reference dataset by downloading genome assemblies classified under the class Clostridia by the GTDB database and extracted from the assemblies the sequences of the genes of interest (dnak1, gyrB and 16S rRNA). We then estimated the variability of each gene and compared it to that of the 16S ribosomal RNA using pairwise identity matrices. A linear regression between pairwise comparison of marker genes belonging to the same assembly allowed us to understand how much resolution is gained by using an alternative marker compared to 16S rRNA sequences. Our results showed that both dnaK1 and gyrB are more variable in their sequence than the 16S rRNA gene and, therefore, may constitute appropriate markers to assess genetic diversity within Clostridia. Other studies evaluating different genes, bacterial groups and ecosystems, consistently confirm that the use of alternative house-keeping genes can help to elucidate finer diversity than what is observed with the traditional 16S rRNA gene. We foresee the use of alternative, house-keeping genes as being complementary to the 16S rRNA approach to answer questions that span different taxonomic levels and address bacterial identification, classification, phylogenetics and evolution.

L4 - Péptidos LL-37 y ATRA-1, potenciales alternativos frente a la resistencia antibiótica en *Staphylococcus aureus*

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Staphylococcus aureus es una bacteria parte de la microbiota humana, no obstante puede llegar a causar una gran variedad de infecciones tanto localizadas como sistémicas. Pese a la cantidad de antibióticos existentes, el tratamiento de este microorganismo suele complicarse, debido a su capacidad para generar resistencia. Este trabajo tiene como objetivo evaluar la capacidad de péptidos LL-37 y ATRA-1 para inhibir el crecimiento in vitro de aislamientos clínicos de S. aureus resistentes a antibióticos. Se realizó el perfil de sensibilidad in vitro a antibióticos para un total de 26 aislamientos usando las normas CLSI M7 y M2. Para cada péptido se determinó la concentración mínima inhibitoria en concentraciones de 64-2 µg/mL en medio PBS (125mM de NaCl) mediante la técnica de microdilución (CMI) y la concentración mínima bactericida (CMB) mediante la técnica de spots, los ensayos se realizaron por triplicado y se seleccionó la concentración más alta para cada aislamiento como su CIM y CMB. Tanto la sensibilidad antibiótica como las concentraciones mínimas inhibitorias y bactericidas se consideraron variable categorías y se realizó prueba de Chi

cuadrado para evaluar relaciones entre estas, con P-value 0,05. El 73 % de los aislamientos fueron resistentes a oxacilina, el 65 % a cefoxitin, el 11 % a eritromicina. El péptido LL-37 presentó actividad en 64-16 µg/mL, mientras que ATRA-1 exhibió actividad en 32-4 µg/mL. Se evidenciaron diferencias en los rangos de actividad a péptidos antimicrobianos en comparación con la sensibilidad antibiótica, sin embargo, estas no fueron significativas. Nuestros resultados muestran que LL-37 y ATRA-1 presentan actividad antimicrobiana en los aislamientos de S. aureus resistentes a antibióticos, además ATRA-1 representa el candidato más prometedor como alternativa terapeutica para el tratamiento de infecciones causadas por este microorganismo, inclusive abre la posibilidad de diseñar variantes de esta molécula con capacidad antimicrobiana que no han sido reportadas previamente.

L6 - Gut bugs matter to viroimmunotherapy: bacterial changes associated to the efficacy of Delta-24-RGDOX against glioblastoma

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Introduction: Glioblastoma is a notoriously invasive and devastating disease that requires new and more effective treatments as less than 5% of patients survive 5 years post-diagnosis. To improve clinical outcomes, the MDACC laboratory developed an oncolytic adenovirus armed with the T-cell activator OX40L, named Delta-24-RGDOX. Objective: Here, we evaluated to which extent there were gut microbiome changes in glioma bearing mice treated with viroimmunotherapy. GL261-5 glioblastoma cells were implanted in the brain of immunocompetent C57BL/6 mice and treated with control or a combination of Delta-24-RGDOX and Indoximod, an inhibitor of indoleamine 2,3-dioxygenase (IDO). Methods: Genomic DNA was isolated from fecal pellets collected from glioma-bearing mice, followed by sequencing of the 16S rRNA gene using the Illumina platform. Results/Discussion: We found significant differences in the gut microbiome community structure of viroimmunotherapy-treated animals compared to those with depleted CD4+ T cells and controls (p-value=0.001). Particularly, an increase in Actinobacteria compared to control-treated mice and those with shorter survival was observed. In fact, we found significantly higher amounts of Bifidobacterium and Lactobacillus in the viroimmunotherapy-treated mice while Parabacteroides and Akkermansia were more dominant in the control group ($p<0.05$). Also, we found significantly higher abundance of Lactobacillus and Alistipes in mice with a survival period 56-86 days, while Ruminiclostridium was more dominant in the mice with shortest survival. Conclusion: Our data suggests bacterial communities play an important role in modulating viroimmunotherapy against glioma. Importantly, increase in certain gut bacteria was associated with a better response to the therapy, likely strengthening antitumor immunity and raising efficacy of Delta-24-RGDOX; thus revealing the benefits of gut microbiome therapeutics in positively influencing the final clinical outcome of viroimmunotherapy.

L7 - Association of oral and environmental fungi with periodontal disease

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Background: Fungi are a major component of the human microbiome that has only recently received increased attention. Abundance of both bacteria and fungi are important in shaping oral health, especially in people with inflammatory diseases such as gingivitis and periodontitis. Imbalance of indigenous fungal communities may have a role in oral dysbiosis. Objectives: We aimed to study the association of oral fungi to periodontal disease. Methods: This cross-sectional study recruited individuals aged 21 to 49 from sexually transmitted infection clinics in Puerto Rico. A total of 95 participants were assessed and a full-mouth periodontal examination was performed following the National Health and Nutrition Examination Survey protocol. Periodontal severity was defined according to the Centers for Disease Control/American Academy of Periodontology. Saliva was collected for genomic DNA extraction and downstream ITS-2 genes were amplified, sequenced, and analyzed with QIITA and Qiime2 platforms. Results: A total of 31% of individuals had some degree of periodontal disease while 69% were healthy. We found significant differences in beta diversity in both composition (p-value: 0.02) and dispersion (p-value: 0.026), however there were no significant differences in alpha diversity. Higher abundance of Debaryomyces, Aspergillus, Candida and Saccharomyces were associated with periodontal disease. Surprisingly we found most of the detected fungi to be filamentous fungi representing the outdoor (Basidiomycetes) and indoor (Ascomycetes) environments. Conclusions: Our preliminary data confirms polymicrobial colonization of yeast and filamentous fungi in the oral biofilm. A significant increase in indoor fungi in periodontal disease severity, may reveal the impact of the indoor environment on the human microbiome and the impacts of non-indigenous taxa on the immune response and disease persistence. Mycotic dysbiosis should be considered when choosing therapeutics for periodontal disease.

L8 - Evaluation of two DNA markers for improving the resolution of microbial diversity in a Colombian population

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A previous characterization of the gut microbiota of a Colombian population showed an enrichment of bacteria belonging to the families Lachnospiraceae and Ruminococcaceae. This diversity characterization was based on the amplification of the V4 fragment of the 16S rRNA gene, and thus may be underestimated due to the limitations of this genetic marker to separate closely related taxa. In order to gain a better resolution of the diversity within these two families, we evaluated the amplicon sequences of two genes that have less conserved sequences than the 16S rRNA gene, DNA kinase1 (dnaK1) and gyrase subunit B (gyrB). We designed primers for each gene, and the amplicons were subjected to Illumina MiSeq sequencing. The resulted reads were pre-processed using Trimmomatic v0.39 and denoised by Deblur, as implemented in Qiime2 v2020.2. The taxonomy was assigned using kraken2 with GTDB-taxonomy data base as implemented in the pipeline STRUO2. We found that both dnak1 and gyrB genes show more diversity in terms of amplicon sequence variants (ASVs) than the 16S rRNA gene, but that it depends on the family under scrutiny. The marker dnak1 shows more diversity of Ruminococcaceae, with prevalence of species belonging to the genera Gemminger (in particular G. quacibialis), Ruminococcus and Faecalibacterium. The marker gyrB shows more variability of Lachnospiraceae, with prevalence of species belonging to the genera Dorea and Blautia. The sequencing of alternative marker genes to 16S rRNA gene is useful to resolve community diversity while keeping the costs and analysis simple, and here we provide two potential markers that may be useful to reveal hidden diversity of important groups in the human gut microbiota.

L9 - New insights into taxonomic and genetic diversity of the *Blautia* genus, found by a phylogenomic approach

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Blautia is a relevant and abundant genus present in the microbiome of human and other mammalian gastrointestinal (GI) tracts. Seventeen accepted Blautia species are currently available, in addition to nine other non-accepted ones. Despite the increasing level of knowledge about Blautia and its role in the GI tract, its genetic and taxonomic diversity is still poorly understood. The growing availability of Blautia genomic sequences in public databases opens the possibility to study this genus from a genomic perspective.

Here, we report a pan-genome analysis and a phylogenomic study of 224 Blautia genomes available in RefSeq. We found 33 different potential species groups at the genomic level, sixteen of them previously unknown. We also confirmed the status of 4 previously proposed new Blautia species by genomic standards and discovered that two accepted species could be fused with other species (e.g., B. coccoides and B. producta are part of the same species group). Our comparative analysis showed that the Blautia pan-genome is open, with a relatively small core genome (722 gene families). Additionally, utilizing a set of representative genomes, we applied a gene family gain/loss model for the genus, showing that some Blautia lineages experienced massive gene gains (up to ~900 genes), whereas that gene loss events were relatively less massive (< 300 genes), suggesting a primary role of gene gain in Blautia evolution. Using the HGTector tool to predict horizontal gene transfer (HGT) events, we found that approximately 22% of the genes from 35 representative Blautia genomes were potentially acquired by HGT, mostly from Clostridiales or other Firmicutes.

L10 - Differential Microbiota of HPV and Non HPV related Penile Cancer

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Penile cancer (PeCa) is a disease with a high morbidity and mortality, among developing countries. Although penile cancer is a relatively uncommon cancer, its incidence is nearly four times higher in Puerto Rico (PR) when compared with other racial and ethnic groups in the United States (US). Infection with human papillomavirus (HPV) has been identified as a risk factor for an average of 48% of PeCa cases. To date, the role of the microbiota in the pathogenesis of PeCa is unknown, as there are no studies on the microbiome of penile cancer. We hypothesized that the penile. Bacterial communities could change with HPV infection and subsequent cancerous lesions. Methods: Genomic DNA was extracted from biopsies of 51 patient biopsy samples, followed by HPV genotyping and microbiota analyses using 16S rRNA genes with the Illumina MiSeq platform with a focus on tumor histology and HPV status. We found HPV positive samples with high grade histology have higher alpha diversity and abundance of Prevotella and Actiobacullum. HPV positive samples had higher levels of Actinobacteria, including Actinomyces europaeus, Mobiluncus sp. or Corynebacterium. HPV negative samples with high grade histology had higher levels of Sneathia, Gardnerella and even Lactobacillus. We found lipophilic and anaerobic bacteria associated with penile dysbiosis, taxa that have been defined as biomarkers of HPV and cervical dysbiosis, which may be involved in triggering inflammatory responses and oncogenesis. Although many challenges must be overcome to dissect the specific interactions of coinfecting bacteria during the penile cancer infectious process, our findings demonstrate that microbes may be involved in these cellular processes.

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CAPAC Cancer Prevention and Control Research Training Program National Cancer Institute Award# 1R25CA240120-01

L11 - Protocolo de modulación de la microbiota intestinal basado en hidroterapia de colón en mujeres jóvenes con sobrepeso

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Introducción: La microbiota intestinal (MI) es objeto de estudio y blanco terapéutico en sobrepeso/obesidad y otras enfermedades crónicas no transmisibles. Objetivo: Determinar cambios fisiológicos benéficos en 12 variables físicas y 9 químicas asociadas a sobrepeso, así como en la razón firmicutes/bacteroidetes de la MI, producidos por un protocolo de modulación de la microbiota bacteriana (PM-MI), para indagar posible asociación entre dicha razón y los primeros. Metodología: Muestra de conveniencia (12 voluntarias, 18-28 años de edad), dividida aleatoriamente en grupos control y experimental. Significancia estádistica cuando $p<0,05$. Todas las participantes se examinaron en tres momentos: inicio del estudio, a los 8-10 días y al mes (M1, M2 y M3, respectivamente). Entre M1-M2, el grupo experimental se sometió al PM-MI, que incluye: 5 irrigaciones transanales del colon, dieta líquida, consumo diario de psyllium y montmorillonita e ingesta de probióticos (Eptavis®). Resultados. Mientras el grupo control, a los momentos M2 y M3, comparado con el M1, experimentó ligeros cambios desfavorables en las variables estudiadas (en algunos casos con significancia estadística), lo opuesto se evidenció en el grupo experimental, en el cual prácticamente todas las variables mostraron cambios favorables estadísticamente significativos. Al comparar ambos grupos en M1, las medias de los valores de todas las variables consideradas (salvo 2) son iguales; en M2, 3 variables físicas, todas las químicas y la biológica son estadísticamente diferentes entre ambos grupos, y, en M3, se conservan las diferencias entre ambos grupos observadas en M2, y 2 variables físicas más muestran diferencia estadísticamente significativa. Discusión: resultados respaldan la hipótesis propuesta por González-Correa et al (2017) de que el PM-MI mejora el estado de salud y bienestar de las personas y permite una cierta modulación de la MI. Conclusiones: los resultados son muy sugestivos del efecto benéfico general del PM-MI y se sugiere otro estudio con una n mayor.

L12 - Situación de la investigación en microbioma humano en América Latina: Una revisión bibliométrica 2015-2020

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Latinoamérica es una región con poblaciones muy diversas, tanto a nivel genético, como de estilos de vida, tradiciones y condiciones socioeconómicas, lo cual supone un interés en el estudio de los microbiomas asociados a sus habitantes. Sin embargo, hay escasos estudios que recopilen información de las investigaciones en el tema de microbioma humano en la región. Por lo tanto, el objetivo de este trabajo es realizar una revisión bibliométrica descriptiva para identificar tendencias de la investigación en el tema de microbioma humano en Latinoamérica. Para esto se efectuó una revisión sistemática en la base de datos PubMed para identificar estudios en este tema en 20 países de América Latina. Los estudios debían incluir una técnica de secuenciación como técnica principal de identificación bacteriana, y efectuarse en una población propia del país. Se analizaron indicadores bibliométricos personales, de productividad, de citación o impacto y de contenido. Se obtuvieron 184 estudios de 14 países, la mayoría perteneciente a Brasil (39%), México (18%), Colombia (10%) y Chile (8%). Desde el 2015, la cantidad de publicaciones aumentó cada año; además, aproximadamente 72% de las publicaciones presentan una predominante participación de autores latinos. Sin embargo, en países con pocas publicaciones, la colaboración internacional es más relevante. Por otro lado, es frecuente la publicación en revistas de alta visibilidad. Respecto al tipo de microbiota estudiada, la microbiota intestinal es la más investigada (56%), seguido de la microbiota oral (15%), y luego la vaginal (8%). Los resultados concuerdan con la tendencia mundial de interés en el tema de microbiota, principalmente la intestinal. No obstante, es necesario incentivar la investigación en este campo en Latinoamérica para generar conocimiento autóctono que permita mejorar la calidad de vida de los habitantes de esta región.

POSTERS SELECTED FOR SHORT PRESENTATIONS

1. The influence of the Doce river mouth on the microbiome of nearby coastal areas three years after the Fundão Dam failure, Brazil.

Luanny Fernandez

Universidade Federal Fluminense

See page 125

2. Globally ubiquitous viruses in oil reservoirs refute burial and isolation theory

Julia Plewka

University Duisburg-Essen

See page 150

3. Integration of bioinformatic tools in a automatized workflow for the search of novel biosynthetic gene clusters

Leonardo Zamora

Universidad Técnica Federico Santa María

See page 187

4. Novel hot spring cyanobacterial genomes from metagenomes unveil genetic adaptations to the high temperature environment

Jaime Alcorta

Pontificia Universidad Católica de Chile

See page 217

5. Taxones bacterianos claves en líquenes Peltigera rufescens creciendo en dos praderas en la región de Aysén, Chile.

Karla Veas

Universidad de Chile

See page 232

6. ¿Afecta la endozoocoria la diversidad de bacterias endófitas en semillas?

Felipe Cruz

Universidad de La Salle

See page 244

7. Agriculture irrigation modified microbial communities and soil functions associated with enhancing C uptake of a semi-arid soil in Patagonia

Luis Wall

Uiversity of Quilmes, Bernal, Argentina

See page 266

8. Bacterial community composition in shallow lakes from Nothofagus pumilio forest (Patagonia, Argentina).

Marcela Bastidas

INIBIOMA (CONICET-UNCOMA)

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9. Dysbiosis and structural disruption of the respiratory microbiota in

COVID-19 patients with severe and fatal outcomes

Alejandra Hernández

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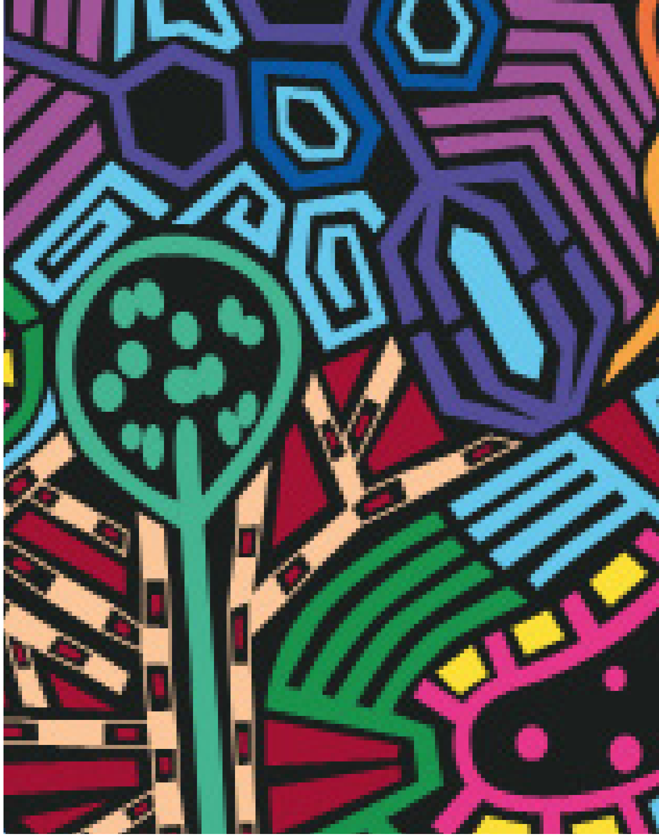
See page 333

PANEL DISCUSSION



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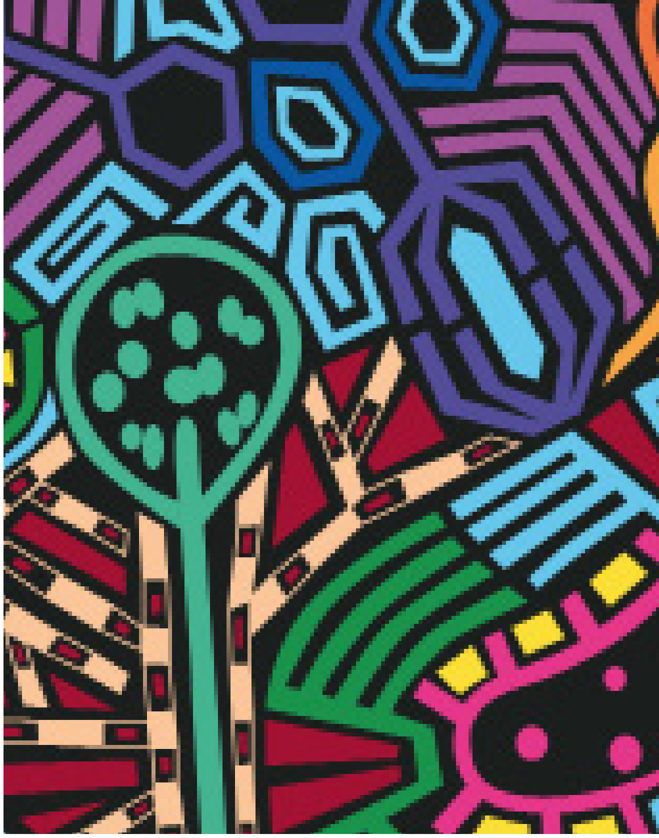
WORKSHOPS



1. QIIME 2 WORKSHOP

MEMBERS OF THE RESEARCH GROUP IN COMPUTATIONAL BIOLOGY AND MICROBIAL ECOLOGY FROM UNIVERSIDAD DE LOS ANDES IN BOGOTÁ, COLOMBIA, WITH SUPPORT FROM THE QIIME 2 TEAM, CARRIED OUT A TWO-DAY ONLINE WORKSHOP ON BIOINFORMATICS TOOLS FOR MICROBIOME SCIENCE IN THE CONTEXT OF THE LATIN AMERICAN ISME CONFERENCE. THE WORKSHOP INCLUDED LECTURES COVERING THEORY AND USE OF QIIME 2, AND PRACTICAL WORK WITH QIIME 2 TO PERFORM MICROBIOME ANALYSIS FROM RAW SEQUENCE DATA THROUGH PUBLICATION-QUALITY STATISTICS AND VISUALIZATIONS. THIS ONLINE COURSE WAS A BLEND OF PRE-RECORDED AND LIVE LECTURES. THERE WERE ALSO INTERACTIVE COMMAND-LINE BASED TUTORIAL SESSIONS, WHERE ATTENDEES PERFORMED MICROBIOME ANALYSES USING QIIME 2 ONLINE. WE ALSO HOSTED LIVE QUESTION-AND-ANSWER SESSIONS.

INSTRUCTORS:

- BCEM GROUP (BCEM.UNIANDES.EDU.CO) – UNIVERSIDAD DE LOS ANDES, BOGOTÁ, COLOMBIA
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  - KEEGAN EVANS PHD
  - LIZ GEHRET PHD
  - CHLOE HERMAN PHD
  - JEFF MEILANDER PHD

DR. CAPORASO GAVE AN OPENING LECTURE AND ALL MEMBERS OF THIS GROUP ANSWERED QUESTIONS IN THE CLOSING Q&A SESSION.

2. DIVULGACIÓN CIENTÍFICA: MÉTODOS Y HERRAMIENTA

EL CURSO DE DIVULGACIÓN CIENTÍFICA RESALTÓ LA IMPORTANCIA DE LA DIVULGACIÓN CIENTÍFICA Y COMPARTIÓ MANERAS DE IMPLEMENTARLA EN LA PRÁCTICA PROFESIONAL. EL CURSO INCLUYÓ EJERCICIOS INTERACTIVOS, ACTIVIDADES DE REFLEXIÓN Y LA OPORTUNIDAD DE CONVERSAR CON INVITADOS CON AMPLIA EXPERIENCIA EN COMUNICACIÓN DE CIENCIA. EL CURSO ESTABA DIRIGIDO A PERSONAS INTERESADAS EN DIVULGAR CIENCIA, INDEPENDIENTEMENTE DE SU ÁREA ESPECÍFICA DE ENTRENAMIENTO.

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ANA MARÍA PORRAS
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3. MEGAN WORKSHOP

THIS WORKSHOP GAVE AN INTRODUCTION TO THE COMPUTATIONAL ANALYSIS OF MICROBIOME SEQUENCING READS. WE BRIEFLY DISCUSSED QUALITY CONTROL, PROCESSING AND SEQUENCE ASSEMBLY. WE THEN DISCUSSED IN MORE DETAIL HOW TO PERFORM DIAMOND ALIGNMENT OF THE DATA AND HOW TO PROCESS THE RESULTING ALIGNMENT FILES SO AS TO BE ABLE TO OPEN THEM IN MEGAN. WE THEN USE MEGAN TO EXPLORE A NUMBER OF DIFFERENT MICROBIOME DATASETS FROM DIFFERENT HOST-ASSOCIATED STUDIES, AND FROM BIO-REACTOR COMMUNITIES. WE CONSIDERED BOTH SHORT-READ AND LONG-READ DATASETS. DIAMOND IS A COMMAND LINE TOOL THAT IS RUN ON A SERVER. MEGAN IS AN INTERACTIVE MICROBIOME EXPLORATION TOOL THAT IS RUN ON A LAPTOP OR DESKTOP. THE DIAMOND+MEGAN PIPELINE IS THE ARCHETYPE OF HOMOLOGY-BASED MICROBIOME ANALYSIS AND SO OBTAINING AN UNDERSTANDING OF THIS APPROACH WILL ALSO PREPARE YOU TO WORK WITH OTHER MICROBIOME ANALYSIS TOOLS THAT FOLLOW THIS APPROACH.

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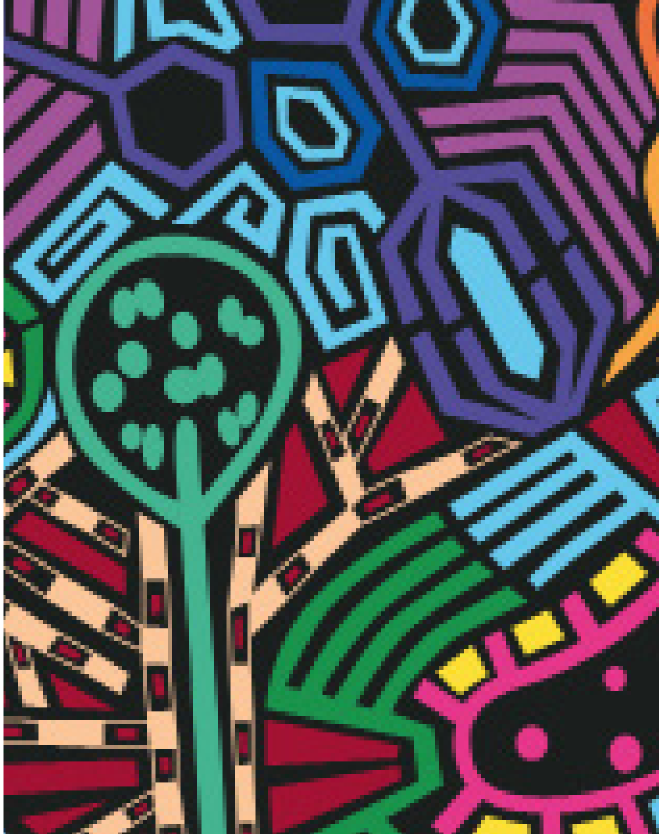

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