XLI Congreso Nacional de Microbiología AMM
Oaxaca 2019

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VI Congreso Rama BBMB-SMB
Oaxaca 2019

Scientific Program

Comité Organizador y
Mesa Directiva 2017 – 2019
Asociación Mexicana de Microbiología

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VI Congreso de Bioquímica y Biología Molecular de Bacterias
Sociedad Mexicana de Bioquímica

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XLI National Microbiology Meeting of the
Mexican Association of Microbiology (AMM)

VI Meeting of Biochemistry and Molecular Biology of Bacteria (BBMB)

P r o g r a m

Oaxaca, Oax, Mexico. October 27 - 31, 2019

Sunday, October 27

11:00 – 17:00	Registration
14:00 – 17:00	Lunch
16:25 – 17:00	Opening Ceremony
17:00 – 18:00	Opening Talk I **Susana López Charretón** **Rotavirus strategies to control the antiviral response of the cell: A dynamic story** Instituto de Biotecnología, UNAM Chair: ***David Romero***
18:00 – 19:00	Opening Talk II **Gabriel Núñez** **Host-Microbiota Interactions in Health and Disease** Department of Pathology, University of Michigan Chair: ***José Luis Puente***
19:00 – 21:00	Welcome Cocktail

Monday, October 28

7:00 – 9:00	Breakfast
	Symposium I **BACTERIAL SIGNALING AND METABOLISM** Chair: ***Gloria Soberón***
9:00 – 9:30	Structure, functional prediction, and phenotyping studies in genes encoding proteins involved in cyclic-di-GMP in *Azospirillum* *Beatriz Eugenia Baca* CICM – Benemérita Universidad Autónoma de Puebla
9:30 – 10:00	Exploitation of public goods and population collapses in *Pseudomonas aeruginosa* *Rodolfo García Contreras* Facultad de Medicina, UNAM
10:00 – 10:30	Rethinking secondary metabolism in bacteria: from evolution to function *Francisco Barona Gómez* Unidad de Genómica Avanzada, LANGEBIO CINVESTAV

10:30 – 11:00	The tRNA fragments exported by *Escherichia coli* cells may be protein synthesis by-products generated on ribosomes *Eva Jacinto Loeza* CINVESTAV Unidad Zacatenco
11:00 – 11:30	Coffee Break
	Symposium II **TUBERCULOSIS** Chair: ***Rogelio Hernández Pando***
11:30 – 12:00	The role of Hepatocyte Growth Factor in experimental pulmonary tuberculosis. Therapeutical implications *Rogelio Hernández Pando* Instituto Nacional de Nutrición "Salvador Zubirán"
12:00 – 12:30	New insights into the methylation of heparin binding hemagglutinin adhesin (HbhA) of *Mycobacterium tuberculosis* *Clara Inés Espitia Pinzón* Instituto de Investigaciones Biomédicas, UNAM
12:30 – 13:00	Towards the constitution of an epidemiological atlas of multidrug-resistant tuberculosis in Mexico *José Antonio Enciso Moreno* Unidad de Investigación Biomédica de Zacatecas, IMSS
13:00 – 13:30	Nicotine induces virulence genes in *Mycobacterium tuberculosis* *Bruno Rivas Santiago* Unidad de Investigación Biomédica de Zacatecas, IMSS
13:30 – 15:00	Lunch
15:00 – 16:00	Plenary Lecture I **Urs Jenal** ***From Cell Polarity to Bacterial Virulence Control*** University of Basel - Biozentrum Switzerland Chair: ***Dimitris Georgellis***
16:00 – 16:15	Coffee break
	Symposium III **CELL DYNAMICS I** Chair: ***Bianca Anabel Amézquita***
16:15 – 16:30	Isolation, genotyping and antimicrobial resistance of Shiga toxin-producing *Escherichia coli* *Bianca Anabel Amézquita López* Facultad de Ciencias Químico Biológicas, Universidad Autónoma de Sinaloa
16:30 – 16:45	*Student presentations* Phenotypic plasticity by reaction norms in *Bacillus* spp. species from wild environments from Cuatro Ciénegas Coahuila desert facing physical

	environmental factors *Enrique Hurtado-Bautista* Laboratory of Molecular Biology and Microbial Ecology - CINVESTAV Irapuato
16:45 – 17:00	Establishment of a protein concentration gradient in the outer membrane requires two diffusion limiting mechanisms *Luis David Ginez* Instituto de Investigaciones Biomédicas, UNAM
17:00 – 17:15	Analysis of Gp37 function of the coliphage mEp021 *Elissa Paulina Ballinas Turrén* CINVESTAV Unidad Zacatenco
17:15 – 18:15	Plenary Lecture II **David Pérez Morga** **Human African Trypanosomiasis evolution and Cell Death in *Trypanosoma brucei brucei*** Université Libre de Bruxelles Belgium Chair: ***Gabriela Olmedo***
18:15 – 20:15	Poster Session Odd Numbers

Tuesday, October 29

7:00 – 9:00	Breakfast
	Symposium IV **BACTERIAL RESISTANCE AND ITS CLINICAL, EPIDEMIOLOGICAL AND ENVIRONMENTAL RELEVANCE** Chair: ***Guadalupe Aguilera***
9:00 – 9:30	Surveillance of *Pseudomonas aeruginosa* *Alejandra Aquino Andrade* Instituto Nacional de Pediatría
9:30 – 10:00	Epidemiology of multidrug-resistant *Neisseria gonorrhoeae* in Mexico City: crisis in a complicated context? *Guadalupe Aguilera Arreola* Escuela Nacional de Ciencias Biológicas, IPN
10:00 – 10:30	Methicillin-resistant *Staphylococcus aureus* and its persistence in hand hygiene *Sara Ariadna Ochoa Pérez* Hospital Infantil de México “Federico Gómez”
10:30 – 11:00	Una vida dedicada al estudio de la Bacteriología Médica en México: en homenaje a la Doctora Silvia Giono Cerezo, politécnica y bacterióloga por convicción *María Teresa Estrada García* CINVESTAV Unidad Zacatenco
11:00 – 11:30	Coffee break

	Symposium V **MICROBIOME** Chair: ***Eria Rebollar***
11:30 – 12:00	Amphibian-Microbial symbioses: understanding the protective role of skin bacteria against emerging diseases *Eria Rebollar Caudillo* Centro de Ciencias Genómicas, UNAM
12:00 – 12:30	Microbiome of cycad's coralloid roots: co-evolution of bacterial communities encoding niche-specific biosynthetic gene clusters *Angélica Cibrián Jaramillo* Unidad de Genómica Avanzada, LANGEBIO CINVESTAV
12:30 – 13:00	The distal colon microbiota of Type 2 Diabetes, Obesity, and Metabolic Syndrome triad in Mexico *Jaime García Mena* CINVESTAV Unidad Zacatenco
13:00 – 13:15	*Student presentations* Bacteria and Archaea distribution in subsurface sediments of the Gulf of Mexico *Adrián Martínez Santana* Instituto de Biotecnología, UNAM
13:15 – 13:30	Recognition of human colostrum bacteria by IgA subtypes and their effect on microbiota establishment in the newborn *Erick Sánchez Salguero* CINVESTAV Unidad Zacatenco
13:30 – 15:00	Lunch
15:00 – 16:00	Plenary Lecture III **Rita Tamayo** ***Mechanisms of Phenotypic Heterogeneity in Clostridioides difficile*** University of North Carolina at Chapel Hill USA Chair: ***José Luis Puente***
16:00 – 16:15	Coffee break
	Symposium VI **GENE REGULATION** Chair: ***Ma. Teresa Estrada***
16:15 – 16:45	Defining the role of toxin-antitoxin systems in the persistence phenotype of the intracellular pathogen *Burkholderia pseudomallei* *Alfredo Torres* University of Texas, USA
16:45 – 17:00	*Student presentations* The CtrA regulon of *Rhodobacter sphaeroides* favors adaptation to particular life styles *José de Jesús Hernández Valle* Instituto de Investigaciones Biomédicas, UNAM

17:00 – 17:15	CreR, an EIL domain-containing protein, positively regulates the expression of the *ecp* fimbrial operon in *Citrobacter rodentium* *María Inés Isidro Coxca* Instituto de Biotecnología, UNAM
17:15 – 17:30	The quorum sensing system NprR-NprRB contributes to spreading and fitness in biofilms of *Bacillus thuringensis* *Abel Alberto Verdugo Fuentes* Centro de Investigación en Alimentación y Desarrollo, A.C.
17:30 – 17:45	Characterization of a *Rhizobium etli* OmpR-type regulator that participates in motility and nitrogen fixation with bean plants *Susana Rodríguez* Centro de Ciencias Genómicas, UNAM
17:45 – 18:00	The CRISPR-Cas system is involved in the synthesis of outer membrane proteins in *Salmonella enterica* serovar Typhi *Sarahi Rodríguez Gutiérrez* Instituto de Biotecnología, UNAM
18:00 – 18:15	ZMP dependent activation of response regulators in *Escherichia coli* *Oscar Jair Vázquez Ciros* Instituto de Fisiología Celular, UNAM
18:15 – 20:15	Poster Session Even Numbers

Wednesday, October 30

7:00 – 9:00	Breakfast
	Symposium VII **FOOD MICROBIOLOGY** Chair: ***Agustín López-Munguía***
9:00 – 9:30	Synthesis of glycopolysaccharides in traditionally fermented foods *Agustín López Munguía* Instituto de Biotecnología, UNAM
9:30 – 10:00	Detection and identification of yeasts from musts of three Mexican distilled beverages *Francisco Ruíz Terán* Facultad de Química, UNAM
10:00 – 10:15	*Student presentations* The effect of the number of chambers on the performance of a *MESynC* that produces succinic acid by *A. succinogenes* Sara Abaunza Alvarado CINVESTAV Unidad Zacatenco
10:15 – 10:30	Development of a methodology for the genetic transformation of *Agave tequilana* Weber var. Azul mediated by *Agrobacterium tumefaciens* and based on organogenesis *Edith Alheli Bernabé Pérez* Instituto Tecnológico de Oaxaca

10:30 – 10:45	Phenotypic trait diversity of budding yeast populations associated to Agave fermentation in Mexico *Porfirio Alberto Gallegos Casillas* Unidad de Genómica Avanzada, LANGEBIO CINVESTAV Unidad Irapuato
10:45 – 11:00	Biosurfactant and/or Bioemulsifier Production by *Gordonia sp*. R4M20CR Utilizing Agro-industrial Waste Products *Isaac Alberto Vigil García* Facultad de Ciencias Químicas, UACH
11:00 – 11:30	Coffee Break
	Symposium VIII **INDUSTRIAL MICROBIOLOGY IN MEXICO: FROM THE EMERGING TO THE TRANSNATIONAL COMPANY** Chair: ***Cesar Hernández***
11:30 – 12:00	Vaccine manufacturing. A global challenge requiring specialized people. A complex journey in a highly regulated industry *Eduardo Estrada Obregón* SANOFI
12:00 – 12:30	Technological platforms based on industrial microbiology and its role solving social problems, a third-party laboratory perspective *Cecilia Padierna Mota* Laboratorio de Especialidades Inmunológicas
12:30 – 13:00	Success cases of biotechnology in Mexico *Néstor Octavio Pérez Ramírez* PROBIOMED
13:00 – 13:30	Different data science approaches for the development and obtaining bacterial functional secrets for industry improvement *Violeta Larios Serrato* Winter Genomics
13:30 – 15:00	Lunch
15:00 – 16:00	Plenary Lecture IV **Cammie F. Lesser** ***Leveraging bacterial secretion systems to develop therapeutic designer probiotics*** Department of Microbiology and Immunobiology Massachusetts General Hospital Harvard Medical School USA Chair: ***Bertha González-Pedrajo***
16:00 – 16:15	Coffee break

	Symposium IX **CELL DYNAMICS II** Chair: ***Juan José Valdez***
16:15 – 16:30	From molecular epidemiology to the biocontrol of *Staphylococcus aureus* in bovine mastitis *Juan José Valdez Alarcón* FMVZ, Universidad Michoacana de San Nicolás de Hidalgo
16:30 – 16:45	*Student presentations* Silencing of unused sectors of the *E. coli* proteome using CRISPRi and its application in synthetic biology *Miguel Ángel Bello González* Centro de Ciencias Genómicas, UNAM
16:45 – 17:00	Study of enzymatic promiscuity at the enzyme level, family and metabolic pathway, and its role in genomic mining of natural products *Nelly Sélem Mojica* LANGEBIO CINVESTAV
17:00 – 17:15	Single-cell plasmid dynamics in fluctuating environments *José Carlos Ramón Hernández Beltrán* Centro de Ciencias Genómicas, UNAM
17:15 – 18:15	Closing Lecture **Antonio Lazcano Araujo** **Oxygen and biological evolution:** **some major biogeochemical consequences** El Colegio Nacional / Facultad de Ciencias, UNAM Chair: ***Cesar Hernández***
18:15 – 18:30	Final Announcements and Closing Ceremony
18:30	Business meeting AMM
21:00	Dinner and Dancing

All oral presentations will be held in the Grand Plaza II & III Rooms

All poster presentations will be held in the Grand Plaza I & Platino Rooms

POSTER PRESENTATIONS

Odd poster board number Presentation: Monday October 28th

Even poster board number Presentation: Tuesday October 29th

CELL BIOLOGY

1.	**Viability assessment and morphological changes of mycobacteria during dormancy induced by hypoxia and starvation.** *Diana Angelica Aguilar Ayala*, Ruben Zaragoza Contreras, Addy Cecilia Helguera Repetto, Jorge Francisco Cerna Cortés, Sandra Rivera Gutiérrez, Robert A. Cox and Jorge Alberto Gonzalez Y Merchand. Instituto Nacional de Perinatología Isidro Espinosa de los Reyes (InPer)
2.	**Cloning, expression and purification of PilW and PilV pilins of the Type IV pili of *Acidithiobacillus thiooxidans***. *Elvia F. Alfaro Saldaña,* J. Viridiana García Meza, J. Alfredo Méndez Cabañas. Geomicrobiología, Metalurgia. Instituto de Física. Universidad Autónoma de San Luis Potosí
3.	**A new proposal for the study of proteins that bind to cell wall of peptidoglycan.** *Arenas Rodríguez Thelma*, Osorio Franco Aurora, Poggio Ghilarducci Sebastián. Department of Molecular Biology and Biotechnology, Biomedical Research Institute**,** UNAM
4.	**Ultrastructural damage in *Streptococcus mutans* incubated with saliva and histatin 5.** Ana María Fernández Presas, *Blanca Esther Blancas Luciano*, Yamili Marquez Torres, Ingeborg Becker Fauser, Roxana Hayde Rodríguez Barrera, Rosmary Toloza Medina, José Delgado Domínguez, Jose Luis Molinarí Soriano. Departamento de Microbiología y Parasitología. Facultad de Medicina, UNAM
5.	**Substrate recognition by the sorting platform in the injectisome.** *Arely Ivonne Marcos Vilchis*, Norma Espinosa Sánchez and Bertha González Pedrajo. Instituto de Fisiología Celular, UNAM
6.	**Induction of the mycelial morphotype in *Candida albicans* yeast cells and activity of Glucosamine-6-phosphate synthase**. *Silvia Gabriela Pérez Ramírez,* Everardo López Romero. División de Ciencias Naturales y Exactas, Universidad de Guanajuato
7.	**Effect of antimicrobial peptide LL-37 and KR-20 on *Trichomonas vaginalis* viability.** *Ramírez Ledesma María Guadalupe*, Arroyo López C. Cecilia, Alva Murillo Patricia Nayeli, Ávila Muro Eva Edilia. Departamento de Biología, División de Ciencias Naturales y Exactas, Universidad de Guanajuato
8.	**Outer membrane vesicles from *Rhodobacter sphaeroides*.** *Benjamín Vega Baray*, Sebastián Poggio, Georges Dreyfus, Laura Camarena. Instituto de Investigaciones Biomédicas, UNAM

STRUCTURAL BIOLOGY

9.	**Analysis of the FlgT-MotF interaction in the flagellar system 1 of *Rhodobacter sphaeroides.*** *David Rodríguez, Méndez*, C. Domenzain, S Poggio, A. Osorio, G. Dreyfus, L. Camarena. Instituto de Investigaciones Biomédicas, UNAM.
10.	**Characterization of the open reading frame *rsp_1315* present in the flagellar set 2 of *Rhodobacter sphaeroides.*** *Fernanda Vélez González,* Benjamín Vega Baray, Sebastián Poggio, Georges Dreyfus, Laura Camarena. Instituto de Investigaciones Biomédicas, UNAM

SYSTEMS BIOLOGY

11.	**Characterization of the temporal variability of the SOS response in individual *Escherichia coli* cells in the presence of beta-lactam antibiotics.** *Oscar Bruno Aguilar Luviano*, Ayari Fuentes Hernández & Rafael Peña Miller**.** Laboratorio de biología de sistemas y biología sintética, Centro de Ciencias Genómicas, UNAM.
12.	**The tragedy of the commons: A selective integration of methods as the best strategy for DNA-sequence-based inference of regulatory networks.** *Juan M. Escorcia Rodríguez*, Maria J. Palma Martínez, Marian Domínguez Mirazo, Elias R. Ruiz Morales, Luis F. Gutiérrez Mondragón, Diego Fernández, and Julio A. Freyre González. Regulatory Systems Biology Research Group, Laboratory of Systems and Synthetic Biology, Center for Genomics Sciences, UNAM.

13.	**Lessons from Abasy Atlas v2.2: complexity, completeness, quality and learning of gene regulatory networks.** *Julio Augusto Freyre González*, Juan Miguel Escorcia Rodríguez, Adrián Isaac Campos González, and Marco Antonio Tello Palencia. Laboratory of Systems and Synthetic Biology, Center for Genomic Sciences, UNAM.
14.	**System-level characterization of the evolution of the gene regulatory networks of *Escherichia coli*, *Bacillus subtilis*, and *Corynebacterium glutamicum.*** *Luis F. Gutiérrez Mondragón*, Gabriel Moreno Hagelsieb, and Julio A. Freyre González. Laboratory of Systems and Synthetic Biology, Center for Genomic Sciences, UNAM.
15.	**Ecological dynamics of auxotrophic microbial populations.** *Daniela Reyes González*, Rafael Peña Miller, Ayari Fuentes Hernández. Laboratory of Systems Biology and Synthetic Biology, Center of Genomic Science, UNAM.
16.	**Inferring gene regulatory networks from transcriptomic data: effects of normalization and combinatorial integration on predictions.** *Juan Miguel Escorcia Rodríguez*, Marco Antonio Tello Palencia, Andrea Zorro Aranda, Roberto Olayo Alarcón, Luis Fernando Altamirano Pacheco, Estefani Gaytán Nuñez, Ericka Montserrat Hernández Benítez, Julio A. Freyre González. Laboratory of Systems and Synthetic Biology, Center for Genomic Sciences, UNAM.

BIOTECHNOLOGY AND INDUSTRIAL MICROBIOLOGY

17.	**Standardization of the conditions of growth and production of the δ endotoxin of *Bacillus thuringiensis* to be used in the biological control of insect pests.** Alma Lilia Antonio Cruz, *Amalia Ventura Almaraz Hernández*, López Sánchez Claudia, Palma Cruz Felipe de Jesús. National Technologic of Mexico/Oaxaca Technologic Institute.
18.	**Characterization of *Rhodococcus ruber* MSA14: a bacterium to degrade high-molecular-weight polycyclic aromatic hydrocarbons.** *Cynthia Lizzeth Araujo Palomares*, Cristina Quezada-Hernández, José Vinicio Macías Zamora, Nancy Ramírez Álvarez, Hortencia Silva Jiménez. Instituto de Investigaciones Oceanológicas, Universidad Autónoma de Baja California
19.	**Plant growth promoting mechanisms from heavy metal tolerant *Micrococcus* strains isolated of contaminated sites in Mexico.** *Ivan Arroyo Herrera*, Brenda Román Ponce, En Tao Wang Hu, Paulina Estrada de los Santos, María Soledad Vásquez Murrieta. ENCB. IPN
20.	**Cytotoxic activity of microalgae isolated from Cuatro Cienegas, Coah. in human cancer cell lines.** Faviola Tavares Carreón, Héctor F. Arocha Garza, Susana de la Torre Zavala, Valeria Souza, *Hamlet Avilés Arnaut.* Facultad de Ciencias Biológicas, Universidad Autónoma de Nuevo León
21.	**Pilot study for the evaluation of antimicrobial and antibiofilm activity of two varieties of walnut shell extracts (*Carya illinoinensis*) from Chihuahua State on a clinical *Staphylococcus aureus* strain.** Sebastián Valdez Gutiérrez, Blanca Estela Rivera Chavira, Carmen Oralia Meléndez Pizarro, Miguel Ángel Flores Villalobos, Angélica Holguín López, Hilda Amelia Piñón Castillo, Erasmo Orrantia Borunda, *Germán Ayala Sandoval.* Universidad Autónoma de Chihuahua.
22.	**Isolation of Steffimycin compound from endophytic *Streptomyces scabrisporus* strain NF3 and screening for their antimicrobial activities.** *Nathalia Badillo Mantilla,* Ajit Kumar Passari, Jose Fausto Rivero Cruz and Sergio Sánchez. Universidad Industrial de Santander, Colombia.
23.	**NP-Hoc protein fusion design and expression in *E. coli* BL21 for a potential influenza A vaccine.** *Francisco de Jesús Balderas Cisneros*, Francisco Ricardo Rodríguez Recio, Carlos Enrique Escárcega González, José Rubén Morones Ramírez. Universidad Autónoma de Nuevo León, Facultad de Ciencias Químicas, Centro de investigación en biotecnología y nanotecnología (CIBYN).
24.	**Engineering *Escherichia coli* membrane lipid composition: towards a robust chassis strain.** *Bedoya Pérez Leidy Patricia*, Utrilla José, Sohlenkamp Christian. CCG. UNAM.
25.	**Spray drying and antibacterial activity of the aqueous extract of *Agave cupreata.*** *Cinthya Vanessa Calderón Peralta*, Liliana Alamilla Beltrán, Mario Márquez Lemus, Ricardo Salazar, Natividad Castro Alarcón, María del Pilar Torres Nicasio, Patricia Álvarez Fitz. Facultad de Ciencias Químico Biológica, Universidad Autónoma de Guerrero.
26.	**Isolation and characterization of the antagonistic strain *Alcaligenes faecalis* MNCu3.** *María Fernanda Cedeño Toscano*, Leslie Mariana Morales Ruìz, Anuar Salazar Gómez, Fernando Uriel Rojas Rojas· Escuela de Ciencias de la Salud. Universidad del Valle de México.
27.	**Production and partial characterization of a cellulase raw extract from a mexican *Streptomyces* strain.**

	Samuel Celaya Herrera, José E. Barboza Corona. Graduate Program in Biosciences. Laboratory of Biotechnology and Molecular Microbiology. Life Science Division. University of Guanajuato
28.	**Potential of biocontrol and molecular characterization of a bacterial agent of the *Pseudomonas* genus.** *Ismael Fernando Chávez Díaz*, Sergio Aranda Ocampo, Andrés Aguilar Granados, Bárbara Hernández Macías, Emma Zavaleta Mejía. Laboratorio de Recursos Genéticos Microbianos, Centro Nacional de Recursos Genéticos INIFAP
29.	**Antifungal activity of *Paenibacillus polymyxa* NMA1017 extracellular metabolites in biological control.** *Belén Chávez Ramírez*, Melissa Mondragón Talonia, María Soledad Vásquez Murrieta, Paulina Estrada de los Santos**.** ENCB IPN.
30.	**Effect of fumarate in microbial communities in sediment microbial fuel cells with sediments from Coatzacoalcos River.** *Alan Cornejo Martell*, Berenice Cruz, Luz Breton Deval, Alberto Álvarez Gallegos, Emmanuel Alvizo, José Fernando García, Katy Juárez. Instituto de Biotecnología, Universidad Nacional Autónoma de México
31.	**Promotion of the *zea mays* growth by mixed bacterial inoculants isolated from jala maize environment.** *Esaú De la Vega Camarillo*, Josimar Sotelo Aguilar, Bibiana Ríos Galicia, Lourdes Villa Tanaca, Ramón Arteaga Garibay, César Hernández Rodríguez. Departamento de Microbiología, Escuela Nacional de Ciencias Biológicas, IPN.
32.	**Improving functional properties of germinated soybean flour by non-lactic acid fermentative bacteria.** *Denisse Escareño Luna*, Vinicius Falleiros, Ana Paula Mejía Victoria, Ramón Núñez Molina, Marcela González Montoya, Fernando Uriel Rojas Rojas. Escuela de Ciencias de la Salud, Universidad del Valle de México
33.	**Lignocellulolytic enzymes by actinomycetes isolated in the extremely oligotrophic desert oasis Cuatro Ciénegas basin, Mexico.** Janneth Escudero Agudelo, Montserrat Orencio Trejo, Argel Gastélum Arellánez, Susana De la Torre Zavala. Facultad de Ciencias Biológicas, Instituto de Biotecnología, Universidad Autónoma de Nuevo León,
34.	**Molecular detection of *Pseudomonas aeruginosa* by test strips coupled to the LAMP technique.** *Daniel Alejandro Ferrusca Bernal*, F. Monica Neri Martínez, J. Joel Mosqueda Gualito, Bertha Isabel Carvajal Gamez. Facultad de Ciencias Naturales, Universidad Autónoma de Querétaro.
35.	**Physicochemical and electrophoretical characterization of endoglucanases obtained from a novel consortia PM-06 for lignocelullose saccharification.** *Ricardo Andrés Flores Briceño*, Rodrigo Guzmán Pedraza, Mónica Noel Sánchez González. Universidad Autónoma de Yucatán..
36.	**Phytochemical profile and antibacterial activity of the acetonic extract of *Phoradendron* sp.** *Paola Rossy García Sosa*, Patricia Álvarez Fitz, Norma Reyna Robledo Quintos, Carlos Villicaña Zuñiga**.** Centro Interdisciplinario de Ciencias de la Salud. Unidad Milpa Alta IPN
37.	**Characterization of endolysin genes and design of an heterologous expression vector for its use against *Staphylococcus aureus*.** *Adriana Carolina Gil Correa*, Nadia Karina Mota Sandoval, Víctor Manuel Baizabal Aguirre, Javier Oviedo Boyso, Rodolfo G. Ríos Díaz, Juan José Valdez Alarcón. Centro Multidisciplinario de Estudios en Biotecnología, FMVZ UMSNH.
38.	**Evaluation of plant growth promoting bacteria in saline conditions.** *Eduardo Gómez Sánchez*, Valentín López Gayou, Laura J. García Barrera, Ada María Ríos Cortés, María M. Solís Oba, Patricia Ibarra Torres. Centro de Investigación en Biotecnología Aplicada. IPN.
39.	***In vitro* analysis of antagonism of a *Trichoderma atroviride* wild strain towards phytopathogen microorganisms.** *Karla Ivonne González Martínez*, Virginia Angélica Robinson Fuentes, Ma. Soledad Vázquez Garcidueñas, Salvador Ochoa Ascencio, Gerardo Vázquez Marrufo. Centro multidisciplinario de Estudios en Biotecnología, Facultad de Medicina Veterinaria y Zootecnia.
40.	**Bioassay to evaluate the production of the C4-HSL autoinductor in strains of *Pseudomonas aeruginosa*.** A. Abigail González Valdéz, Miguel Cocotl Yañez, Martin P. Soto Aceves, Gloria Soberón Chávez. Instituto de investigaciones Biomédicas, UNAM.
41.	**Search of extremozymes from halophilic and halotolerant microorganisms for their biotechnological application.** *Joseph Guevara Luna*, Paulina Estrada de los Santos, María Soledad Vásquez Murrieta. Laboratorio de Biotecnología Microbiana, ENCB. IPN.
42.	**Metagenomic screening and characterization of bacterial lipases from sediments of the Gulf of Mexico.** *Isaac Guzmán Becerril*, Libertad Alejandra Adaya García, José Luis Rodríguez Mejía, Liliana Pardo López. Laboratorio de Investigación en Programas Institucionales, Instituto de Biotecnología, UNAM.
43.	**Enzymatic and metasecretomic model of lignocellulose degradation from a novel microbial consortium PM-06.** *Rodrigo Guzmán Pedraza*, José Germán Serrano Gamboa, Rafael Antonio Rojas Herrera, Mónica Noel Sánchez González. Universidad Autónoma de Yucatán.

44.	**Endemic igneous rock as a proposal of bracket material media for the growth of a microbial oxidizing sulphate consortium.** *Benjamín Hernández Figueroa*, Antonino Pérez Hernández, Velvett G. Domínguez Ménde, Francisco Javier Zavala Díaz de la Serna, Beatriz A. Rocha Gutiérrez, Lourdes Ballinas Casarrubia, Héctor A. López Aguilar, Jorge Gómez, Ma. Del Rosario Peralta Pérez. Facultad de Ciencias Químicas. Universidad Autónoma de Chihuahua
45.	**Biodirected phytochemical fractionation and antibacterial activity of fraction from *Agave cupreata.*** *Ana Karen Herrera Vargas,* Patricia Álvarez Fitz, Luis Chávez Almazán, Ma. Elena Moreno Godínez, Natividad Castro Alarcón. Laboratorio de Investigación en Microbiología, UAGro,
46.	**Search of genes encoding for bioactive components by transposon mutagenesis in *Burkholderia cenocepacia* TAtl-371.** *Jeniffer Chris Kerber Díaz*, Fernando U. Rojas Rojas, Paulina Estrada de los Santos, José Antonio Ibarra García. Escuela Nacional de Ciencias Biológicas, IPN.
47.	**Analysis of the enzyme Lytic Polysaccharide Monooxygenase during the enzymatic degradation of the maize pericarp.** *Ángel Licona Segura*, Rodrigo Guzmán Pedraza, Mónica Noel Sánchez González. Facultad de Ingeniería Química. Universidad Autónoma de Yucatán.
48.	**Kinetic characterization of the radial growth of *Ganoderma lucidum* on different supplements and media culture.** *Ramos Juárez Eduardo*, López Sánchez Claudia, Palma Cruz Felipe de Jesús. National Technologic of Mexico/Technologic Institute of Oaxaca.
49.	**Generation of an immune library fragments of single-chain antibodies of mouse against prostate specific antigen.** *Denisse Anaí López Sosa*, José Oscar Zavala Tapia and Naún Lobo Galo. Universidad Autónoma de Ciudad Juárez
50.	**Morphological and electrogenic analysis of bacteria isolated from the Lagos de Moreno river, Jalisco.** *Adriana Araceli Macías Reynoso*, Erbin Eduardo Vázquez Villa, Juana Elizabeth Alba Cuevas, Héctor Pérez Ladrón de Guevara y Virginia Villa Cruz. Centro Universitario de los Lagos, Universidad de Guadalajara.
51.	**Metagenomic and chemical analyses of microbial communities from coastal karstic swamp sediments to assess their biosynthetic potencial for PKS and NRPS production.** *Miguel Marfil Santana*, Claudia Remes Rodríguez, Angélica Márquez Velázquez, Alejandra Prieto Davo. Unidad Sisal-Yucatán, Facultad de Química, UNAM.
52.	**Isolation of wild bacteria from nodules of *Phaseolus vulgaris* and analysis of their potential use as biofertilizers**. *Cecilio Mauricio Ramos*, Analilia Arroyo Becerra, Lorena Jacqueline Gómez Godínez, Andrea Salvador Muñoz, María de Lourdes Girard Cuesy, Selma Ríos Meléndez, Miguel Ángel Villalobos López**.** Centro de Investigación en Biotecnología Aplicada, IPN
53.	**Bactericidal effect of purified products of soil bacterias against Gram-positive bacterias.** *Abigail Méndez Martínez*, Jonathan Isaí Delgado López, Victor E. Aguirre Arzola, Julia Mariana Márquez Reyes. Facultad de Agronomía, UANL
54.	**Isolation and molecular characterization of a strain with 2,3-extradiol dioxygenase activity and heterologous expression of the enzyme responsible of the activity.** *Karla Sofía Millán López,* Selma Julieta Rodríguez Salazar, Ernestina Godoy Lozano, Liliana Pardo López. Instituto de Biotecnología, UNAM.
55.	**Search for lactic acid bacteria capable of degrading glucosinolates.** *Ignacio Eduardo Monsivais Rodriguez,* Adriana C. Flores, Juan A. Ascasio, Cristóbal N. Aguilar, Raúl Rodriguez, Leonardo Sepúlveda, Jesús Morlett, Julia R. Medrano Macías. Departamento de Investigación en Alimentos, Universidad Autónoma de Coahuila
56.	**Bacterial hydrocarbon-responsive transcriptional factors and their application for the design of biosensors.** *Luis Felipe Muriel Millán*, José Luis Rodriguez Mejía, Carlos Guillermo Garnier Rocha, Paul Gaytan, Liliana Pardo López. Instituto de Biotecnología, UNAM
57.	**Characterization of cultivable yeasts in the production of a traditional mezcal from Oaxaca.** *Alexa Yunuen Nieves Arízaga*, Rodrigo Campos Rivera, Claudia Ivette Cisneros Reyes, Julia del Carmen Martínez Rodríguez. DDCyT. Universidad Autónoma de Guadalajara.
58.	**Anticancer potential of two sediment Actinobacteria extract from Puerto Vallarta and Veracruz, México.** *Irasema Oroz Parra*, Natalie Millán Aguiñaga, Alfredo Castellanos Ibarra, Alexei Fedórovish Licea Navarro, Paul R. Jensen. Marine Sciences Faculty, Autonomous University of Baja California
59.	**Screening of cellulose-degrading wild molds for cellulase production from lignocellulosic agroindustrial residues.** *Rosa Jazmín Osuna Cisneros*, Francisco Javier Delgado Virgen, Oscar Fernando Vázquez Vuelvas. TecNM/Instituto Tecnológico de Colima.
60.	***Bacillus subtilis* as promoter of volatile organic compounds (VOCs) applied in blackberry crop (*Rubus fruticosus*).** *Samuel Macario Padilla Jiménez*, María Valentina Angoa Pérez, Hortencia Gabriela Mena Violante, Guadalupe Oyoque Salcedo, Ernesto Oregel Zamudio. CIIDIR IPN Unidad Michoacán.
61.	**Whole-genome sequence of strain *Streptomyces thermocarboxydus* and their heavy metal resistance**

	biosorption property. *Ajit Kumar Passari*, Maria Paula Gómez Roman,Nathalia Badillo Mantilla, José Fausto Rivero Cruz, Sergio Sánchez. Instituto de Investigaciones Biomédicas, UNAM.
62.	**Molecular identification of yeasts in cider from Zacatlán.** Jaquelinne Montiel Rivera, Amanda Gabriela Alarcón Barios, Ernestina Valadez Moctezuma, *Guillermo Pérez Esteban.* Departamento de ingeniería en industrias alimentarias. Instituto Tecnológico Superior de la Sierra Norte de Puebla.
63.	**Influence of heavy metals on biofilm production in bacteria isolated from contaminated soils.** *Adriana Perez Sanchez*, María Soledad Vásquez Murrieta, Paulina Estrada de los Santos. Escuela Nacional de Ciencias Biológicas, IPN.
64.	**Effect of *Pseudomonas aeruginosa* rhamnolipids over mature biofilms of multirresistant clinical isolates.** *Alejandro Plascencia Terrazas*, Guadalupe Virginia Nevárez Moorillón, Jair Carrazco Palafox, María Olga González Rangel. Laboratorio de Microbiología III, Facultad de Ciencias Químicas, Universidad Autónoma de Chihuahua,
65.	**A case study: Obtainment of minimally functional microbial consortia from CR1 consortium using dilution to extinction for Lignocelullose degradation***. Ángel Rafael Pool Cen*, Rodrigo Guzmán Pedraza, Mónica Noel Sánchez González. Universidad Autónoma de Yucatán. Facultad de Ingeniería Química.
66.	**Identification, expression and characterization of a biosynthetic cluster involved in the production of a lantipeptide in *Micromonospora purpurea***. *Ramírez Rendón Dulce María*, Ruiz Villafán Beatriz, Sánchez Sergio**.** Instituto de Investigaciones Biomédicas, UNAM.
67.	**A tRNA-utilizing enzyme is involved in the synthesis of the protease inhibitor thiolstatin (livipeptin) in *Streptomyces lividans* 66.** César Aguilar, *Hilda E. Ramos Aboites*, Karina Verdel Aranda, Nelly Sélem Mojica, Francisco Barona Gómez, Evolution of Metabolic Diversity Laboratory, Unidad de Genómica Avanzada (Langebio), CINVESTAV, IPN.
68.	**Evaluation of astaxanthin production by *Xanthophyllomyces dendrorhous* XR4 in saccharified lignocellulosic biomass.** *Yeily Adriana Rangel Basto*, Ana C. Ramos Valvidia, Carlos M. Cerda García Rojas, Odilia Pérez Avalos, María Teresa Ponce Noyola**.** Departamento de Biotecnología y Bioingeniería. Departamento de Química. CINVESTAV-IPN.
69.	**Effect of the growth temperature on proteomic and structural response of the rHuGM-CSF inclusion bodies of *E. coli* under thermoinduction.** *Sara Restrepo Pineda*, Norma A. Valdez Cruz, Néstor O. Pérez, Mauricio A. Trujillo Roldán. Unidad de Bioprocesos, Instituto de Investigaciones Biomédicas, UNAM.
70.	**Growth evaluation of lentinan producer mycelium of *Lentinula edodes* (Berk.) Pegler, in solid and submerged fermentation médium.** *Emilene Reyes Rodríguez*, Claudia López Sánchez, Felipe de Jesús Palma Cruz. National Technologic of Mexico/Technologic Institute of Oaxaca.
71.	**Isolation and characterization of the lipolytic activity of a marine *Pseudomonas alcaligenes* from Gulf of Mexico.** *José Luis Rodríguez Mejía*, Itzel Anahí Manzano Hidalgo, Luis Felipe Muriel Millán, Nancy Rivera Gómez, Elizabeth Ernestina Godoy Lozano, Liliana Pardo López. Instituto de Biotecnología, UNAM.
72.	**Marine Dioxygenases: Who thinks crude oil is delicious?.** *Julieta Rodríguez Salazar*, Katya Ornelas Ocampo, Sofía Millán López, José Luis Rodríguez Mejía, Luis Felipe Muriel Millán, Liliana Pardo López**.** Instituto de Biotecnología, UNAM.
73.	**Characterization of biological control agents for diseases of importance in cacao crops in Chiapas.** Nadia Denisse Rodríguez Velázquez, Belén Chávez Ramírez, Carlos Hugo Avendaño Arrazate, Paulina Estrada de los Santos**.** Laboratorio de Biotecnología Microbiana, ENCB, IPN.
74.	**Growth promotion in wheat (*Triticum turgidum* L. *subsp. durum*) by co-inoculation of native *Bacillus* strains isolated from the Yaqui Valley, Mexico***. Jonathan Rojas Padilla,* Luis Abraham Chaparro Encinas, Rosa Icela Robles Montoya, Fannie Isela Parra Cota, Sergio de los Santos Villalobo. Laboratorio de Biotecnología del Recurso Microbiano, Instituto Tecnológico de Sonora.
75.	**Effect of volatile organic compounds synthesized by *Pseudomonas rhodesiae* GRC140 on the root architecture of *Arabidopsis thaliana.*** *Gisela Adelina Rolón Cárdenas*, Jackeline Lizzeta Arvizu Gómez, Juan Ramiro Pacheco Aguilar, Alejandro Hernández Morales. Facultad de Ciencias Químicas, Universidad Autónoma de San Luis Potosí.
76.	**Synthetic bacterial consortium to degrade monocyclic aromatic compounds.** *Jaime Rosas Díaz*, Libertad Alejandra Adaya García, Grisel Alejandra Escobar Zepeda, Elizabeth Ernestina Godoy Lozano y Liliana Pardo López. Instituto de Biotecnología, UNAM
77.	**Selection of operating conditions for palm oil mill effluent treatment in microbial fuel cells.** Jorge Alberto Albarracin Arias, *Viviana Sanchez Torres.* Universidad Industrial de Santander, Bucaramanga, Colombia.
78.	**Polyhydroxybutyrate production by heavy metals-resistant bacteria strains.** *Juan Francisco Sánchez López*, Osiel Salvador Recoder Meléndez, César Osiris Arias López, Aurelio Álvarez Vargas, Ulises Emiliano

	Rodríguez Castrejón, Carmen Cano Canchola. Unidad Profesional Interdisciplinaria de Ingeniería Campus Guanajuato. IPN.
79.	**Expression of a 3-hydroxyacyl-ACP thioesterase and a mcl-CoA ligase in *Azotobacter vinelandii* for the production of medium chain length polyhydroxyalkanoates*:* new degradable bioplastics.** Gabriela Morales Flores, Josefina Guzmán Aparicio, Carlos Peña Malacara, Guadalupe Espín Ocampo, *Daniel Segura González.* Instituto de Biotecnología, UNAM.
80.	***Pseudomonas stutzeri* MLA9, a marine bacterium with high potential to degrade pyrene.** Cynthia Lizzeth Araujo Palomares, Ileana Sarahí Ramos Mendoza, *Hortencia Silva Jiménez.* Instituto de Investigaciones Oceanológicas, Universidad Autónoma de Baja California.
81.	**Phenotypic analysis of the fur_{1398} mutant in *Gluconacetobacter diazotrophicus* Pal5 strain.** María Sofía Pardo Reyes, Luis Javier Martínez Morales, Beatriz Eugenia Baca, *Lucía Soto Urzúa.* Centro de Investigaciones en Ciencias Microbiológicas, ICUAP-BUAP
82.	**Characterization of *Cupriavidus* strains isolated from nodules with biotechnological potential.** *Erika Yanet Tapia García*, Verónica Hernández-Trejo, Ma. Soledad Vásquez Murrieta y Paulina Estrada de los Santos. Escuela Nacional de Ciencias Biológicas, IPN
83.	**The pH shift affects the production and architecture of inclusion bodies of recombinant phospholipase A2 expressed in *Escherichia coli.*** Norma Adriana Valdez Cruz, Carlos Calcines Cruz, Alejandro Olvera, Alejandro Alagón, *Mauricio A. Trujillo Roldán.* Instituto de Investigaciones Biomédicas, UNAM
84.	**Resonant acoustic mixing improves oxygen transfer in shake flasks and production of a recombinant phospholipase A2 in *Escherichia coli.*** Mauricio A. Trujillo Roldán, Mayra Herrera de los Santos, Sara Restrepo Pineda, Greta I. Reynoso Cereceda, Alejandro Olvera, Alejandro Alagón, *Norma A. Valdez Cruz.* Instituto de Investigaciones Biomédicas, UNAM

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85.	**Emergent properties of a synthetic community of *Bacillus* or how the context changes the dynamics in the study of interactions.** *Aguilar Salinas Bernardo*, Ortega Aguilar Jaime, Islas Robles Africa, Olmedo Álvarez Gabriela. Laboratory of Molecular Biology and Microbial Ecology – CINVESTAV.
86.	**Etiological agent prevalence for ecosystem health monitoring in mangroves of the Yucatán peninsula, México.** Muhilan Mahendhiran, Joanna María Ortiz Alcántara, Javier Apodaca Hernández, Germán Giacoman Vallejo, Jorge Herrera Silveira*, María Leticia Arena Ortiz.* Facultad de Ciencias, UNAM.
87.	**Isolation and pre-characterization of microorganisms from "Cerro El Toscano" soil, Michoacán**. *Héctor Avalos Flores*, César Darío Méndez Horta, José O. Reyes Sánchez. Universidad de la Ciénega del Estado de Michoacán de Ocampo.
88.	**A new biosynthesis pathway for the sulfolipid sulfoquinovosyl diacylglycerol in *Sinorhizobium meliloti.*** Jessica Y. Cuevas Rivas, Diego Rodríguez Terrones, Napoleón González Silva, Ángeles Moreno Ocampo, Ed Bergström, Jane E. Thomas Oates, Otto Geiger and Isabel M. López Lara. Centro de Ciencias Genómicas, UNAM
89.	**Geographic distribution and diversity of *Fusarium* species in the state of Colima, México.** *Andrea Viridiana Estrada Zaragoza*, Omar Adalid Reyes Vuelvas, Jorge Roberto Velázquez Milanés, Juan Enrique Cortés Valle, Ana Cecilia Ramírez López, Luis Ignacio Hernández Chávez, Francisco Javier Delgado Virgen. TecNM/Instituto Tecnológico de Colima.
90.	**Bacterial diversity in karst sinkholes (cenotes) from the Puerto Morelos and Tulum touristic zones.** *Karina Hernández-García*, Jazmín Santillán, Rafael López Martínez, Martín Merino Ibarra, Rocio J. Alcántara-Hernández. Posgrado en Ciencias del Mar y Limnología, Instituto de Geología, UNAM
91.	**Experimental evolution to explore phenotypic plasticity to temperature in wild type strains from a natural environment.** *Enrique Hurtado Bautista*, Laura Sánchez Pérez, África Islas Robles, Gabriel Moreno Hagelsieb, and Gabriela Olmedo Álvarez**.** Laboratory of Molecular Biology and Microbial Ecology - CINVESTAV
92.	**Identification and biochemical characterization of the putative XPG/Rad2 nuclease of *Giardia duodenalis.*** *María Teresa Izaguirre Hernández,* **María** Luisa Bazán Tejeda, Rosa María Bermúdez Cruz. Departamento de Genética y Biología Molecular. CINVESTAV IPN.
93.	**Study of RNA Degradosome *in vivo* dynamics using FRET.** *Marcos Emmanuel Jaso Vera*, Emmanuel Solis Romo, Liliana Domínguez Malfavon, Ben Luisi, Jaime García Mena. Departamento de Genética y

	Biología Molecular, CINVESTAV.
94.	**A highly conserved *16S rRNA* region reveled a new strain of *Acidithiobacillus ferrooxidans* from a biohydrometallurgy residual solution.** *Andrea E. Jiménez Paredes*, Elvia Alfaro, Marizel G Astello García, J Alfredo Méndez, J Viridiana García Meza. Geomicrobiología, Ingeniería, Metalurgia, UASLP
95.	**Horizontal transference of virulence genes in *E. coli* strains isolated from a same geographical area.** *Jonathan Josué López Islas*, Estela T. Méndez Olvera, Carlos A. Eslava Campos, Daniel Martínez Gómez, Andrés López Pérez. División de Ciencias Biológicas y de la Salud, UAM Xochimilco.
96.	**Specific genetic background is required for acquisition of virulence genes in *Escherichia coli.*** *Jonathan Josué López Islas*, Estela T. Méndez Olvera, Carlos A. Eslava Campos, Daniel Martínez Gómez. División de Ciencias Biológicas y de la Salud, UAM Xochimilco
97.	**Isolation of halophilic archaeas from Cuatro Ciénegas Basin: the lost world hotspot.** *Nahui Olin Medina Chávez,* Valeria Souza, Susana De la Torre Zavala**.** Instituto de Biotecnología, Facultad de Ciencias Biológicas, Universidad Autónoma de Nuevo León.
98.	**Assessing the biotechnological potential of Antarctic and sub-Arctic sediment cores.** *Natalie Millán Aguiñaga*, Holger H. Buchholz, John Howe, Paul A. Hoskisson, Katherine R. Duncan. Universidad Autónoma de Baja California
99.	**Biofertilization of *Bonellia macrocarpa* with native bacterial strains and its effect on the growth and content of bonediol.** *Saidy Monjaraz Penn,* Reiner Rincón Rosales, Clara Ivette Rincón Molina. Tecnológico Nacional de México, Campus Tuxtla.
100.	**Design and validation of a multiplex PCR assay for MAT idiomorph determination within *Fusarium fujikuroi* species complex.** *Amelia C. Montoya Martínez*, Gerardo Rodríguez Alvarado, Sylvia P. Fernández Pavía, Robert H. Procto, Hye Seon Kim, Kerry O'Donnell. Laboratorio de Patología Vegetal, IIAF, Universidad Michoacana de San Nicolás de Hidalgo
101.	**Environmental conditions and organisms associated to the coloration change in the "La Salina" lagoon of Bajos de Coyula, Oaxaca.** *Andehui Danay Morales Flores*, Ivonne Sandra Santiago Morales*, Yolanda Huante González, Barbara Zavala Trujillo, Ernesto García Mendoza, Aramis Olivos Ortíz, Amayaly Becerril Espinosa. Universidad del Mar
102.	**pH dependent Predation by *Bdellovibrio bacteriovorus* 109J.** *Tae Moriya*, Junichi Yoshimura, Yuki Hoshiko, Rodolfo García Contreras, Toshinari Maeda. Department of Biological Functions Engineering. Kyushu Institute of Technology, Japan
103.	**Sphingolipids required for survival of *Caulobacter crescentus.*** *Roberto J. Olea Ozuna*, Sebastian Poggio Ghilarducci, Ed Bergström, Elva Quiroz Rocha, Jonathan Padilla Gomez, Lourdes Martínez Aguilar, Isabel M. López Lara, Jane E. Thomas Oates and Otto Geiger. Centro de Ciencias Genómicas, UNAM.
104.	**Phenotypic plasticity evaluated in bacteria in a classic G x E study comparing lineages from contrasting natural environments.** Enrique Hurtado Bautista, África Islas Robles, Gustavo Santoyo, *Gabriela Olmedo Álvarez.* Laboratory of Molecular Biology and Microbial Ecology - CINVESTAV Irapuato.
105.	**Molecular identification and characterization of bacteria isolated from biofilms in Atetelco, Teotihuacan.** Martínez Calixto Yunuen, Ojeda Rivera Guadalupe, Medina Jaritz Nora, Hernández Rodríguez César H., *Olvera Ramírez Roxana*. Departamento de Botánica. ENCB. IPN.
106.	**Isolation, and molecular identification of plant growth promoting bacteria in vegetables and *Salix sp*. from Chinampa agricultural system in Mexico City, Mexico.** *Beatriz Mónica Pérez Ibarra,* Raúl Motte Nava**.** Escuela Nacional Colegio de Ciencias y Humanidades, UNAM.
107.	**Structural genomics and molecular characterization of symbol bacteria resistant to heavy metals.** *Rebeca Pérez Martínez*, Edgar Dantán González, María de Lourdes Girard Cuesy,José Augusto Ramírez Trujillo, Ramón Suárez Rodríguez. Center for Research in Biotechnology, UAEM.
108.	**ISSR-based assessment of the genetic diversity of *F. mexicanum,* causal agent of mango and big-leaf mahogany malformation diseases in Mexico.** *Daniela Pineda-Vaca*, Ricardo Santillán-Mendoza, Sylvia Patricia Fernández-Pavía, Juan Carlos Montero Castro, Nuria Gómez-Dorantes, Gerardo Rodríguez-Alvarado. Laboratorio de Patología Vegetal, Universidad Michoacana.
109.	**Lambda red system adjustment for *pilA* gene mutation in *Klebsiella pneumoniae*.** *Denisse Ramírez Mendoza*, César I. López Reynoso, Patricia Lozano Zaraín, Rosa del C. Rocha Gracia, Ygnacio Martínez Laguna, Margarita M. P Arenas Hernández and Claudia F. Martínez de la Peña. Centro de Investigacion en Ciencias Microbiológicas, BUAP.
110.	**Plant growth-promoting bacteria associated to pioneer plants from El Chichón volcano, Chiapas (Mexico).** *Clara I. Rincón Molina*, Esperanza Martínez Romero, Encarna Velázquez, Marco A. Rogel Hernández, Reiner Rincón Rosales. Tecnológico Nacional de México, Campus Tuxtla.
111.	**Development of SCAR markers by Inter-Simple Sequence Repeat (ISSR) analysis for identification of**

	***Fusarium mexicanum* and *F. pseudocircinatum*.** Ricardo Santillán Mendoza, Amelia Cristina Montoya Martínez, Daniela Pineda Vaca, Sylvia Patricia Fernández Pavía, Miguel Martínez Trujillo, María Gloria Solís-Guzmán, *Gerardo Rodríguez Alvarado.*[1]Laboratorio de Patología Vegetal, Universidad Michoacana
112.	**Prevalence Of *Campylobacter jejuni* and *Campylobacter coli* From Environmental Samples in Culiacan, Sinaloa, Mexico.** Marcela Soto Beltrán, *Celica Antonela Rodríguez López*, Hilary Beltrán Sauceda, Beatriz Quiñones, Ángel Ibarra Rodríguez, Bianca Anabel Amézquita López. Facultad de Ciencias Químico Biológicas, Universidad Autónoma de Sinaloa.
113.	**Plasmid construction for CRISPR genetic edition in a no model fungal phytopathogen *Sclerotium cepivorum* Berk.** *Luis Mauricio Salazar García*, Sandra E. González Hernández, José A. Martínez Álvarez, Mitzi Flores Ponce, Patricia Ponce Noyola. Departamento de Biología. Universidad de Guanajuato.
114.	**Shift of the species in a microalgae community exposed to Cu and Zn.** *Manuel A Sánchez Olvera*, Paola Pérez Castro, Andrea E Jiménez Paredes, Marizel Astello García G, J Viridiana García Meza. Geomicrobiología, Metalurgia, UASLP.
115.	**Study of the microbial communities of the swamp de Sisal and the El Palmar State Reserve in the Yucatan Peninsula using Next Generation Sequencing tools.** *Erika Sánchez Ramos* and Mario Alberto Martínez Núñez. UMDI-Sisal, Facultad de Ciencias, UNAM
116.	**Study of the interaction between RNase II and RNase PH with RNase E of *Escherichia coli in vivo*.** *Emmanuel Solís*, Marcos E. Jaso Vera, Lilianha Domínguez Malfavón, Jaime García Mena, Ben F. Luisi. CINVESTAV IPN Zacatenco
117.	**Bacteriological quality in fresh fish from different aquatic systems from Tabasco State.** *María de Lourdes Torres Pérez*, Rosa Martha Padrón López, Lucero Vázquez Cruz, Luis José Rangel Ruiz**.** División Académica de Ciencias Biológicas, Universidad Juárez Autónoma de Tabasco.
118.	**Pathogenic bacteria in tilapia (*Oreochromis niloticus*) cultivation**. *María de Lourdes Torres Pérez*, Rosa Martha Padrón López y Lucero Vázquez Cruz. División Académica de Ciencias Biológicas, Universidad Juárez Autónoma de Tabasco.
119.	**Characterization of antagonistic bacteria of phytopathogenic fungi obtained from a strawberry orchard with organic management.** *Alejandra Torres Lara*, Mayra Niño González, Francisco Córdoba Andrade, Ulises Esquivel Naranjo, Fidel Landeros Jaime, Rosario Abraham Juárez, José Antonio Cervantes Chávez. Degree in Biology. Autonomous University of Queretaro
120.	**Ribosome profiling analysis of a Pth (Ts) *E. coli* mutant strain.** *Augusto Uc-Mass*, Yuritza Olguín, Eva Jacinto-Loeza, and Gabriel Guarneros. Departamento de Genética y Biología Molecular, CINVESTAV IPN.
121.	**Cloning, purification and production of polyclonal antibodies for the detection of Bap adhesin in enterohemorrhagic *Escherichia coli.*** *Sergio Iván Vázquez Arellano*, María Lilia Cedillo Ramírez, Ygnacio Martínez Laguna, Jorge Alberto Girón Ortiz, Cristina Lara Ochoa. Centro de Detección Biomolecular-BUAP.
122.	**Identificación de genes involucrados en la hidroxilación de lipidos de membrana en *Burkholderia cenocepacia* J2315.** *Maritza Lorena Vences Guzmán*, Miguel Ángel Vences Guzmán, Christian Sohlenkamp. Centro de Investigación en Dinámica Celular, UAEM.
123.	**Studies of microbial communities associated to the root of *Typha spp.* exposed to a mixture of diclofenac and naproxen in a horizontal wetland of subsurface Flow.** *Ana Laura Zapata Morales*, Ma. Catalina Alfaro de la Torre. Hernández Morales Alejandro. Facultad de Ciencias Químicas, Universidad Autónoma de San Luis Potosí.
124.	**Safety of *Pseudomonas* spp. and *Bacillus* spp. strains that inhibit the growth of *Fusarium* spp. and promote maize growth.** Mario Blanco Camarillo, Ramón I. Arteaga Garibay*, Lily X. Zelaya Molina*. Centro Nacional de Recursos Genéticos INIFAP.

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125.	**Functional analysis of the aminoacid sequence involved in localization of the hybrid protein CdgB of *Azospirillum brazilense* Sp 245.** *Acatitla Jácome Iris*, Viruega Góngora Víctor I., María Luisa Xiqui Vazquez Beatriz E. Baca, Alberto Ramírez Mata. Centro de Investigaciones en Ciencias Microbiológicas, BUAP
126.	**An exploration of tRNA utilizing enzymes using EvoMining reveals novel antibiotic biosynthetic gene clusters in *Actinobacteria.*** *César Aguilar*, Hilda E. Ramos Aboites, Nelly Sélem Mojica, Paulina M. Mejía Ponce, Pablo Cruz Morales. Francisco Barona Gómez. Unidad de Genómica Avanzada. CINVESTAV. IPN.
127.	**Ureolytic bacteria as Geological Agents: Their role in metal carbonates formation in mine tailings.** *Jose Luis Aguirre Noyola*, Gustavo Cuaxinque Flores, Esperanza Martinez Romero, Oscar Talavera

	Mendoza**.** Centro de Ciencias Genómicas, UNAM
128.	**Changes observed in insulin and IL-15 levels in patients with pulmonary tuberculosis with or without type 2 diabetes mellitus.** Eduarda Cerón, Julia Moreno, Manuel Castillejos, Demetrio Bernal, *Noé Alvarado*. Instituto Nacional de Enfermedades Respiratorias "Ismael Cosío Villegas".
129.	**Functional identification of two operon related to the use of specific carbohydrates of tissues of animal origin, in *Avibacterium paragallinarum.*** *Alma Gabriela Bárcenas Villalobos*, María Elena Cobos Justo, Patricia Sánchez Alonso, Erasmo Negrete Abascal, Candelario Vázquez Cruz. Centro de Investigaciones en Ciencias Microbiológicas. BUAP
130.	**The cytotoxicity of Thymus vulgaris in eukaryotic cells.** Jesús Rodrigo Morales Baéz, Mirian Becerril Ramírez, *Luis Eduardo Canul Chulim*, Germán Rubén Aguilar Gutiérrez, Carlos Cabrera Maldonado, Marcos Flores Encarnación. Facultad de Medicina. BUAP
131.	**Mutation and phenotypic study of the gene AMK58_RS02950 that encodes a proposed hybrid protein (GGDEF-EAL) of *Azospirillum brasilense* Sp7.** *Diana Carolina Castro Fernández,* Alberto Ramírez Mata and Beatriz Eugenia Baca. Centro de Investigaciones en Ciencias Microbiológicas, BUAP.
132.	**Indole-3-acetic acid biosynthesis by the bacterium *Azospirillum brasilense* cultured under a biogas atmosphere allows its beneficial association with microalgae.** Jorge Alejandro Barbosa Nuñez, Oskar Alejandro Palacios, Raúl Snell Castro, Rosa Isela Corona González, *Francisco Javier Choix Ley.* CUCEI-Universidad de Guadalajara.
133.	***iorA* gene is involved in IAA biosynthesis in *A. brasilense* Sp7.** *Ricardo Cuatlayotl Olarte*, Cynthia Marcos Jimenez, Alberto Ramirez Mata, Beatriz Eugenia Baca. Centro de investigaciones en ciencias microbiológicas, BUAP.
134.	**The effect of different carbon sources in *Kluyveromyces marxianus* growth kinetics.** *Pablo Diaz de León Trujillo*, Rafael de la Huerta Benites, Veronica Corssen Blando, Claudia Ivette Cisneros Reyes, Rafael Torres Guardado, Julia del Carmen Martínez Rodríguez. DDCyT. Universidad Autónoma de Guadalajara,
135.	**Physicochemical analysis of four mixed cultures prepared with different strain combinations.** Blanca Estela García Caballero, Raúl Rodríguez Herrera, Silvia Marina González Herrera, Cristóbal Noé Aguilar González, Olga Miriam Rutiaga Quiñónes and Adriana Carolina Flores Gallegos. Chemical Sciences Faculty. Coahuila Autonomus University
136.	**Bioprospecting for Actinobacterias isolated from tropical soils with antimicrobial properties.** *Viviana Gutiérrez Foronda*, Evvy Rico Velazco, Navila De la Cruz Ceferino, Susana De la Rosa Garcia, Sergio Gómez Cornelio. División Académica de Ciencias Biológicas, Universidad Juárez Autónoma de Tabasco
137.	**Seeding public goods is essential for maintaining cooperation in *Pseudomonas aeruginosa.*** *Luis Daniel Loarca Alvarez,* Rodolfo García Contreras. Departamento de Microbiología y Parasitología, Facultad de Medicina. UNAM.
138.	**Engineering a biosynthetic pathway for the production of novel bioactive diterpenoids.** *Dalia Magaña-Van Den Hengel*, Verónica Rodríguez-Celestino, Sergio Sánchez, Sara Centeno Leija, Hugo Serrano Posada. Tecnoparque CLQ, Universidad de Colima.
139.	**Characterization of PGPR isolated from rhizospheric soils of *Agave angustifolia.*** *Cristian Medina Nieto*, Erick Marrón Montiel. Tecnológico de Estudios Superiores de Villa Guerrero
140.	**Antimicrobial metabolites from fungal strains isolated from agroindustrial waste products.** Benjamín Hernández Figueroa, Luis Fernando Sepúlveda Sáenz, *Guadalupe Virginia Nevárez Moorillón.* Facultad de Ciencias Químicas. Universidad Autónoma de Chihuahua.
141.	**Antioxidant peptides from whey fermentation and bacteriocin production by *Enterococcus faecium* strains.** María Georgina Venegas Ortega, Adriana Carolina Flores Gallegos, Raul Rodriguez Herrera, Jose Luis Martínez Hernández, Cristóbal Noe Aguilar González, *Guadalupe Virginia Nevárez Moorillón*. Facultad de Ciencias Químicas. Universidad Autónoma de Chihuahua.
142.	**Proteins of *Helicobacter pylori,* which scavenge iron from human sources.** *José de Jesús Olivares-Trejo*, Juan Mosqueda, Cristhian Sánchez Cruz, Marco Antonio González López. Posgrado en Ciencias Genómicas, Universidad Autónoma de la Ciudad de México
143.	**Efecto sobre el crecimiento de células de las líneas celulares de cáncer HCT15, MDA-MB231, MCF-7, PC3, HeLa y HEP-G2 de metabolitos secundarios producidos por Actinobacterias.** *Dolores Viridiana Patiño Parra***.** BUAP
144.	**Participation of phosphatases in the solubilizing activity of phosphates in *Gluconacetobacter diazotrophicus* Pal5.** *Alma Rosa Pérez Rodríguez*. Luis Javier Martínez Morales. Lucía Soto Urzúa. Centro de Investigaciones Microbiológicas, Instituto de Ciencias, BUAP**.**
145.	**The hemolysin of *Gluconacetobacter diazotrophicus.*** *Ailyn María Fernanda Ramírez González*, Marcos Flores Encarnación, Ricardo Carreño López, Silvia del Carmen García García. Facultad de Medicina. BUAP.

146.	**The participation of the pyruvate carboxylase and phosphoenolpyruvate carboxylase enzymes in the aerobic metabolism in *Rhizobium phaseoli* CIAT652.** *Alma Ruth Reyes González*, Carmen Vargas Lagunas, Michael Dunn, Lourdes Girard, Jaime Mora. Laboratorio de Biología de Sistemas y Biología Sintética, Centro de Ciencias Genómicas, UNAM
147.	**Biochemical characterization of two proteins involved in the metabolism of polyhydroxybutyrate (PHB) in *Azotobacter vinelandii.*** *Jessica Ruiz Escobedo*, Holjes Salgado Lugo, Josefina Guzmán, Libertad Adaya García, Alma Reyes González, Guadalupe Espín, Daniel Segura. Instituto de Biotecnología, UNAM
148.	**Purification of the recombinant Fur1248 protein of *Gluconacetobacter diazotrophicus* Pal5 strain: Factors that affect the oligomerization state.** Brenda Estefany Roldán León, Luis Javier Martínez Morales, Beatriz Eugenia Baca, *Lucía Soto Urzúa***.** Centro de Investigaciones en Ciencias Microbiológicas, ICUAP-BUAP.
149.	**Flow cytometry assessment of membrane integrity of lactic acid bacteria maintained under preservation.** José Martín Ruvalcaba Gómez, *Lily Xochilt Zelaya Molina*, Edith Rojas Anaya, Bibiana Ríos Galicia, Ramón Ignacio Arteaga Garibay. Centro Nacional de Recursos Genéticos-INIFAP.

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150.	**Nodules of *Phaseolus vulgaris*: the unexpected place for *Rhizobium* conjugation.** *Luis Alfredo Bañuelos Vazquez*, Gonzalo Torres Tejerizo, Lourdes Girard, Laura Cervantes de la Luz, David Romero, Susana Brom. Centro de Ciencias Genómicas, UNAM
151.	**Structural genomics for nonribosomal peptide synthetases analysis in symbiotic bacteria**. *Brandon Bueno Hernández*, Edgar Dantán González**.** Centro de Investigación en Biotecnología, Universidad Autónoma del Estado de Morelos,
152.	**Genomic analysis of *Rhizobium* prophages.** *Patricia Bustos*, Rosa I. Santamaría, Arun Reverte Vera, Luis Lozano, Gabriela Guerrero, Víctor González. Centro de Ciencias Genómicas, UNAM
153.	**Intra- and inter-plasmid regulation of conjugative transfer in *Sinorhizobium.*** *Laura Cervantes De la Luz*, Gonzalo Torres Tejerizo, Eunice López Fuentes, Fabiola Miranda Sánchez, Susana Brom Klanner. Centro de Ciencias Genómicas, UNAM.
154.	**Unveiling the elusive nature of *Clavibacter michiganensis* subsp. *michiganensis* pathogenicity after a functional phylogenomics approach.** *Ámbar G. Gómez Díaz*, Alan G. Yañez Olvera, Francisco Barona Gómez. Unidad de Genómica Avanzada LANGEBIO CINVESTAV IPN
155.	**Bioinformatic analysis of aerobic carbon monoxide dehydrogenase from *Streptomyces thermocarboxydus*.** *Maria Paula Gómez Román,* Ajit Kumar Passari and Sergio Sánchez. Instituto de Investigaciones Biomédicas, UNAM
156.	**Translation efficiency and codon usage bias among prokaryotes.** *González Serrano Francisco Maximiliano*, Delaye Arredondo Luis José**.** Laboratorio de Genómica Evolutiva, CINVESTAV.
157.	**Evolutionary and Transmission Dynamics of a highly prevalent Acinetobacter baumannii lineage (ST758) in Mexico**. *Lucía Graña Miraglia,* Santiago Castillo Ramírez
158.	**Identification of the gene involved in biosynthesis of polysaccharide produced by *Lactobacillus hilgardii* WKGMX in water kefir.** *Pamela Heredia del Orbe*, Violeta Larios Serrato, Lourdes Villa Tanaca, César Hernández Rodríguez. Escuela Nacional de Ciencias Biológicas, IPN.
159.	**Metagenomic analyses uncover the differential effect of azide treatment on bacterial community structure by enriching a specific Cyanobacteria present in a saline-alkaline environmental sample.** *Luis Mario Hernández Soto*, Francisco Martínez Abarca, Daniel Montiel Lugo, Hugo Ramírez Saad, José Félix Aguirre Garrido. Universidad Autónoma Metropolitana-Lerma.
160.	**Transcriptome analysis of a conditional knockdown mutant in an essential gene participating in cell division and cell polarity in *Rhizobium etli* CFN42.** *Sofía Martínez Absalón*, Carmen Guadarrama, Araceli Dávalos, Susana Brom, David Romero. Centro de Ciencias Genómicas UNAM
161.	**A detailed analysis of the sets of essential genes in *Pseudomonas aeruginosa* strains PAO1 and PA14.** *Enrique Martínez Carranza*, Luis David Alcaráz Peraza, Luis Servín González, Gloria Soberón Chávez. Instituto de Investigaciones Biomédicas, UNAM
162.	**The essential genes of *Pseudomonas aeruginosa* are well conserved in *Azotobacter vinelandii*.** *Enrique Martínez-Carranza*, Luis David Alcaráz Peraza, Luis Servín González Gloria Soberón Chávez. Instituto de Investigaciones Biomédicas, UNAM
163.	**Stability of Drug Resistance in Bacterial Population.** *Sandra Mayoral Álvarez*, Rafael Peña Miller y Ayari

	Fuentes Hernández**.** Centro de Ciencias Genómicas, UNAM
164.	**Transcriptional expression and phylogenetic analysis of outer membrane protein genes (OMP) *alpA* and *alpB in Helicobacter pylori*.** *Daniela Meléndez Sánchez,* Margarita de la Luz Camorlinga Ponce, Jorge Alberto Gonzalez y Merchand. Escuela Nacional de Ciencias Biológicas, IPN.
165.	***In silico* approach of potential like binding proteins of Cry *Bacillus thuringiensis* in mammals** *Arnold Mendoza Osorno*, Carlos Javier Sanchez, Gabriela E Olguin Ruiz, Hilda Perez Cervantes Ernesto Alarcon Hernandez E, Gloria G Guerrero M. Escuela Nacional de Ciencias Biológicas. IPN.
166.	**Environmentally driven gene content convergence and the *Bacillus* phylogeny**. Ismael Hernández González, *Gabriel Moreno Hagelsieb*, Gabriela Olmedo Álvarez, Department of Genetic Engineering, CINVESTAV Irapuato
167.	**Characterization of local adaptations in the genus Virgibacillus through pangenomic analysis.** *Marisol Navarro Miranda*, Manuel García Ulloa Gámiz, Mariette Viladomat Jasso, Valeria Souza Saldiva. Instituto de Ecología, UNAM
168.	**Genomic analysis reveals genetic markers that can be used for the specific identification of *Campylobacter fetus*, an important livestock pathogen.** *Daniel Rivera Mendoza*, Víctor H. Bustamante, Deyanira Pérez Morales. Centro de Investigación en Biotecnología, Universidad Autónoma del Estado de Morelos
169.	**Cophylogenetic analysis suggests cospeciation between scorpions and their Mollicutes symbionts.** *Mónica Rosenblueth*, Luis M. Bolaños, Tonalli García Santibañez, Amaranta Manrique de Lara, Analí Migueles Lozano, Citlali Gil Aguillón, Valeria Mateo Estrada, Francisco González Serrano, Carlos E. Santibáñez López, Esperanza Martínez Romero. Programa de Ecología Genómica, Centro de Ciencias Genómicas, UNAM
170.	**Gut microbiome from *Goepherus berlandieri* tortoises contain nitrogen fixing *Klebsiella variicola.*** *Mónica Rosenblueth*, Diana Paola Montes Grajales, Esperanza Martinez Romero. Programa de Ecología Genómica, Centro de Ciencias Genómicas, UNAM.
171.	**Whole genome sequencing of *Mycolicibacter kumamotonensis*: in search of structural and functional characteristics of this potentially pathogenic microorganism**. *Ricardo Sánchez Estrada*, Mauricio Flores Valdez, Alfonso Méndez Tenorio, Ana Laura Cortés Cueto, Diana Angélica Aguilar Ayala, Jorge Francisco Cerna Cortés, Sandra Rivera Gutiérrez, Jorge Alberto González y Merchand. Departamento de Microbiología. ENCB IPN
172.	**Genomic Diversity of Bacteriophages Associated to Rhizobium a Nitrogen-Fixing Bacteria** . *Rosa I. Santamaría*, Jannick Van Cauwenberghe, Patricia Bustos, Soledad Juárez, & Víctor González. Centro de Ciencias Genómicas, UNAM.
173.	**Potential of novel polyketide and non-ribosomal peptide production in marine-derived actinomycetes from the coast of Yucatan.** *Remes-Rodríguez, C.A.*, Márquez-Velázquez N. A., Prieto-Davó, A. Posgrado en Ciencias del Mar y Limnología, UNAM
174.	**Study of enzymatic promiscuity at the enzyme level, family and metabolic pathway, and its role in genomic mining of natural products.** *Nelly Sélem Mojica*, César Aguilar, Eduardo Martínez, Hilda E. Ramos Aboites, Francisco Barona Gómez. LANGEBIO. Unidad de Genómica Avanzada. CINVESTAV, IPN.
175.	**Two genetic variants of a D6-like plasmid-prophage are associated with specific IncA/C plasmid types in the emerging *Salmonella* Typhimurium ST213 genotype in Mexico**. *Claudia Silva*, Edmundo Calva, Marcos Fernández Mora, José L. Puente, Pablo Vinuesa. Departamento de Microbiología Molecular, Instituto de Biotecnología, Programa de Ingeniería Genómica, Centro de Ciencias Genómicas UNAM.
176.	**Comparative genomics of bacterial endosymbionts of the Mexican medicinal leeches.** *Víctor Manuel Sosa Jiménez*, Alejandro Francisco Oceguera Figueroa. Instituto de Biología, UNAM.
177.	**How to live under strong selection pressures and be successful? The case of Pseudomonas mendocina P6115, a bacterium isolated from mine tailings.** *Lizbeth Victoria Vazquez Hernandez*, Violeta Larios Serrato, Alejandra Miranda Carrazco, María de Lourdes Villa Tanaca, César Hugo Hernández Rodríguez. Departamento de Microbiología. ENCB. IPN.
178.	**Plant Cell Wall Degrading Enzymes diversity of Mexican *Clavibacter michiganensis* subsp. michiganensis strains.** *Alan G. Yañez Olvera*, Lorena Rodríguez Orduña, Francisco Barona Gómez. Evolution of Metabolic Diversity Laboratory, Unidad de Genómica Avanzada LANGEBIO, CINVESTAV-IPN.

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179.	**Associated bacteria to urethritis in men who have sex with men (MSM).** *Aguilera Arreola Ma. Guadalupe*, Peña Toribio Arturo, García Mendiola Rebeca Eunice, Contreras Rodríguez Araceli. Laboratorio de Bacteriología Médica, ENCB, IPN.
180.	**Effect of metabolites produced by *Bacillus atrophaeus* on the activity of enzymes involved in the defense system of Hass avocado (*Persea Americana*).** *Bañuelos González, Miriam del Carmen,* Aguilera Aguirre, Selene, López García, Ulises, Montalvo González, Efigenia, Chacón López, Alejandra. Tecnológico Nacional de México Instituto Tecnológico de Tepic.
181.	**Infection of *Phratylenchus spp*. in roots colonized by native arbuscular mycorrhizal fungi of *Zea mays* L.** Mónica Alvarado Herrejón, John Larsen, Mayra E. Gavit, Pablo Jaramillo Lopé, Miguel Martínez Trujillo, *Yazmín Carreón Abud.* Universidad Michoacana de San Nicolás de Hidalgo.
182.	**Arbuscular mycorrhizal fungi protect plants of heavy metals.** Nancy Rosita Rosas Jacuinde, María de los Ángeles Beltrán Nambo, Patricia Ríos Chávez, Miguel Martínez Trujillo, *Yazmín Carreón Abud*. Facultad de Biología. Universidad Michoacana de San Nicolás de Hidalgo.
183.	**The role of different amino acid residues of the SehB antitoxin on the virulence of *Salmonella enterica serotype Typhimurium.*** *Fernando Chimal Cázares,* Jorge A. González y Merchand Miguel A. De la Cruz. Hospital de Pediatría. Centro Médico Nacional Siglo XXI.
184.	**Analysis of the expression of SNAP23 and SNAP25 proteins during infection in macrophages by *Brucella melitensis*.** *Josué Saúl Cruz Rabadán*, Alfredo Castañeda Ramírez, Antonio Verdugo Rodríguez. Facultad de Medicina Veterinaria y Zootecnia, UNAM.
185.	**Induction of *Salmonella* Typhimurium expression of PDL1 on B cells is independent of the mechanisms involved in its persistence.** *Alonso Daniel Cruz Cruz*, Leopoldo Flores Romo y Vianney Ortiz Navarrete. Departamento de Biología Celular. CINVESTAV IPN
186.	***Rhizobium rhizogenes* to transform *Capsicum annuum* and protection against root pathogens using bacteria or fungus as biocontrol agents.** *Yadira Yumiko De la Cruz Rodríguez*, Jaime Sagredo Beltrán, Alejandro Alvarado Gutiérrez, Miguel Alvarado Rodríguez, Saúl Fraire Velázquez. Universidad Autónoma de Zacatecas.
187.	**Distinct phenotypic and genomic characteristics of two Mexican *Pectobacterium carotovorum* strains of the subspecies *brasiliensis.*** *De Sandozequi Andrés*, Delia Narváez Barragán, Mabel Rodríguez, Karel Estrada, Omar E. Tovar Herrera, Lorenzo Segovia and Claudia Martínez Anaya. Instituto de Biotecnología, UNAM
188.	**Vaccine efficacy of BCG in bovine tuberculosis by monitoring response to ESAT-6 and CFP-10 antigens.** *Fernando Díaz Otero*, Laura Jaramillo Meza, Anabelle Manzo Sandoval, Rafael Pérez González. CENID-SAI, INIFAP.
189.	**Effect of coinfection by *Fasciola hepatica* and *Mycobacterium bovis* on bovine tuberculosis immunodiagnosis.** *Fernando Díaz Otero*, Laura Jaramillo Meza, Xitli García López, Héctor Quiroz Romero, Fernando Diosdado Vargas. CENID-SAI, INIFAP.
190.	**Monitoring autophagic flux induced by *Haemophilus influenzae* on HEp-2 cells observed by TEM.** *María del Rosario Espinoza Mellado*, Judith Taba Santos, Edgar Oliver López Villegas, Silvia Giono Cerezo. Departamento de Investigación ENCB. IPN
191.	**Saliva an innate defense in oral cavity: Study of histatin 5 effect in *Streptococcus mutans* morphology and Cystatin C in the immunomodulation of human gingival fibroblasts incubated with *Porphyromonas gingivalis.*** *Ana María Fernández Presas*, Yamilli Márquez Torres, Blanca Blancas Luciano, Lourdes Lanzagorta Rebollo. Facultad de Medicina. UNAM
192.	**Actinobacteria associated with indigenous maize soil from the traditional *milpa* agroecosystem display antagonistic activity against the phytopathogenic fungus *Fusarium graminearuM.*** *Héctor García López*, Rosina Cabrera, Jesus Antonio Orozco Avitia, Eneas Aguirre von Wobeser, Mayra de la Torre. Centro de Investigación y Desarrollo en Agrobiotecnología.
193.	**Study of the virulence of fungi of medical interest in *Galleria mellonella.*** *Romina Guzmán Barrón*, Nancy E. Lozoya-Pérez, Jessica Ornelas Gutiérrez, Andrea Johana Falcón Aguirre, Leonardo Padró Villegas, Héctor Manuel Mora Montes. Universidad de Guanajuato
194.	**Interaction in the production of biofilm between *Candida kefyr*, *Escherichia coli* and *Streptococcus dysgalactiae* isolated from bovine mastitis.** Israel Daniel Ricardo González, *Laura Hernández Andrade*, Ana Lilia del Monte Gutiérrez, Marco Antonio Santillán Flores, Miguel Ángel Blanco Ochoa, Luis Octavio Campuzano Reyes, Alberto Oswaldo Jiménez Saavedra. Facultad de Medicina Veterinaria y Zootecnia UNAM.
195.	**Immune response of vaccinated calves against bovine tuberculosis defined *Mycobacterium bovis* antigens.** *Jaramillo Meza Laura*, Díaz Otero Fernando, Clara I. Espitia Pinzón Rafael Pérez González,

	Anabelle Manzo Sandoval· CENID-SAI, INIFAP,
196.	**Antigenic recognition in vaccinated calves with BCG, or with protein extract of *Mycobacterium bovis.*** *Jaramillo Meza Laura*, Díaz Otero Fernando, Hernández Andrade Laura, Manzo Sandoval Anabelle· CENID-SAI, INIFAP.
197.	***In silico* characterization of *Mycobacterium tuberculosis* PE_PGRS18 protein and its immunogenicity.** *Eva Nélida Jimenez Ruiz*, Andrea Monserrat Negrete Paz, Gerardo Vázquez Marrufo, Ma. Soledad Vázquez Garcidueñas. Universidad Michoacana de San Nicolás de Hidalgo
198.	**Curli, a fitness factor of uropathogenic *Escherichia coli.*** *Víctor M. Luna Pineda*, Vicenta Cázares Domínguez, Sara Ariadna Ochoa Pérez, Ariadnna Cruz Córdova, Mextli Bermejo Haro, Karina Espinosa Mazariego, Gerardo Escalona Venegas y Juan Xicohtencatl Cortes. Hospital Infantil de México "Federico Gómez".
199.	**Effect of *Salmonella* Newport internalized in cherry tomatoes in the colonization of the gastrointestinal tract of Balb/c mice.** *Mancilla Becerra L*. M., Barba León J, Armas Puente P., Ramírez Jiménez C. L., Pedroza Roldán C. Ruiz López M. A., González Aguilar D. G. and Martínez Chávez L. and Martínez Gonzáles N. CUCBA. Universidad de Guadalajara
200.	**C*ampylobacter fetus* induces proinflamatory response in bovine endometrial epithelial cells.** Campos Múzquiz Lizeth Guadalupe, Méndez Olvera Estela Teresita, *Martínez Gómez Daniel*· División de Ciencias Biológicas y de la Salud, UAM Xochimilco,
201.	***Helicobacter pylori* and expression of miR-411-5p, miR-548d-3p and miR-892c-5p in patients with chronic gastritis and gastric cancer.** Sandra Inés Lorenzo Nazario, Judit Alarcón Millán, Josefina Atrisco Morales, Salomón Reyes Navarrete, José María Tremes Roche, Hilda Jiménez Wences, Julio Ortíz Ortíz, Miguel Ángel Mendoza Catalán, Berenice Illades Aguiar, *Dinorah Nashely Martínez Carrillo*, Gloria Fernández Tilapa. Facultad de Ciencias Químico Biológicas, Universidad Autónoma de Guerrero.
202.	**Chemokine dysregulation during HIV and TB Co-infection.** *Yazmin B. Martinez Martinez* Matt B. Huante, Sadhana Chauhan, George Golovko, Yuriy Fofanov, Benjamin Gelman, Janice J. Endsley. Department of Microbiology and Immunology, UTMB, Galveston, TX, USA.
203.	**Rescue of the thermosensitive mutation of peptidyl t-RNA hydrolase from *Escherichia coli* by three Pths from *Entamoeba histolytica* modified by directed mutagenesis**. *Karina Moreno Escandón*, Sara Abaunza Alvarado, María Elizabeth Reséndiz Juárez, María Margarita Carranza Cruz, Milagros Gómez Nieto, Armando Pérez Rangel, José Manuel Hernández, Gloria León Avila. Departamento de Zoología, ENCB, IPN
204.	**Selection, characterization and evaluation of TCR-like domain antibodies against Ag85Bp$_{199-207}$/HLA-A*0201 and ESAT6$_{p82-90}$/HLA-A*0201 OF *Mycobacterium tuberculosis.*** *Paola A. Ortega*, Cristina Parada, Kees Franken, Tom H.M. Ottenhoff, Juraj Ivanyi· Clara Inés Espítia**.** Instituto de Investigaciones Biomédicas, UNAM
205.	**Development of an *in vitro* granuloma model for the study of *Mycobacterium tuberculosis* antigens.** *David Ortega Tirado*, Aldo Arvizu Flores, Carlos Velázquez, Clara Espitia, Adriana Sumoza Toledo, Adriana Garibay Escobar. Departamento de Ciencias Químico Biológicas, Universidad de Sonora.
206.	**Recombinant enolase from *Haemophilus influenzae*: characterization as a binding protein to collagen, fibronectin and human plasmatic proteins.** *Yesenia Osorio Aguilar,* María Cristina González Vázquez, Diana Elizabeth Hernández Cerón, Deysi Alejandrina Cabrera Segura, Alejandro Carabarín Lima, Ygnacio Martínez Laguna. Patricia Lozano Zaraín, Rosa del Carmen Rocha Gracia. Centro de Investigaciones en Ciencias Microbiológicas. BUAP.
207.	**Suppression of the Peptidyl tRNA hydrolase (*Ts*) mutation of *Escherichia coli* by Pths A and B of two parasitic protozoa: *Giardia lamblia* and *Trypanosoma cruzi.*** *María Elizabeth Reséndiz Juárez***,** Karina Moreno Escandón, Armando Pérez Rangel, Milagros Gómez Nieto, José Manuel Hernández, Gloria León Avila**.** Escuela Nacional de Ciencias Biológicas. IPN
208.	**Mitochondrial antiviral signaling protein (MAVS) expression in MDCK cells infected with Canine Parvovirus**. *Reyes Cruz Tania*, Méndez Olvera Estela Teresita, Martínez Gómez Daniel. Ciencias Biológicas y de la Salud. División de Ciencias Biológicas y de la Salud, UAM Xochimilco.
209.	**Non-tuberculous mycobacteria of various environmental origin: their interaction with human macrophages.** *Sandra Rivera Gutiérrez*, Ana L. Cortés Cueto, Jorge F. Cerna Cortés, L. Patricia Salas Rangel, Jorge A. González y Merchand. Departamento de Microbiología, ENCB-IPN.
210.	**Molecular toolbox for harnessing plant-microbe interactions with biotechnology potential.** *Jorge Rocha*, Daniel Solis, Gabriela Gastelum, Lori R. Shapiro, Gustavo Viniegra and Mayra de la Torre· Centro de Investigación y Desarrollo en Agrobiotecnología Alimentaria.
211.	**Induction of autophagy by *Listeria monocytogenes* strains isolated from clinical products.** *Oscar*

	Rodolfo Rodas Suárez, Edith Johana Ortiz Reyes, Edson Resendiz Ortiz, María del Rosario Espinoza Mellado· Central de Instrumentación de Microscopía. ENCB–IPN
212.	**LngA, CstH, and FliC in the ETEC E9034A participate in adherence to intestinal cells HT-29 and LS174T.** *Ricardo Rodriguez Martínez*, Ariadnna Cruz Córdova, Sara Ochoa Pérez, Karina Espinosa Mazariego, Gerardo Escalona Venegas, Víctor Luna Pineda, Vicenta Cázares Domínguez, Graciela Castro Escarpulli, Juan Xicohtencatl Cortes. Hospital Infantil de México Federico Gómez.
213.	**Interferon-gamma-activated macrophages present antigens of *Burkholderia cenocepacia* to T-cells by class I and II major histocompatibility complex molecules.** *Roberto Rosales Reyes*, Paola Garza Villafuerte, Daniela Vences Vences, Rubi Aca Teutle, Daniel F. Aubert, Vianney F. Ortiz Navarrete, Laura C. Bonifaz, Julio Cesar Carrero Sánchez, Alfonso Olivos García Miguel A. Valvano, José Ignacio Santos Preciado. Facultad de Medicina, UNAM.
214.	**Isolation and molecular identification of *Pseudomonas sp* from larvae of *Aedes aegypti*, an arbovirus vector.** *Angel Rubio Miranda*, Lorena González López, Antonio Celestino Montes, Daniel A. Estrada Barcenas, Juan Carlos Estrada Mora, Bibiana Chávez Munguia, Fidel de la Cruz Hernández Hernández. Departamento de Infectómica y Patogénesis Molecular. Colección Nacional de Cepas Microbianas y Cultivos Celulares. *CINVESTAV IPN.*
215.	**Participation of α5β1/FAK Integrin Pathway in the *Staphylococcus aureus* Internalization Regulated by Fatty Acids in Bovine Mammary Epithelial Cells.** Monica Guadalupe Sánchez Ceja, *María Guadalupe Salgado Lora*, Alejandra Ochoa Zarzosa, Joel Edmundo López Meza. Centro Multidisciplinario de Estudios en Biotecnología-FMVZ. Universidad Michoacana de San Nicolás de Hidalgo.
216.	**Regulation and role in colonization of the *csu*-like fimbrial operon of *Citrobacter rodentium*.** *Zeus Saldaña Ahuactzi*, Karla Fernanda Ramírez-González, Gustavo G. Caballero-Flores, Liliana Medina-Aparicio, Stephanie Ortiz-Jiménez, Alejandra Vázquez Ramos, José Luis Puente. Instituto de Biotecnología, UNAM
217.	**Prolactin and 17β–estradiol induce pro-inflammatory cytokines in bovine mammary epithelial cells inhibiting *Staphylococcus aureus* internalization and modulating epigenetic marks.** *María Guadalupe Salgado Lora*, Ricardo Ivan Medina Estrada, Joel Edmundo López Meza, and Alejandra Ochoa Zarzosa. Facultad de Medicina Veterinaria y Zootecnia, Universidad Michoacana de San Nicolás de Hidalgo.
218.	**Role of miR-200a in *Mycobacterium tuberculosis* H37Rv infection".** *Brisa Marcela Sánchez Camacho*, Olga Noemi Hernández de la Cruz, Mauricio Castañón Arreola. Universidad Autónoma de la Ciudad de México.
219.	**Phenotypic characterization of multidrug-resistant *Salmonella enterica* serovar Typhimurium sequence type (ST) 213 strains isolated in Mexico.** *Isela Serrano Fujarte*, Claudia Silva Romero, Francisco García del Portillo, José Luis Puente. Instituto de Biotecnología, UNAM.
220.	**Functional analysis of the Type VI Secretion Systems in the opportunistic pathogen *Enterobacter cloacae.*** *Jorge Soria Bustos*, Jorge A. González y Merchand, and Miguel Ángel De la Cruz. Hospital de Pediatría. Centro Médico Nacional Siglo XXI.
221.	**Epidemiological and clinical characteristics of Coronavirus infections in patients treated at INER (November 2013- March 2018).** *Daniel Valencia Trujillo*, Eduardo Becerril Vargas, Arturo Martínez Orozco, Christian Mireles Dávalos, Mario Mujica Sánchez, Elena Jiménez Martínez, Andrea Delgado Cueva, Elia Flores Pérez. Instituto Nacional de Enfermedades Respiratorias.
222.	**miR-24-3p and miR-142-3p expression and *Helicobacter pylori* infection in patients with gastric pathology.** *Gladys W. Valente Niño*, Dinorah N. Martinez Carrillo, Carlos A. Castañón Sánchez, Josefina Atrisco Morales, Hilda Jiménez Wences, Oscar Peralta Zaragoza, Salomón Reyes Navarrete, Gloria Fernández Tilapa. Facultad de Ciencias Químico Biológicas, Universidad Autónoma de Guerrero.
223.	**Imaging analysis of the simple and double mutants in *fliC*, *fimH*, and *csgA* genes of uropathogenic *Escherichia coli* using Transmission Electronic Microscopy.** *Rubí Gabriela Vega Hernández*, Víctor Manuel Luna Pineda, Vicenta Cazáres Domínguez, Sara Ochoa Pérez, Karina Espinosa-Mazariego, Gerardo Escalona-Venegas, Ariadnna Cruz-Córdova and Xicohtencatl Cortes Juan. Hospital Infantil de México "Federico Gómez".
224.	**Macrophages infection with dormant *Mycobacterium tuberculosis*: transcriptional analysis.** *Samantha Yong-Mendoza,* Angélica Yong Mendoza, Xaremi Pamela Montiel Zúñiga, Emiliano Campoy Flores, Claudia Verónica Zaga Clavellina, Moisés León Juárez, Rodrigo García Herrera, Sandra Rivera Gutiérrez, Jorge Francisco Cerna Cortés, Jorge Alberto González y Merchand, Addy Cecilia Helguera Repetto. Departamento de Microbiología, ENCB, IPN.
225.	**Effect of a monoclonal antibody IgA anti-lipid A in the polymyxin B sensitivity of *Salmonella*.** *Martha Elena Zaragoza Martìnez*, María de los Ángeles Padilla Mendoza and Emma Isabel Melendro Lozano. Facultad de Medicina, UNAM. Hospital General de México Dr. Eduardo Liceaga SS.

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227.	**Detection of *Serratia marcescens* isolates obtained from pediatric patients in a tertiary care hospital in Mexico City.** *Acosta Méndez Héctor Emmanuel*, Aparicio Ozores Gerardo, Merida Vieyra Jocelin, Tapia Reyes Alejandro, De Colsa Ranero Agustín, Aquino Andrade Alejandra. Instituto Nacional de Pediatría (INP).
228.	**Osteomyelitis with Panton- Valentine Leukocidin producing *Staphylococcus aureus* strains, experience in a tertiary pediatric hospital in Mexico city.** *Nancy Evelyn Aguilar Gómez*, Alejandra Aquino Andrade, Guillermo José Vázquez Rosas, Jocelin Mérida Vieyra, Oscar Daniel Isunza Alonso, Oscar Tamez Rivera, Agustín de Colsa Ranero. Department of Pediatric Infectious Diseases, Instituto Nacional de Pediatría.
229.	**Detection of some virulence factors in *Salmonella* sp strains of environmental origin.** Denisse Flores Martínez, *Ana Karen Álvarez Contreras*, Iván Natividad Bonifacio, Carlos Vázquez Salinas, Elsa Irma Quiñones Ramírez. Departamento de Microbiología, ENCB. IPN.
230.	**Presence of virulence markers in *Vibrio parahaemolyticus* strains isolated from oysters.** David Anselmo Nava, Iván Natividad Bonifacio, *Ana Karen Álvarez Contreras*, Marcos Francisco Hernández Robles, Elsa Irma Quiñones Ramirez, Carlos Vázquez Salinas. Departamento de Microbiología, ENCB, IPN.
231.	**Comparison of internalization in cherry tomatoes between *Salmonella* Montevideo, Newport, Saintpaul and non-pathogenic *E. coli.*** *Aurora Dolores Arista Regalado*, Jeannette Barba León, Víctor Humberto Bustamante, Lilia Mercedes Mancilla Becerra, Rocío Acosta Martínez. Centro Universitario de Ciencias de la Salud. Universidad de Guadalajara
232.	**Epidemiological characterization of virulence factors of Pseudomonas spp. from the "Hospital Central Ignacio Morones Prieto" of San Luis Potosí, SLP.** *Nallely Sarai Badillo Larios*, Edgar A. Turrubiates Martínez, Luis Fernando Pérez González, Perla del Camen Niño Moreno. Centro de Investigación de Ciencias de la Salud y Biomedicina, UASLP.
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235.	**Genotyping of uropathogenic *Escherichia coli* (UPEC) strains isolated from urinary tract infections during pregnancy in Culiacan, Sinaloa.** *Ana María Castañeda Meléndrez*, Ignacio Osuna Ramírez, Patricia Catalina García Cervantes, Rodolfo Bernal Reynaga. Facultad de Ciencias Químico-Biológicas. Universidad Autónoma de Sinaloa.
236.	**Isolation and identification of bacterial pathogens from yellow tail snapper (*Ocyurus chrysurus*) and whiteleg shrimp (*Penaeus vannamei*).** *Patricia Isidra Cauich Sánchez,* Amelia Isabel Paredes Trujillo, Oswaldo de Jesús González Yam, Rosa Cristina Canul Puc, Ma. Leopoldina Aguirre Macedo. ENCB, IPN.
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240.	**Antimicrobial activity from *Lactococcus lactis* 115 isolated from atole agrio, from Villahermosa, Tabasco.** Carlos A. Sosa Aguilar, Carmen Wacher Rodarte, *Gloria Díaz Ruiz.* Departamento de Alimentos y Biotecnología, Facultad de Química, UNAM.
241.	**Detection of *Trypanosoma cruzi* by municipality of the state of Morelos in donors of the Hospital General Regional No. 01, del Instituto Mexicano del Seguro Social (IMSS) of Cuernavaca, Morelos.**

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242.	**Effect of the association on co-cultivation of *Listeria monocytogenes* with *Bacillus cereus* in the biofilm formation.** *María del Rosario Espinoza Mellado*, Mariana Macías Romero, Gloria Abigail Vilchis Garduño, Oscar Rodolfo Rodas Suárez. Departamento de Microbiología, ENCB. IPN.
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244.	**Incidence of *Chlamydia trachomatis* infections in medical students of third and fourth semester in a private University.** *Janeth Gómez García*, Julieta Ivonne Castro Romero, María Crystal Columba Palomares, Nallelyt Segundo Arizmendi. Universidad Autónoma del Estado de Morelos.
245.	**Determination of *C. difficile* from diarrheal samples of hospitalized patients during the period July 2018-July 2019.** *Nancy Gómez Rivera*, Margarita M.P Arenas Hernández, Rosa Del C Rocha Gracia, María Lilia Cedillo Ramírez, Ygnacio Martínez Laguna, Claudia Fabiola Martínez De La Peña. Centro de Investigación en Ciencias Microbiológicas, BUAP.
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250.	**Prevalence of *vacA / cagA* genotypes *of Helicobacter pylori* in saliva of mystical asymptotic children 6 to 12 years of age (Palo Blanco Guerrero, Mexico).** Ana Karen Salgado Moreno., *Sharon Danne Hernández Becerra*., Tomas Manuel Poblete López., Gloria Fernández Tilapa., Sandra Inés Lorenzo Nazario., Diana Guillermina Soto Flores. Universidad Autónoma de Guerrero
251.	**Characterization of antimicrobial resistance and AIEC phenotype in *Escherichia coli* strains isolated from patients with Inflammatory Bowel Disease in Puebla.** *Norarizbeth Lara Flores* , Edwin Barrios Villa, Julieta Martínez García , Francisco Uriel Navarrete Gutiérrez , Patricia Lozano Zarain , Rosa del Carmen Rocha Gracia. Posgrado en Microbiología, CICM, ICUAP.
252.	**Evaluation of the effect of silver nanoparticles (AgNP's) against pathogenic bacteria causing. foodborne diseases.** *Gloria León Tello*, Enrique Rodríguez Zitlalpopoca, Yasmín Perlita Muñíz Soperánez, Juan Carlos Benítez Serrano, Laura Martínez Pérez. Universidad Autónoma de Puebla.
253.	**Comparative stress response among *Salmonella enterica* strains of ST19 and ST213 genotypes to host digestive tract environment.** *Cristina Linares Salgado*, Diego Alejandro Duarte Ortíz, Adrián Gómez Baltazar, Ma. Soledad Vázquez-Garcidueñas, Gerardo Vázquez Marrufo. Facultad de Ciencias Médicas y Biológicas "Dr. Ignacio Chávez". Universidad Michoacana de San Nicolás de Hidalgo
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258.	***sabA* diversity of *Helicobacter pylori* strains isolated from patients with chronic gastritis.** *Verónica I. Martínez-Santos*, Amairany Carrasco-López, Jocelyn Néstor-Damián, Diana G. Soto-Flores, Salomón Reyes-Navarrete, Dinorah N. Martínez-Carrillo, Carlos A. Castañón-Sánchez, Gloria Fernández-Tilapa. Facultad de Ciencias Químico Biológicas, Universidad Autónoma de Guerrero.
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260.	**Obtention of an IgG monoclonal antibody against the *Brucella abortus* lipopolysaccharide.** *Ivette Mendoza Salazar*, Héctor Romero Ramírez, Shantal Lizbeth Baltierra Uribe, Martha Cecilia Moreno Lafont and Rubén López Santiago. Laboratorio de Inmunología Celular, ENCB, IPN
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265.	**Evaluation of disinfectants on bacterial strains isolated in sheep and goats by the rideal and modified walker method.** Rodolfo Alberto Perea Cantero, *Ivonne Barrera Jiménez*, Jesús Manuel Tarín Ramírez. Universidad Autónoma Metropolitana Xochimilco.
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271.	**Probiotic potential of *Lactobacillus* strains isolated from an artisanal raw-milk cheese.** José Martín Ruvalcaba-Gómez, *Edith Rojas-Anaya*, Lily Xochilt Zelaya-Molina, Dalia Vanesa Pérez-Hernández, Jacqueline Díaz-Padilla, Ramón Ignacio Arteaga-Garibay. Centro Nacional de Recursos Genéticos-INIFAP.
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274.	**Phenotypic and genotypic characterization of bacteria in meat for human consumption in a population of the Sierra Sur of Oaxaca, 2019-2020.** *Elidet Salinas Robles*, Ana María González Villoria, Patricia Lozanos Sarain, Guilibaldo Gabriel Zurita Vásquez. Maestría en Salud Pública Universidad de la Sierra Sur.
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276.	**Structure-function relationship of *Streptococcus infantarius* subsp. *infantarius* amylopullulanase.** *Alma Asiri Santiago Gutiérrez*, Daniel Guillén, Romina Rodríguez Sanoja**.** Departamento de Biología Molecular y Biotecnología. Instituto de Investigaciones Biomédicas, UNAM.
277.	**Correlation between Polymerase Chain Reaction and Cervical Cytology Results in Patients from Oaxaca, Mexico.** *Juana A. Sarmiento Porras*, Perla M. Martínez Cruz, Sergio R. Aguilar Ruiz, Lisandro Sosa Velasco, Cristóbal Ortíz, Lucía Martínez Martínez. Centro de Investigación. Facultad de Medicina, UNAM-UABJO.
278.	**Effect of a Hand-washing Workshop on the decrease of total aerobes on the hands of social service students of the Pharmacy Degree.** Diana Hazel Tapia Mazón, Janeth Gómez-García, Carlos Antonio Arjona Canul, Blanca Estela Duque Montaño, Oscar Torres Angeles*, Nallelyt Segundo Arizmendi*. Universidad Autónoma del Estado de Morelos
279.	**Comparison of the microbiological and chemical characteristics of pulque from Claveles, Guanajuato in two seasons.** *Luis Fernando Sepúlveda Sáenz*, Carlos Alan Hernández, Luisa Fernanda Moriel Cano, Hilda Amelia Piñón Castillo, Joan Sebastián Salas Leiva, Martha Graciela Ruíz Gutiérrez, Layla Nayzzel Muñoz Castellanos y Reyna Reyes Martínez. Facultad de Ciencias Químicas, Universidad Autónoma de Chihuahua
280.	**Determination of virulence profile of Shiga toxin-producing *Escherichia coli* from Chicken Carcasses from Retail Markets in Culiacan, Sinaloa, Mexico.** Amézquita-López B. A, *Terrazas-Alcaraz C. A*, Soto-Beltrán M, Lugo-Melchor O. Y, García-Caldera T. Y, Domínguez-Esquerra W. E & Quiñones B**.** Facultad de Ciencias Químico Biológicas. Universidad Autónoma de Sinaloa
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285.	**Characterization of UPEC clinical isolates in pregnant women.** *Villavicencio Carrisoza O*, León Juárez, García Correa A. Sosa González I, Villeda Gabriel G, Martínez Salazar M.G, González y Merchand J. A, Helguera Repetto A. Departamento de Microbiología. ENCB. IPN.
286.	**Drug susceptibility testing of *Mycobacterium mucogenicum* isolates from different sources.** Elizabeth Arana-Medina, Diana Angelica Aguilar-Ayala*, Samantha Yong-Mendoza*, Addy Cecilia Helguera-Repetto, Jorge Francisco Cerna-Cortés1, Sandra Rivera-Gutiérrez, Jorge Alberto González-y-Merchand. Laboratorio de Microbiología Molecular. ENCB. IPN

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297.	**Microbial profiling of gestational diabetes pathophysiology: First steps towards dysbiosis characterization using amniotic fluid, placenta, meconium and colostrum samples**. *July Stephany Gámez Valdez*, Raúl Piñeiro Salvador, Gelacio Jiménez Blanco, Dalia Liliana Rodríguez Reyes, Alan Heriberto Montoya Rincón, Marion Brunck, Víctor Javier Lara Díaz, Cuauhtémoc Licona Cassani. Centro de Biotecnología FEMSA, Tecnológico de Monterrey
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299.	**Prevalence of *Porphyromona gingivalis* and *Tannerella forsythia* bacterial species in *E. gingivalis*-ST1 and/or ST2-kamaktli subtypes carriers.** *Gabriela García Pérez,* Fernando Ramos Reyes**.** Facultad de Medicina,
300.	**Linking up the metabolically active versus total *Vibrio* spp. population in the digestive tract of *Litopenaeus vannamei* during their post-larval development.** *Estefania Garibay-Valdez*, Luis Rafael Martinez-Cordova, Marco A. Lopez-Torres, F. Javier Almendariz-Tapia, Marcel Martinez-Porchas, Kadiya Calderón. Centro de Investigación en Alimentos y Desarrollo A.C.
301.	**Contribution of hospitals in the microbiome inside Mexico City Subway System.** *Carolina González Cedillo*, Luis D. Alcaraz Peraza, Mariana Peimbert. Facultad de Ciencias. UNAM.
302.	**Distribution of rhizospheric bacterial diversity of corn from a production area of Jalisco.** *Jairo Eder Guerra-Camacho*, Aremi Rebeca Contreras-Toledo, Carlos Ivan Cruz-Cárdenas, Lily Xochilt Zelaya-Molina, César Hugo Hernández-Rodríguez, Ramón Ignacio Arteaga-Garibay. ENCB. IPN.
303.	**Impact of bacteriophages associated with childhood obesity in the intestinal microbiome in a model murine.** *Abigail Hernández-Reyna*, Shirley Bikel, Fernanda Cornejo-Granados, Filiberto Sánchez, Luigui Gallardo-Becerra, Adrián Ochoa-Leyva. Instituto de Biotecnología, UNAM.
304.	**Mycobiota associated with dieback in Mexican Lime (*Citrus aurantifolia)* affected by Huanglonbing (HLB).** *Julio Cesar Herrera Ortiz,* Karina de la Paz García Mariscal, Manuel de Jesús Bermúdez Guzmán, José Joaquín Velázquez Monreal, Mario Orozco Santos, Francisco Javier Delgado Virgen. Instituto Tecnológico de Colima.
305.	**Dynamic and Asymmetric Changes of the Microbial Communities after Cohousing in Laboratory Mice.**

	Roberta Caruso, Masashi Ono, Marie E. Bunker, Gabriel Núñez, *Naohiro Inohara.* Department of Pathology, University of Michigan Medical School
306.	**Characterization of bacterial diversity of healthy individuals and patients with ocular surface infection.***Silvia Bernardina López-Gaytán*, Juan Campos-Guillén, Rosa Paulina Calvillo-Medina, Diana Gabriela Ponce-Angulo, Luis Antonio Bautista-Hernández, Dulce Karina Rico-Amador, Victor Manuel Bautista-de Lucio. Faculty of Chemistry, Autonomous University of Querétaro.
307.	**Microbiota response to stress situations.** *Jael López Martínez*, María del Pilar Gabriel-de la Torre, Miguel-Ángel Mayoral-Chávez. Centro de Investigación UNAM-UABJO
308.	***Lactobacillus gasseri* and *Sneathia sanguinegens* in women non-squamous intraepithelial lesion and cervical cancer with HR-HPV infection.** *Dinorah Nashely Martínez Carrillo*, Iraly Yarizbet Sotelo Ortiz, Elvis Uriel González Marroquín, Ángel Said Hipólito Valenzo, Julio Ortiz Ortiz, Javier Sánchez Rendón, Francisco Israel Torres Rojas, Miguel Ángel Mendoza Catalán, Berenice Illades Aguiar, Gloria Fernández Tilapa, Adolfo Román Román, Hilda Jiménez Wences. Facultad de Ciencias Químico Biológicas, UAGro.
309.	**Microbial diversity and structure of the parasitic plants *Phoradendron velutinum* and *Arceuthobium gilli.*** *Erika Mendez Manzano*, Noé Flores Hernández, Luis Mario Hernández Soto, Jose Abraham Canales Meza, José Félix Aguirre Garrido. Universidad Autónoma Metropolitana Unidad Lerma.
310.	**Metagenomic Analysis of Gut Microbiota Associated with Obesity.** *Alma Delia Nicolás-Morales*, Yaneth Castro-Coronel, Arturo Ramírez-Peralta, Hugo Castelán-Sánchez, Yordanis Pérez-Llano, Natividad Castro-Alarcón**.** Laboratorio de Investigación en Microbiología-UAGro.
311.	**Metagenomic analysis of Actinobacteria phylum in patients with Irritable Bowel Syndrome.** *Braulio Manuel Fitz González*, Yolanda López Vidal, Patricia Orduña Estrada. Programa de Inmunología Molecular Microbiana, Facultad de Medicina, UNAM.
312.	**Fecal bacterial profile of the Merriam´s kangaroo rat, *Dipodomys merriami*, in the Chihuahuan Desert.** Irene Pacheco-Torres, Cristina García-De la Peña, Felipe Vaca-Paniagua, Clara E. Díaz-Velásquez, Claudia Fabiola Méndez-Catalá , César A. Meza-Herrera, Luis Antonio Tarango-Arambula, Cameron W. Barrows. Unidad Regional Universitaria de Zonas Áridas, Universidad Autónoma Chapingo
313.	**Fecal bacterial microbiota of the pallid bat, *Antrozous pallidus*, in the Chihuahuan Desert.** *Irene Pacheco-Torre*, Cristina García-De la Peña, Felipe Vaca-Paniagua, Clara E. Díaz-Velásquez, Claudia Fabiola Méndez-Catalá, César A. Meza-Herrera, Luis Antonio Tarango-Arámbula, Cameron W. Barrows. Unidad Regional Universitaria de Zonas Áridas, Universidad Autónoma Chapingo
314.	**Oral sodium butyrate induces substantial intestinal changes in IL-17 / IFNγ and stabilizes tight junction proteins in an experimental model of cholestatis.** *Marcela Peña Rodríguez*, Natali Vega Magaña, Leonel García Benavides, Lucero González Hernández, Jaime Andrade Villanueva, Sergio Zepeda, Susana del Toro Arreola, Juan Manuel Benavides y Miriam Ruth Bueno Topete. Instituto de Investigación en Enfermedades Crónico Degenerativas, CUCS, U de G.
315.	**Evaluation of domestic canaries (*Serinus canaria*) gut microbiota. Potential zoonotic pathogens and antibiotic resistance patterns.** *Marian Ramos-Rivera*, Melissa Fierro-Loera, Norma Lizeth Soriano-Oviedo, Erica Karime Ventura-García, Claudia Isela Avitia-Domínguez, Alfredo Téllez-Valencia, Mónica Andrea Valdez-Solana, Erick Sierra-Campos. Facultad de Ciencias Químicas, UJED.
316.	**Prevalence of bacterial communities and potential pathogens in surface waters of the Rio Grande/Bravo in Reynosa Tamaulipas.** *Requena-Castro Rocío,* Aguilera-Arreola María Guadalupe, Cruz-Hernández María Antonia, Martínez-Vázquez Ana Verónica, Bocanegra-García Virgilio. Centro de Biotecnología. Genómica, IPN.
317.	**Gut microbiome in small ruminants.** *Edith Rojas-Anaya*, Elizabeth Loza-Rubio, Rodrigo J. Barrón Rodríguez, Rocio Parra-Laca, José Luis Gutiérrez-Hernández, Efrén Díaz-Aparicio, Moisés A. Cortes-Cruz MA. Centro Nacional de Recursos Genéticos, INIFAP.
318.	**Identification of actinobacterial strains isolated from rhizosphere of experimental wheat varieties from CIMMYT by MALDI-TOF mass spectrometry and 16s gene sequencing.** Julia del Carmen Martínez Rodríguez, Claudia Ivette Cisneros Reyes, Jessica Viridiana Galvez Calvario*, César Salgado Lozada,* DDCyT. Universidad Autónoma de Guadalajara
319.	**Bioprospection of actinobacteria and study of bacterial diversity from Calakmul *aguadas* (wetlands-like) using comparative genomics and metaprofiling.** *Karina Verdel-Aranda*, Joel Lara Reyna, Aída Martínez Hernández, Cuauhtemoc Licona Cassani. Colegio de Postgraduados, Campus Campeche.
320.	**Bacterial flora in stool of a captive manatee calf.** *Lucero Vázquez Cruz,* Rosa Martha Padrón López, María de Lourdes Torres Pérez, Julia María Lesher Gordillo, Adolfo López Hernández, León David Olivera Gómez y Darwin Jiménez-Domínguez. Universidad Juárez Autónoma de Tabasco

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322.	**Study of the regulation of polyhydroxybutyrate (PHB) depolymerization in *Azotobacter vinelandii.*** *Thalía Barrientos Millán,* Libertad Adaya García, Holjes Salgado Lugo Josefina Guzmán Aparicio, Soledad Moreno León, Carlos Peña Malacara, Guadalupe Espín Ocampo, Daniel Segura González. Instituto de Biotecnología. UNAM
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324.	**In silico and functional analyses of GrlR, the LEE pathogenicity island repressor in enteropathogenic** *Escherichia coli. Jordan Euler Bernaldo Agüero*, Carmen A. Contreras García, José Luis Puente. Instituto de Biotecnología, UNAM
325.	**Differences in HBsAg detection and oxidative stress gene expression between wild type and C107R mutant of Hepatitis B Virus genotype H.** *Marina Campos-Valdez,* Sina Feustel, Carolina Barrientos-Salcedo, Hugo Christian Monroy Ramírez, Belinda Gomez Meda, Juan Armendáriz Borunda, Laura Sánchez Orozco. Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara
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330.	**Analysis of a putative operon in *A. brasilense* Sp245 involved in growth and motility.** Yessica I. Cosme-Herrera, Carlos D. Cordero-Rivera, Ma. Luisa Xiqui-Vázque, Alberto Ramírez-Mata, and Beatriz E. Baca. Centro de Investigaciones en Ciencias Microbiológicas, BUAP.
331.	**Study of the activity of select promoters by the transcriptional regulator TyrR of *Azospirillum brasilense* Sp7.** *Enrique Cruz Aparicio*, Sandra R. Reyes Carmona, Saúl Jijón Moreno, Alberto Ramírez Mata and Beatriz Eugenia Baca. Centro de Investigaciones en Ciencias Microbiológicas, BUAP.
332.	**Study of the motility of bacteria of the genus *Vibrio* under different salinity conditions**. *Leticia Cruz Mendoza*, Francisco Javier de la Mora y Georges Dreyfus. Instituto de Fisiología Celular, UNAM
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335.	**Identification of a gene encoding for a phosphodiesterase and likely diguanylate cyclase hybrid protein in *Azospirillum brasilense* Sp245.** Jesús Uriel Espino Aldaba, Antonio de Jesús Salazar García, Sandra Raquel Reyes-Carmona, Ma. Luisa Xiqui-Vázquez, Beatriz Eugenia Baca and Alberto Ramírez Mata. Centro de Investigaciones en Ciencias Microbiológicas, BUAP
336.	**A new alternative against urinary tract infection: design and generation of uroplakin-silenced bladder cells line.** *Marco Antonio Flores Oropeza*, Víctor Manuel Luna Pineda, Ariadnna Cruz Córdova, Sara Ariadna Ochoa Pérez, Vicenta Cázares Domínguez, Karina Espinosa Mazariego, Gerardo Escalona Venegas, Guillermo Aquino Jarquín, and Juan Xicohtencatl Cortes. Programa Doctorado Directo en Ciencias Biomédicas, UNAM
337.	**Co-expressed gene modules share similar function and regulation.** *Edgardo Galán Vásquez*, Ernesto Pérez Rueda. Instituto de Investigaciones en Matemáticas Aplicadas y en Sistemas, UNAM
338.	**Functional gene association networks analysis suggests that the ORF VCA0231 from *Vibrio cholerae* codes for a common iron uptake regulator in proteobacteria.** Bernardo Sachman Ruiz, Alexia Torres

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340.	**The LEE-encoded regulator GrlA, promotes the expression of the type III secretion effector gene *nleH1* in enteropathogenic *Escherichia coli***. *Fabiola González Lara,* José Luis Puente. Instituto de Biotecnología, UNAM.
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342.	**Study of the gen Avin_15460 (*gacS2*) involved in the synthesis of alginates in *A. vinelandii*.** *Lennis Hernández Campos*, Miguel Castañeda Lucio. Centro de Investigaciones en Ciencias Microbiológicas. BUAP
343.	**Characterization of GSU1771 regulator involved in electron transfer and energy generation in *Geobacter sulfurreducens.*** *José Alberto Hernández-Eligio*, Sergio Martínez Bahena, Guillermo Huerta, Margarita Miranda-Hernández and Katy Juárez López. Instituto de Biotecnología, UNAM.
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345.	**Molecular characterization of SehB, a type II antitoxin of *Salmonella enterica* serotype Typhimurium.** *Gabriela Hernández-Martínez*, José A. Ibarra-García, and Miguel A. De la Cruz. Hospital de Pediatría, CMN Siglo XXI, IMSS.
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348.	**CreR, an EIL domain-containing protein, positively regulates the expression of the *ecp* fimbrial operon in *Citrobacter rodentium.*** *María Inés Isidro-Coxca*, Verónica I. Martínez-Santos, Andrés Escalera Maurer, Gustavo Caballero Flores, Alejandra Vázquez Ramos, José Luis Puente. Instituto de Biotecnología, UNAM.
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367.	**A novel MarR-like transcriptional regulator of *Klebsiella oxytoca* represses expression of genes involved in biosynthesis of tilivalline.** *Diana Ivonne Rodríguez Valverde*, Jorge Alberto González y Merchand, Miguel Ángel de la Cruz Villegas, Miguel Ángel Ares Jiménez. Hospital de Pediatría, CMN Siglo XXI, IMSS
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	Ixchell Yureimy Sedillo Torres, Dulce Martínez Cortés, Jonathan Vera Pérez, Joaquín Tamaríz Mascarua, César H. Hernández Rodríguez, Yolanda Gómez y Gómez, José Antonio Ibarra García. ENCB. IPN.
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423.	***Burkholderia pseudomallei* identification in México.** Georgina Meza Radilla, Ausel Méndez Canarios, J. Eduardo Solis Hernández, J. Antonio Ibarra, *Paulina Estrada de los Santos.* ENCB – IPN.
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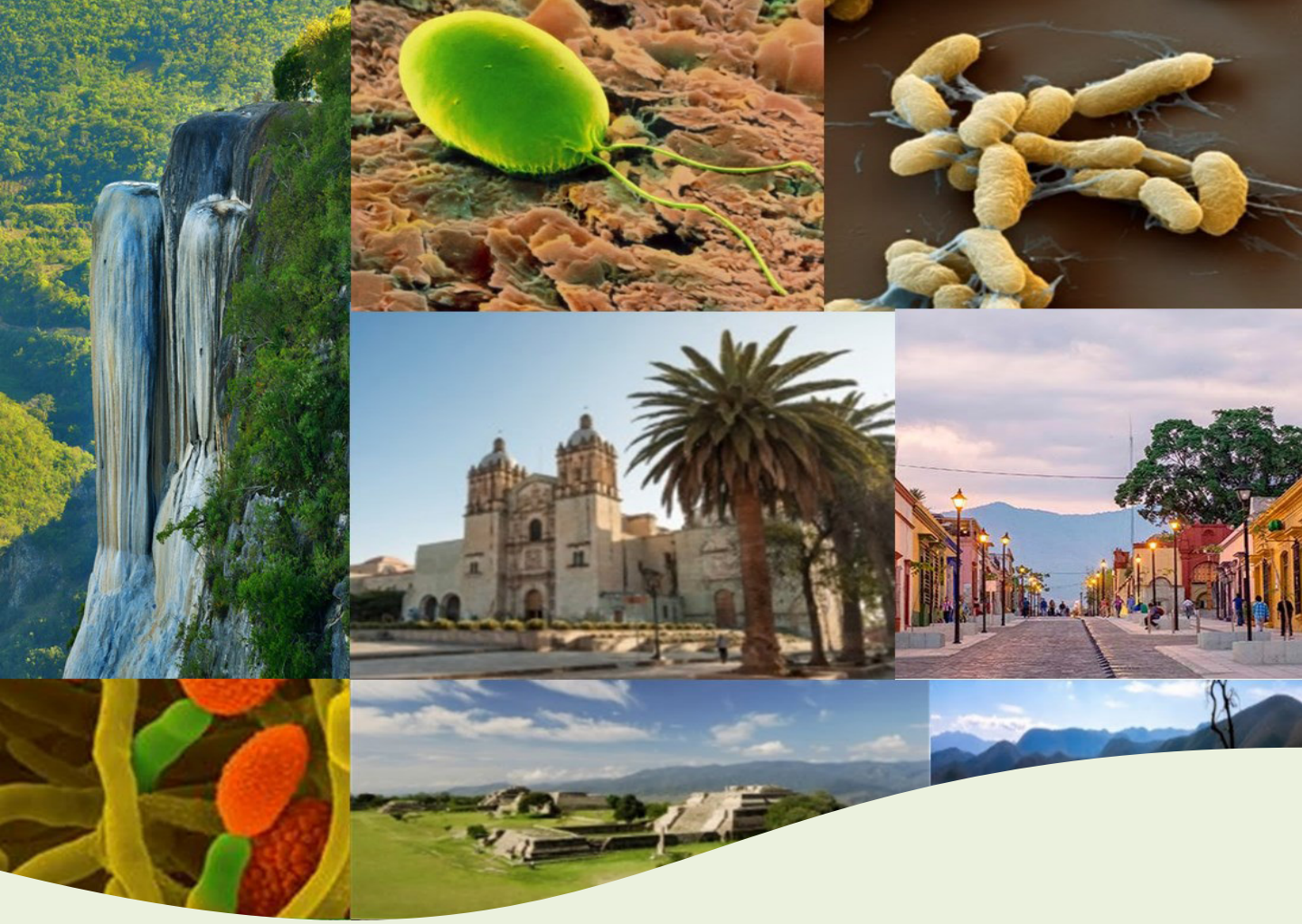

Invited Abstracts

XLI National Meeting of the Mexican Association of Microbiology (AMM)
VI Meeting of Biochemistry and Molecular Biology of Bacteria (BBMB)

Oaxaca, Oax. October 27 - 31, 2019.

Epidemiology of multidrug-resistant *Neisseria gonorrhoeae* in Mexico City: crisis in a complicated context?

Ma. Guadalupe Aguilera-Arreola, Arturo Peña Toribio, Maryjose Perez Bautista, Brenda Lizeth Ballesteros Astorga, Rebeca Eunice García-Mendiola, Araceli Contreras-Rodríguez.

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Gonorrhea is an actual global public health concern because it causes more than 78 million new cases among adults every year. The etiological agent of gonorrhea is *Neisseria gonorrhoeae*: this bacterium has developed resistance to almost all of the antimicrobials previously used for the treatment of gonorrhoeae, including penicillins, tetracyclines and fluoroquinolones. Currently, emergence of resistance to third-generation cephalosporins and azithromycin has been described in different countries.

Since both, epidemiology of gonorrhoeae and resistance profiles of *N. gonorrhoeae* are unknown in Mexico, our workgroup has focus it to research these important issues. In the last years, using traditional and molecular approaches we are detected not only an increase in the number cases of gonorrhoeae but also an alarming presence of multidrug resistant strains isolated from men who have sex with men.

Widespread antimicrobial resistance (AMR) of *N. gonorrhoeae* strains has continuously compromised the management and control of gonorrhea. Therefore, development of prevention and control strategies, targeting the groups at risk, should be reinforced in order to prevent the problem from getting worse.

Isolation, genotyping and antimicrobial resistance of Shiga toxin-producing *Escherichia coli*

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Shiga toxin-producing *Escherichia coli* (STEC) is an enteric pathogen linked to outbreaks of human gastroenteritis with diverse clinical spectra. We have examined the currently methodologies and molecular characterization techniques for assessing the phenotypic, genotypic and functional characteristics of STEC O157 and non-O157. Traditional culture and isolation methods, inclyding selective enrichment and differential plating, have enabled the effective recovery of STEC. Following recovery, immunological serotyping of somatic surface antigens (O-antigens) and flagellum (H-atigens) are employed for the classification of the STEC isolates. Molecular genotyping methods, including multiple-locus variable-number tandem repeat analysis, arrys, and whole genome sequencing, can discriminate the isolate virulence profile beyond the serotype level. Virulence profilling is focused on the identification of chromosomal and plasmid genes coding for adhesins, cytotoxins, effectors, and hemolysins to better assess the pathogenic potential of the recovered STEC isolates. Important animal reservoirs are cattle and other small domestic ruminants. STEC can also be recovered from other carriers, such as mammals, birds, fish, amphibians, shellfish and insects. Finally, antimicrobial resistance in STEC is a matter of growing concern, supporting the need to monitor the use of these agents by private, public and agricultural sectors. Certain antimicrobials can induce Shiga toxin producing and thus promote the onset of severe disease symptoms in humans. Together, this information will provide a better understanding of risks associated with STEC and will aid in the development of efficient and targeted intervention strategies.

Surveillance of *Pseudomonas aeruginosa*

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To the problem of the high incidence and severity of *Pseudomonas aeruginosa* infections in the hospital environment, the resistance of this microorganism to conventional antimicrobial treatments is added. Antimicrobial resistance in *P. aeruginosa* is multifactorial; some main mechanisms are recognized such as: enzymatic inactivation of the antibiotic, target alterations, and changes in membrane permeability Surveillance of this microorganism in the hospital environment allows to establish multidisciplinary teamwork, to improve the interpretation of the antibiogram and to observe the emergence of clones and antimicrobial resistance mechanisms.

Structure, functional prediction, and phenotyping studies in genes encoding proteins involved in cyclic-di-GMP in *Azospirillum.*

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Bacteria that live in the plant rhizosphere and possess a large array of potential mechanisms to enhance plant growth are considered as PGPR. *Azospirillum* represents a well-characterized genus of PGPR due to its capacity of fixing atmospheric nitrogen. Another main characteristic of *Azospirillum* proposed to explain plant growth promotion has been related to its ability to produce phytohormones. The effective use of *Azospirillum brasilense* as bio-fertilizers requires the ability to achieve effective colonization to root-plants.

Important phenotypes are controlled by a second messenger the cyclic-di-GMP, which is involved in control of biofilm formation, synthesis of exopolysaccharides (EPS), and motility that are essential properties for the establishment of mutualist relationships of bacteria with their plant hosts.

The role of c-di-GMP is now established in the transitioning of bacterial lifestyle from planktonic to sessile, cellular development, host cell adherence, and motility, among other functions. The c-di-GMP is synthesized and degraded by proteins containing GGDEF and EAL domains, respectively, named after the conserved signature motifs Gly-Gly-Asp-Glu- Phe (GGDEF) and Glu-Ala-Leu (EAL). The GGDEF and EAL domains are typically linked to non-enzymatic domains that are involved in the signal transduction system. In addition, there are hybrid proteins harboring both enzymatic domains (GGDEF-EAL).

A systematic study accomplished in our group in the genomes of *A. brasilense* Sp245 and Sp7 strains showed that the bacteria encompassed several genes potentially encoding for the three signaling domain-containing the c-di-GMP proteins. Phenotyping studies carried out in six genes performed with their mutants generated and compared with the wild-type strains, showed that regulate swimming motility, biofilm formation, and colonization to wheat roots.

These findings deepen our understanding of the role of c-di-GMP signaling mechanisms in the adaptation of PGPR to the host environment.

ACKNOWLEDGMENTS
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Rethinking secondary metabolism in bacteria: from evolution to function

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Abstract:

The forces of biochemical adaptive evolution operate at the level of genes, manifesting in complex phenotypes and the global biodiversity of proteins and metabolites. While evolutionary histories have been deciphered for some other complex traits, the origins of natural product (NP) biosynthesis, or secondary metabolism, largely remain a mystery. This fundamental knowledge gap is surprising given the many decades of research probing the genetic, chemical, and biophysical mechanisms of bacterial natural product biosynthesis. Recently, evolutionary thinking has revolutionized this otherwise mechanistically dominated field. NPs are now sometimes referred to as 'specialized' rather than 'secondary' metabolites, reinforcing the importance of their biological and ecological functions. Here, I will present what is known about the evolutionary mechanisms underlying the overwhelming chemical diversity of bacterial secondary metabolism, focusing on enzyme promiscuity and the evolution of enzymatic domains that enable metabolic traits. I will discuss the mechanisms that drive the assembly of NP biosynthetic gene clusters (BGCs) and propose formal definitions for 'specialized' and 'secondary' metabolism. I further explore how biosynthetic gene clusters evolve to synthesize related molecular species, and in turn how the biological and ecological roles that emerge from metabolic diversity are acted on by selection. Finally, I will reconcile chemical, functional, and genetic data into an evolutionary model, the Dynamic Chemical Matrix Evolutionary (DCME) hypothesis, in which the relationships between chemical distance, biomolecular activity (function), and relative fitness shape adaptive landscapes.

Microbiome of cycad's coralloid roots: co-evolution of bacterial communities encoding niche-specific biosynthetic gene clusters

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Abstract:

Cycads are the only early seed plants that have evolved a specialized root to host endophytic bacteria that fix nitrogen. To provide evolutionary and functional insights into this million-year old symbiosis, we investigated endophytic bacterial sub-communities isolated from coralloid roots of species from *Dioon* (Zamiaceae) sampled from their natural habitats. We employed uncultured taxonomic profiling and co-culture experimental metagenomics to reveal both predominant and rare bacteria, which were characterized using phylogenomics and metabolic annotation. Diazotrophic plant endophytes, but also other symbiotic bacteria, dominated the epiphyte-free sub-communities. Draft genomes of several cyanobacteria were obtained from selected sub-communities, suggesting two *Dioon*-specific monophyletic groups. This speaks to a level of specialization characteristic of co-evolved symbiotic relationships, which may be also present in the guts of symbiotic cycad insects, implying a tripartite co-evolved system. Furthermore, the genomes of cyanobacteria were found to encode unique biosynthetic gene clusters, predicted to direct the synthesis of specialized metabolites (peptides and siderophores) that could help the plant rapidly adapt to soils with low nutrients. Genome mining in combination with multi-photon excitation fluorescence microscopy showed that *Caulobacter* species co-exist with cyanobacteria, and may interact by means of a novel indigoidine-like metabolite. Overall, I will provide an unprecedented view of the composition of the cycad coralloid root microbiome, important for the evolution of ancient symbiotic adaptations.

"Towards the constitution of an epidemiological atlas of multidrug-resistant tuberculosis in Mexico"

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According to the annual report of the World Health Organization in 2017, 10.5 million new cases and 1.7 million deaths are related to tuberculosis (TB), being TB the infectious disease with the greatest impact on human health. Epidemiological surveillance suggests that drug-resistant tuberculosis is a global problem, from which Mexico does not escape. The growing number of cases of multidrug-resistant tuberculosis (MDR-TB) and extensively drug-resistant (TB-XDR), has the consequence that in several endemic countries, MDR-TB has evolved to pharmacological incurable tuberculosis (fully drug-resistant tuberculosis). Thus, every yearc about 25% of cases of TB worldwide show resistance to at least one of the antibiotics used in the first-line treatment against TB. Of these isolates, 5% evolve to MDR-TB, presenting a combined resistance to isoniazid and rifampin, with propensity to more severe forms of TB-XDR, with simultaneous resistance to a flouroquinolone and at least one of the three injectable drugs of second line (amikacin, kanamycin and capreomycin). Mexico has the third highest contribution of tuberculosis in Latin America, including aggravated forms of TB-R, MDR-TB and XDR-TB. In 2016, 22,869 new cases of TB were reported in Mexico, with an incidence of 22 cases per 100,000 inhabitants. Of these, 2.5% showed MTB-DR with primary resistance, with 610 individuals with MDR-TB, and an increasing number of cases of XDR-TB. To ensure the confirmatory diagnosis and epidemiological monitoring of cases of emerging, reemerging and endemic diseases such as tuberculosis, a network of epidemiological surveillance and research laboratories was build in 2008 at the Mexican Institute of Social Security (IMSS). The Biomedical Research Unit of Zacatecas (UIBMZ) was integrated into this network as a National Reference Center for the Diagnosis of Tuberculosis (TB). In this center, the complete diagnostic algorithm is performed on pulmonary and extrapulmonary samples with suspected tuberculosis from all over the Mexican Republic. In Mexico there is a considerable diversity of mutations associated with drug-resistant MTB, which are presented as predominant variations linked to certain geographic regions. Complete genome sequencing (WGS) provides accurate information on polymorphisms, insertions and deletions with potential relevance for the rapid prediction of drug resistance phenotypes related to clinically important drugs. In a recently published study (PLOSOne https://doi.org/10.1371/journal.pone.0213046 June 5, 2019), Doctors Roberto Zenteno (Institute of Health Sciences Universidad Veracruzana, Mexico), and Iñaki Comas (from the Biomedicine Institute in Valencia Spain) and Us showed the utility of algorithms applied to WGS to predict drug resistance in MTB-MDR, pre-XDR and XDR mexican strains. In addition, WGS revealed polymorphisms related to resistance to second-line drugs, and its specific lineages were classified in a single analysis and with great precision in several DR and XDR isolates, allowing epidemiological-genomic surveillance studies. The results will be discussed in this presentation.

New insights into the methylation of heparin binding hemagglutinin adhesin (HbhA) of *Mycobacterium tuberculosis*

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The heparin binding hemagglutinin adhesin (HbhA) of *Mycobacterium tuberculosis* is an important surface antigen which mediates adhesion to epithelial cells and leads to extrapulmonary dissemination of bacilli. The protein binds to cell sulfated glycoconjugates through its C-terminal Lys-rich repeats, which can be modified by methyl groups that are involved in protection against *M. tuberculosis* challenge in mice. Although, methylation of non-histone proteins in prokaryotes have been associated with different bacteria physiological processes the role of methylation in HbhA remains unknown. The presence of *M. tuberculosis* HbhA orthologue in *Rhodococcus opacus* PD630, the triacylglycerol accumulation deficient protein (TadA) involved in assembling and maturation lipid droplets (LDs), prompted us to clone and express the HbhA gene in the *Rhodococcus erythropolis* L88 strain, previously developed for heterologous protein expression. The recombinant HbhA was methylated in *R. erythropolis* and was found associated to LDs, induced when recombinant bacteria were grown in media with limited nitrogen and excess of carbon supplies. The r*Rho*HbhA was recognized by both IgG and IgM antibodies from tuberculosis patients and BCG vaccinated individuals. It was also found that the recombinant non-methylated protein expressed in *E. coli* was able to inhibit the entrance of BCG to human epithelial cell line while only an small percentage of inhibition was observed when cells were previously incubated with methylated r*Rho*HbhA. In addition, both r*Rho*HbhA and *rE.coli*Hbha were able to bind specifically to stearic acid independent of its methylation status, in contrast with recently observations that showed that only the modified protein interacted with phosphatidylinositol. Together these results suggest that Lys methylation of HbhA can interfere with the recognition of the protein by proteoglycans and therefore could be regulating the attachment and entrance of mycobacteria to epithelial cells. This work, also points out the importance of having heterologous expression systems in order to obtain methylated proteins that will allow a deeper understanding about the role these molecules are playing in *M. tuberculosis* host-pathogen relationship.

VACCINE MANUFACTURING

A global challenge requiring specialized people.

A complex journey in a highly regulated industry

The vaccine industry is composed of companies that are engaged in any of the following activities: research (including that performed in industry and biotech), development, Regulatory affairs, manufacture, quality systems and quality control, sales, marketing, and distribution of vaccines.

The vaccine industry is relatively small, compared to the pharmaceutical industry, but growing. We estimate that total infectious disease vaccine sales in 2013 were more than $25 billion worldwide and expected to grow to about $35 billion by 2020.
Every year, 10.6 million children die before the age of five years; 1.4 million of these are due to diseases that could have been prevented by vaccines.
Immunization saves more than 3 million lives (children and adults) worldwide each year, and it saves millions more from suffering illness and lifelong disability.
After clean water, vaccination is the most effective public health intervention in the world for saving lives and promoting good health.

Vaccines are sophisticated biological products.
Vaccines have complex production process with particularly long production cycles and require sophisticated equipment, technologies and analytical methods to consistently ensure finished products of the highest quality. **To ensure this, highly trained and qualified employees are also required. Specialist, Ph´s, master's degrees, with technical knowledge including soft skills are required** to assure high quality standards, vaccines production demands a strict adherence to international quality requirements and must remain compliant to non-harmonized regulatory requirements worldwide.

Vaccine development is difficult, complex, highly risky, and costly, and includes clinical development, process development, and assay development.
Today researchers have alternatives to integrate into the vaccine production industry through scholarships, public/private or public/private institutions agreements and governments, development projects. The vaccine production industry is in the aftermath of having technical staff in problem solving and decision-making areas that proactively solve technical and business solutions

Exploitation of public goods and population collapses in *Pseudomonas aeruginosa*

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Pseudomonas aeruginosa is an opportunistic pathogenic bacterium, multi-resistant to antibiotics and one of the main causes of nosocomial infections. It is considered by the WHO as a critical priority for the development of new effective therapies for the treatment of their infections. *P. aeruginosa* has a very extensive network of virulence factors, mostly controlled by quorum sensing, among these are a variety of exoproteases such as elastases LasA and LasB, collagenase AprA and protease IV, as well as siderophores such as pyoverdine.

These factors are public goods since they are shared among all the members of the bacterial community regardless of whether the individuals produce them or not, hence their production is susceptible to being exploited by non-producing mutants (social cheaters), and may even completely stop the growth of the community due over exploitation.

In the present work it will show that during the daily sequential growth in minimum medium with caseinate as the sole carbon source, which requires the production of exoproteases to maintain cellular duplication, QS defective mutants (*lasR*$^{-}$) arise and accumulate, occasionally promoting the population collapse of about 40% of the cultures after 30 sequential passes and that these collapses are much more frequent (100%) and early (pass 7) if the exoprotease present in the inoculum is removed. This is probably related to the greater production of exoprotease (LasB) by the producing individuals in conditions of nutrient deficiency.

In addition, in minimal medium with low concentrations of free iron, non-producers of siderophore pyoverdine arise, which exploit the producers and cause population collapses, whose frequency seems to increase with the addition of gallium, which sequesters pyoverdine.

"The distal colon microbiota of Type 2 Diabetes, Obesity, and Metabolic Syndrome triad in Mexico"

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The research on microbes has been an important aspect of science which has taken different approaches through the time, and microbes have been exposed as responsible agents of several human maladies and problems in agriculture, industry and other food production activities. However, recent times have brought to popularity interesting aspects of microbial activities, especially those from bacteria mostly present in the human microbiota which contributes to health. At population level, Mexicans are severely affected by metabolic disorders such as obesity, type 2 diabetes and even metabolic syndrome, a condition increasing the risk of heart disease, stroke and type 2 diabetes, ranking our country among the top list of countries in the world with these problems. In at least one decade, science has shown in several published studies in the world, the importance of a functional microbiota, to maintain human health, especially bacteria from the gut microbiota. In this presentation we report our published advances of the last five years, characterizing the distal colon microbiota and even the microbiome of Mexicans affected of type 2 diabetes, obesity, or the complex metabolic syndrome. We have found that Mexicans have cosmopolitan bacteria in their guts, but also, we carry indigenous bacteria in the dysfunctional microbiotas of the studied diseases, which exhibit abundances of genes whose expression contributes importantly to the unhealthy conditions.

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The role of Hepatocyte Growth Factor in experimental pulmonary tuberculosis. Therapeutical implications.

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Hepatocyte growth factor (HGF) is a multifunctional cytokine with important roles in cell proliferation, survival, motility and morphogenesis that is produced by cells of mesenchymal origin. HGF is the specific ligand of the tyrosine-kinase receptor c-MET (cellular mesenchymal-epithelial transition). HGF is a potent mitogenic factor for hepatocytes but it is also highly produced after lung injury and it has several activities on the immune system, such as central regulation of monocyte–macrophage functions and promoting Th-1 cells activity. Thus, this growth factor could have relevant functions in tuberculosis (TB). We determined the HGF kinetics and cellular source during progressive pulmonary TB using a murine model. In this model, during the first month of infection there is a temporal control of bacillary growth with granuloma formation; gene expression kinetic determined by RT-PCR showed high expression of both HGF and c-MET after one week of infection, raised their maximal expression at two weeks when granulomas started their formation. Then, their expression decreased when bacillary growth and pneumonia progressively increased. This active progressive phase is well established after two months of infection, when the expression of HGF and c-MET is the lowest, at this time the intraperitoneal administration of recombinant HGF once per week during two months, produced significant decrease of bacterial burdens in coexistence with high expression of the protective cytokines IFN and TNF.
At the present the raise of TB cases produced by multidrug-resistant strains (MDR) is increasing, which is frequently produced by the abandon of long treatment of drug sensible TB. Considering that HGF is efficient to prevent liver toxicity induced by the two principal antibiotics used in TB (isoniazid and rifampicin), in a second part of this work BALB/c mice infected with drug sensible or MDR strains were treated after two months of infection with supra-pharmacological doses of rifampicin and isoniazid (administrated by gavage or intratracheal routes), in combination with HGF. This high dose of antibiotics administered during three months, permitted to shorten conventional chemotherapy in drug sensible TB and more importantly, overcome the resistant threshold of the MDR strain producing a significant reduction of bacillary loads but induced liver damage, which was totally prevented by the administration of HGF. To address the long-term efficiency of this combined treatment, groups of animals after one month of treatment termination were immunosuppressed by glucocorticoid administration, and after one month mice were euthanized and in lungs determined bacillary loads. In comparison with animals treated only with high dose of antibiotics, animals that received the combined treatment showed significant lower bacterial burdens. Thus, HGF is produced by the tuberculous lungs during early infection inducing protective immunity followed by striking decrease, when this growth factor is administrated during active late progressive disease it has a significant therapeutic effect. Moreover, HGF has synergic effect with high doses of the primary antibiotics isoniazid and rifampicin, particularly administrated by aerial route, producing very good therapeutic effect in drug sensible and MDR TB preventing hepato-toxicity, becoming in a new treatment modality.

The tRNA fragments exported by *Escherichia coli* cells may be protein synthesis byproducts generated on ribosomes

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Secretion of biomolecules has been associated to intra- and inter-species cell to cell communication. These secreted entities may act as molecular signals in quorum sensing, pathogenicity and other population communication functions. *Escherichia coli* exports different signaling effectors including fragments of tRNA, free or enclosed in outer membrane vesicles, but the origin of these fragments and its role in population behavior is not understood. The use of deep sequencing of RNA has made possible to identify fragments derived from mature tRNAs, named tRNA halves or tRNA fragments (tRFs). tRFs have been found in many biological systems such as bacteria, archaea, protozoa, plants and animals, including human tissues, but the mechanism of their generation has not been elucidated.

We noticed that a large group fragments of about 35 to 50 nucleotides-long in cell-free extracts corresponded with 5' or 3' tRNA sequences. All tRNA isoacceptors in the cell seem to be represented in the group and its presence correlated with active protein synthesis. Conditions that result in arrest of protein synthesis also reduce the generation of tRNA halves in the extracts. Cell extracts resolved through sucrose gradients showed that most tRFs were in the ribosome free fraction and, in less proportion, in the 30S ribosomal subunit fraction. Interestingly, the tRNAs present in monosomes and polysomes seem to be cleaved to halves by reducing Mg++ concentration, a condition that disassembles ribosomes into 30S and 50S subunit components. Addition of external tRNAs to the disassembling reactions results in complete degradation of tRNAs whereas the intrinsic tRNAs are cleaved to halves. RNaseI, a nuclease that associates with ribosomes, may not be responsible for cleaving tRNAs in halves because mutants defective for *rna*, the gene encoding RNase I, retain the ability to produce tRFs. How the cells export RNA halves and what possible role they play in bacterial communities needs more investigation.

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From Cell Polarity to Bacterial Virulence Control

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Cyclic dinucleotides are highly versatile signaling molecules that control and coordinate a range of important biological processes in bacteria and eukaryotes. The best studied example is cyclic di-GMP (c-di-GMP), a near ubiquitous second messenger that coordinates diverse aspects of bacterial growth and behavior, including motility, cell cycle progression, virulence, and biofilm formation. In this lecture, I will give a brief overview on c-di-GMP signaling principles and will highlight examples of how c-di-GMP controls growth and behavior of different bacteria. The first illustrates how oscillating levels of c-di-GMP determine cell polarity, morphogenesis, and cell cycle progression of *Caulobacter crescentus*, an aqueous bacterium with a characteristic bi-modal life cycle. Work in this non-pathogenic model organism has provided a basic molecular and cellular understanding of the c-di-GMP network that has guided our studies of experimentally less tractable systems like the human pathogen *Pseudomonas aeruginosa*. In the second part, I will provide an update on how *P. aeruginosa* makes use of c-di-GMP to induce its full virulence potential. In particular, our studies have disclosed novel strategies, through which this organism optimizes host tissue colonization.

Different data science approaches for the development and obtaining bacterial functional secrets for industry improvement

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Winter Genomics is a Mexican company focused on consulting, development and bioinformatic analysis of data generated in the life sciences field. The multidisciplinary team of bioinformatics and genetic consultants of Winter Genomics, generate ideas and strategies to harness the potential of the genetic information of bacteria used in the industry. The fact of being a national and international recognized company has allowed us to acquire great experience in the data science field. We selected two interesting success stories that use Next-generation Sequencing (NGS) and different strategies in order to analyze the large amount of the generated data. In the first case, we analyzed a wood industry bacteria that participates in the process of by-products involved in the treatment of raw material for paper production. The genomic analysis showed an important part of its metabolic pathway that eliminates the chlorinated compounds that damage the environment. On the other hand, in the second case associated with the pulque industry, the bioinformatic analysis of a bacteria demonstrated an important association of its genome with the production of this beverage. In both cases, we focused on the art of asking specialists from different industry fields in order to collaborate and generate new bioinformatics solutions and achieve the aims of interest.

Oxygen and biological evolution: some major biogeochemical consequences

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Prior to the evolution of the evolution of oxygenic photosynthesis, sources of free oxygen were scarce. Free molecular oxygen constitutes 21% of present-day terrestrial atmosphere and its main source is, essentially, oxygenic photosynthesis. Accumulation of free atmospheric oxygen during the Precambrian is, undoubtedly, one of the major changes in the history of the planet and may be considered the most significant biogeochemical process after the origin of life itself. The evolution of oxygenic photosynthesis during Precambrian times entailed the diversification of strategies minimizing reactive oxygen species-associated damage and, eventually, the emergence of oxygen-dependent metabolic pathways which evolved first in bacteria and are pervasive in contemporary eukaryotes.

Understanding the biogeochemical consequences of the transformation of the primitive atmosphere depends on a variety of perspectives that include the study of atmospheric evolution, comparative sedimentology, paleontological studies, isotopic geochemistry, microbial ecology, comparative biochemistry and physiology, evolutionary genomics, proteome analysis and molecular phylogenies. Using these different approaches, it will be argued that the accumulation of free oxygen in the terrestrial atmosphere may have led to the extinction of many ancestral lineages (?); a spatial redistribution of microbial species; O_2-sensing mechanisms, including haemoglobins & hemerythrins;
the development of protection mechanism of polyphyletic origin, including the emergence of archaeal Dps-like protein; protein (msrA, msrB) and DNA repair mechanisms; and the development of eukaryotic membranes and compartments.

Leveraging bacterial secretion systems to develop therapeutic designer probiotics

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Type III secretion systems are complex nanomachines common to numerous bacterial pathogens that enable the bacteria to directly inject proteins into host cells. These systems are essential virulence determinants that enable pathogens to usurp host cell processes such that they can establish a successful infection. Efforts of the Lesser Lab, which are the subjects of this talk, are focused on determining how the secreted proteins are defined within the bacterial cytosol, defining how individual bacterial proteins manipulate host cells and lastly, on applying these findings towards the development of novel designer probiotics capable of directly injecting therapeutic payloads into the intestinal lumen.

Rotavirus strategies to control de antiviral response of the cell: A dynamic story

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General stress responses and innate immune responses are intimately linked and interface at many levels. The outcomes of these responses serve to reprogram host expression patterns to prevent viral invasions. In turn, viruses counter-attack these cell responses to ensure their replication. The mechanisms by which viruses attempt to control host cell responses are as varied as the number of different virus families.
Interestingly, the first step to control the antiviral response of the cell, and a very resorted solution used by several virus families is to hijack the translation machinery of the host, such that the translation of viral proteins is ensured, while the expression of the stress and antiviral responses of the cell are blocked at the translation level.
As in any other viral infection, rotaviruses the most important cause of acute gastroenteritis in childhood, trigger an antiviral response in their host cell. We are interested in learning how these viruses deal with the different branches of this response that are turned on upon infection. We have found that early on infection rotavirus induces a shut-off of the cell protein synthesis in which several cellular components of the translation machinery are compromised by the virus. Also, we have found that the organization of the cellular RNA granules is disturbed by the infection, and the OAS-RNAse L system, which is one of the initial antiviral measures of the cell upon sensing dsRNA becomes disabled during rotavirus infection. In this talk I will discuss some of our recen advances in these topics.

FOOD MICROBIOLOGY

Synthesis of glycopolysaccharides in traditionally fermented foods.

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The origins of microbiology date back to the discovery of how microorganisms transform natural products to more stable "fermented foods". Food securiry has also one of its major concerns in the toxicological implications of contaminated food with patogens. Modern food science, through advances in molecular microbiology, human physiology and metagenomics have revealed not only that microorganisms in our interior spaces are fundamental for our health and well being, but also that our relation with our intestinal microbiota requires a permanent attention to what we eat. The "*hygiene hypothesis*", stablishes how "*exposure since our childhood to microorganisms protects us of allergic diseases by contributing to the development of our immune system*". Paradoxicaly, while the main concerns of Food Security are health deseases derived from food contamination with patogens, according to the hygiene hypothesis, it is the lack of contact with certain "benefical patogens" which is responsable for many modern deseases. In effect, most industrialized fermented products, are safe, as they follow ISO international norms of quality and security control.

In this context, traditionally fermented products still consumed all over the world present interesting properties, now the subject of intensive research by different groups. I refer here of course of metagenomic studies that allow knowledge of the microbial bodiversity of natutaly fermented systems and their interaction and influence with our gut microbiota. Similarly, complex carbohydrates represent the largest component of fermented based foods now recognized for their dietary importance, not only in terms of human nutrition, but also as par of soluble fiber, and more importantly, as the basis of prebiotics, modulating the gut microbiome. Some of these carbohydrates are inherent components of the fermented products (starch, cellulose & hemicellulose, pectin, fructans, glucans and complex oligosaccharides, amomg others). Nevertheless, in some fermented products, the synthesis of complex glycopolysaccahrides are part of the main microbal transformation.

In my research group we have studied the properties of bacteria associated to the synthesis of glucans and fructans in traditionally fermented foods. This is the case of *natto* (a soya fermented product), *pulque* (fermeted zap obtained from agave) and *pozol* (fermented corn), where sucrose is the substrate of enzymatic transformations leading to products such as *glucans* (dextrans, alternans or reuterans), as well as *fructans* (microbial inulin or levan). Nevertheless, these type of transformations also occur in fermented systems studied all over the world (eg *sourdough, kimchi*, …) carried out mainly by bacteria from the *Leuconostoc, Lactobacillus, Bacillus* and *Weissella* genus. In this conference we will review some of the main properties of these important componente of fermented foods, their microbial origin, describing the properties of some of the species we have isolated and characterized from fermented foods, specifically, the properties of their enzymes and the way they synthesize complex carbohydrates.

Host-Microbiota Interactions in Health and Disease

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The intestinal tract of mammals is colonized by a large number of microorganisms including trillions of bacteria that are referred to collectively as the gut microbiota. These indigenous microorganisms have co-evolved with the host in a symbiotic relationship. In addition to metabolic benefits, symbiotic bacteria provide the host with several functions that promote immune homeostasis and protection against pathogen colonization. Our laboratory is using *Citrobacter rodentium*, a mouse pathogen that models human infections by enteropathogenic *E. coli* to understand the mechanisms by which the microbiota promote clearance of the pathogen in the gut. Owing to immature immune systems and impaired colonization resistance mediated by the microbiota, infants are more susceptible to enteric infection. We will show new results demonstrating that pathogen-specific IgG in breast milk induced during maternal infection or maternal immunization protects neonates against infection with *C. rodentium*. Bacterial symbionts can also promote disease including inflammatory disorders such as Crohn's disease in genetically susceptible individuals. We will show results that demonstrate that particular symbiotic bacteria can accumulate in the intestine and trigger Crohn's disease-like colitis in mice with mutations relevant to the development of inflammatory bowel disease.

Methicillin-resistant *Staphylococcus aureus* and its persistence in hand hygiene

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Abstract. Healthcare-associated infections (HCAIs) are a significant cause of mortality worldwide, affecting 4 to 20 out of every 100 patients admitted to acute care hospitals. Bacteria from the ESKAPE group with multidrug-resistance characteristics are common causes of life-threatening HCAIs. Hand hygiene is the most important measure for preventing nosocomial infections and has proven to be effective in reducing the attack rate of methicillin-resistant *S. aureus* (MRSA). The aim of this work was to describe the impact of hand hygiene adherence, HCAIs rates and MDR organisms, including pulsed field gel electrophoresis (PFGE)-molecular typing of MRSA strains. The program included Infection Control by Integration and Innovative Strategies based on a multimodal hand hygiene strategy and the evaluation of the clonality of MRSA, by genetic diversity techniques such as pulsed field gel electrophoresis (PFGE). The results showed that the hand hygiene adherence during the first 8 months was 34.9%, increasing trend throughout the study period up to 80.6%. The rate of HCAIs decreased from 7.54 to 6.46/ 1000 patient-days. The attack rate for MDR-ESKAPE group bloodstream infections significantly decreased, from 0.54 to 0.20/100 discharges at the end of the study period. There were significant decreases in the attack rates for MRSA, but this pattern was not observed for Gram-negative pathogens. A total of 17 DNA pulsotypes that grouped into three clusters (I–III) were identified. Briefly, 33.33% (7/21) of the pulsotypes grouped in cluster I, 9.52% (2/21) grouped in cluster II and 57.14% (12/21) grouped in cluster III. A clonal relationship among MRSA clinical strains was observed in pulsotypes 6 and 7 in cluster III during this study. In addition, the other MRSA strains were diverse and located in the other subgroups. A reduction in the number of MRSA strains was observed during the first year after implementing the multimodal hand hygiene programme; however, pulsotypes 6 and 7 were still identified during this 12-month period. Interestingly, the most prevalent pulsotypes, 6 and 7, were no longer detected after one year with sustained hand hygiene adherence above 60 %, but new, unrelated MRSA pulsotypes were identified. Conclusions. A multimodal hand hygiene programme in a paediatric hospital in a middle-income country was effective in improving adherence and reducing HCAIs, and MDR-ESKAPE bloodstream infections. Sustaining hand hygiene adherence at a level of >60% for one year limited MRSA clonal transmission.

Technological platforms based on industrial microbiology and its role solving social problems, a third-party laboratory perspective.

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While industrial microbiology continues to add different types of knowledge and disciplines as work tools, paths open to the application of science. These paths are opportunities to consolidate technological platforms that systematically fulfill social needs; the case of Laboratorios de Especialidades Inmunológicas.

Human African Trypanosomiasis evolution and Cell Death in *Trypanosoma brucei brucei*.

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Humans can survive bloodstream infection by African trypanosomes, such as *Trypanosoma brucei brucei*, owing to the trypanosome-killing activity of serum complexes. The two trypanosome subspecies that are responsible for human sleeping sickness, *T. b. rhodesiense* and *T. b. gambiense*, can evade this defence by expressing distinct resistance proteins. In turn, sequence variation in the gene ApoL1 that encodes the trypanosome-killing component in human serum, has enabled populations in western Africa to restore resistance to *T. b. rhodesiense*, at the expense of the high probability of developing kidney sclerosis. These findings highlight the importance of resistance to trypanosomes in human evolution. Apolipoprotein L1 (APOL1) induces both lysosomal and mitochondrial membrane permeabilization (LMP and MMP) and cell death coincides with MMP and consecutive release of the mitochondrial TbEndoG endonuclease to the nucleus, where it mediates DNA fragmentation. APOL1 is associated with the kinesin TbKIFC1, of which both the motor and vesicular trafficking VHS domains are required for MMP, but not for LMP. The presence of APOL1 in the mitochondrion is accompanied by mitochondrial membrane fenestration, which can be mimicked by knockdown of a mitochondrial mitofusin-like protein (TbMFNL). Thus, cell death by APOL1 is linked to apoptosis-like MMP. A very recent update on this project will also be presented.

Success cases of biotechnology in Mexico

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Biotechnology is part of the tertiary sector of the economy. It is a high tech industry that produces high value products. Requires the use of highly educated professionals and high capital investments. The contribution of this sector to the economy is very important in developed countries.

Mexico is an emerging economy that has already a critical mass for the development of this industry, counts with several academic institutions that produce professionals and many potential products. However, the number of biotechnology-based industries in Mexico is low. In order to increase this industry, is necessary to have better and stronger relationships between the academy and industry.

This talk reviews three cases of success collaboration between the academy and industry. That produced a clear knowledge and technology transfer. Each case represents a clear way to collaborate with the industry and includes entrepreneurship, consulting and technology transfer.

Each country has regulatory and political frame work that impulse, or not, the creation of new products and enterprises, a better frame work could impulse the creation of spin-offs in Mexico, that could contribute in the creation of economic value to take our country to the first world.

Amphibian-Microbial symbioses: understanding the protective role of skin bacteria against emerging diseases

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Chytridiomycosis, caused by the pathogen *Batrachochytrium dendrobatidis* (Bd) and *B. salamandrivorans* (Bsal), has led to population declines and extinctions of frog species around the world. While it is known that symbiotic skin bacteria can play a protective role against pathogens, we still know very little about how these defensive bacteria are integrated into the bacterial community on the amphibian skin and how they exert their protective role. In my lab, we want to understand the factors shaping skin microbiomes and the antifungal capacity of skin bacteria through the use of next generation sequencing technologies. We are analyzing the protective functions present on symbiotic bacterial strains through the use of genomic and functional *in vitro* assays. We are also describing the interactions occurring between microbial communities and their hosts with the aim of understanding the nature of these symbioses and their evolutionary implications. In this talk, I will give an overview of the factors influencing bacterial communities in amphibians. Also, I will talk about the projects we are developing in my lab using 16S rRNA gene amplicon sequencing, culturing and fungal inhibition bioassays to characterize the communities of skin bacteria in different amphibian species. We are currently addressing three main questions: How does the host shapes its microbiome? What ecological interactions are occurring within the community? How does abiotic and biotic factors shape the structure and function of skin communities. To answer these questions, we are studying several Mexican salamander and frog species including the endangered neotenic species *Ambystoma altamirani*.

Nicotine induces virulence genes in *Mycobacterium tuberculosis*.

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Tobacco consumption is a worldwide health problem causing millions of direct or indirect deaths. The nicotine is a chemical contained in cigarette smoke. Smoking increased the risk of heart diseases, lung cancer and risk of bacterial infections such as tuberculosis.

Tuberculosis is a bacterial infection caused by Mycobacterium tuberculosis (Mtb). Although it has been well described the physiological and pathogenic effects of nicotine in the smokers, scarce information has been provided regarding how Mtb responses to the interaction with nicotine and whether this interaction promotes virulence factors expression.

Our results show that nicotine enters and is distributed evenly in the cytoplasm of type II pneumocytes and in infected cells the physical interaction between nicotine and Mtb intracellular.

To assess whether the presence of nicotine has a direct effect on the growth of Mtb, its optical density is evaluated for 29 days. The results show that the bacterium increases its growth and reversing the effect with nicotinic receptor antagonists in mammals, is proposes the bacterium can have a structure capable of recognizing nicotine.

It is proposed to perform an RNA sequencing of the bacterium exposed to nicotine and compare them with a bacterium without exposure to obtain a complete panorama of the effect.

Detection and identification of yeasts from musts of three Mexican distilled beverages.

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The use of *Saccharomyces cerevisiae* strains as starters at industrial level to produce alcoholic drinks as beer, wine or spirits as tequila or whisky is a common practice. Selected strains could be isolated either from the same must used to produce a specific beverage or from other kind of industrial process where ethanol is produced. When selected strain is added, fermentation is better controlled and the final product has good quality and high yields are obtained. Yeasts sold, generally by international companies, came in bags as dry yeasts, which are hydrated and then added to the fermentation tanks. However, industrial fermentation is not a sterile process therefore selected strains used as inoculum could be lost during the process or may coferment with other microorganisms, which are resident in pipes, or in the fermentation tanks and these microbiota could have better performance than the selected inoculum.

We have analyzed two industrial processes where selected yeasts are used to produce tequila; samples were taken from the propagation tanks until the end of the fermentation. Yeast with different morphologies were selected from WL agar an then identified by RFLP analysis of the 5.8S rRNA gene and the two ribosomal internal transcribed spacers followed by D1-D2 sequence of the 26S rRNA gene. *S. cerevisiae* yeasts were typed by interdelta fragments using 12δ and 21δ primers.

Selection of yeast strains were analysed from natural fermentations of mezcal and sotol, which are two kind of distilled alcoholic drinks, produced from plants of *Agave* genera the first one and, *Dasyrilion* genera the second one. Studies were carried out to identify yeasts and typify *S. cerevisiae* species from spontaneous fermentations. Yeasts from mezcal were first grouped using restriction fragments of the 26rRNA gene, then identified by D1-D2 region of the 26rRNA gene. Different yeast genera were used to ferment sterile agave must and volatile compound were identified and quantified using gas chromatography.

Eighteen *S. cerevisiae* strains previously isolated from natural sotol musts fermentations were first, identified by RFLP analysis of the ITS1, ITS2 and 5.8SrRNA gene. Yeasts strains were then typified and three strains showing different MS-PCR with GTG_5 and M13 and Interdelta patterns were selected. These three selected yeasts were put under different temperature, osmotic and ethanol stress conditions. Thereafter, fermentations in sterile sotol must were carried out and ethanol yield and fructose consumption was recorded.

Mechanisms of Phenotypic Heterogeneity in *Clostridioides difficile*

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Phenotypic heterogeneity within a genetically clonal population allows many mucosal pathogens to survive within their hosts, balancing the need to produce factors that promote colonization with the need to avoid the recognition by the host immune system. Our work has shown that the human intestinal pathogen *Clostridioides difficile* employs phase variation by site-specific DNA recombination at multiple genetic loci, suggesting vast potential for phenotypic heterogeneity. Recombination at these loci results in defined, reversible DNA inversions that control the expression of adjacent genes. Among these loci is a large operon of genes required for flagellum biosynthesis, and phase variation at this site results in a mixed population of *C. difficile* with and without flagella. More recently, we found that *C. difficile* reversibly differentiates into rough and smooth colonies. Bacteria derived from the isolated colony types display distinct motility behaviors. We linked these phenotypes to a reversible DNA inversion that controls the expression of genes encoding a putative signal transduction system, which we named CmrRST. Over-expression of the response regulator genes *cmrR* and *cmrT* indicated that they similarly regulate colony morphology and motility behaviors. However, inactivation of the individual genes revealed that they are not redundant and have discrete functions. In a hamster model of acute *C. difficile* disease, the CmrRST system was required for disease development, and we observed evidence of CmrRST phase variation during infection. These results suggest that the intestinal environment impacts the proportion of CmrRST-expressing *C. difficile*. Our studies indicate that *C. difficile* employs phase variation to generate phenotypic heterogeneity during infection, with concomitant effects on bacterial physiology and pathogenesis.

Defining the role of toxin-antitoxin systems in the persistence phenotype of the intracellular pathogen *Burkholderia pseudomallei*.

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Burkholderia pseudomallei is the causative agent of melioidosis, a disease that has high mortality rates if left untreated and despite the ability of certain antibiotics to control infection, relapse occurs in 15-23% of treated patients. The inability for the antibiotics to kill *B. pseudomallei* is due to persistence, a mechanism used by bacteria to enter a dormant state and evade the effects of antibiotics and host defenses. This evasion mechanism has been implicated in nearly all bacterial infections that result in relapses or chronic stages of infection. Testing clinically relevant antibiotics showed that up to 40% of a *B. pseudomallei* population can survive in a persister state. The major modulators of persistence are known as toxin-antitoxin systems, which act by inhibiting transcription, translation, replication, and altering the metabolome, when activated by environmental stresses. Because there was no predictive model to determine which toxins are essential for bacterial survival in the host in response to different environmental stresses, we used existing bioinformatic data to define the expression levels of the 106 toxins found in *B. pseudomallei*. Investigation of over 82 different conditions showed that at least 5 novel toxins are highly expressed in host-associated conditions. Of the 5 highly expressed toxins, 3 are functional when over-expressed and functions are currently investigated. Because our data also showed that numerous toxins are induced with antibiotic exposure, targeting toxins associated with antibiotic persistent is not ideal for drug development; however, toxins associated with persistence in the host may be viable for drug design.

FROM MOLECULAR EPIDEMIOLOGY TO THE BIOCONTROL OF *Staphylococcus aureus* IN BOVINE MASTITIS

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Staphylococcus aureus is an exciting model for genetic diversity and pathogenesis studies because of its versatility as a pathogen. It is the causal agent of human enteric infections, hyperimmune responses (toxic shock syndrome), community-acquired (CA) infections in skin and soft tissue, health care-acquired (HA) infections as bacteraemia, endocarditis and osteomyelitis and animal infections as livestock-associated (LA) or those affecting companion animals. The onset of molecular typing techniques as multilocus sequence typing (MLST), single-nucleotide polymorphism analysis of the *spa* gene (*spa*-typing) and macro-restriction analysis in pulse-field gel electrophoresis (PFGE), along with whole genome sequencing (WGS) approaches, had contributed to identify specific genotypes associated with host range or a particular pathology, functional polymorphisms in virulence genes and understand the evolution of the pathogen. *S. aureus* is also classified by World Health Organization in the “Priority 2 (Elevated)” level group for which novel antibiotic agents are needed. Bovine mastitis in its clinical and subclinical forms, is an elusive disease that impacts milk production economy. In the state of Michoacan, the production systems are largely based on low-scale family farms. In a survey of bovine mastitis cases in the milk production region surrounding Morelia City, all resulted to be methicillin-sensitive *S. aureus* (MSSA) strains grouped mainly to Clonal Complex (CC) 5, subgroup ST97 (ST97, ST352), and subgroup ST126 (ST126), both reported as related with bovine mastitis. Strains from CC 8 (ST8) related with a successful genotype from CA infections were also observed. The strains showed different *spa*-types, PFGE profiles and antimicrobial resistance patterns. We used this information to select strains from the most prevalent genotypes for lytic bacteriophage isolation. A collection of 28 lytic bacteriophages was analysed to evaluate its host range, restriction fragment length polymorphism profiles and stability under a range of pH and temperatures. Bacteriophages were genotype-specific, since those isolated with ST97 or ST352 strains do not infected ST8 strains and showed host ranges according to the strain from which they were isolated. Endolysin gene sequences from bacteriophages were analysed, showing that they were homologous to previously reported LysK endolysin. They were highly conserved at their catalytic domains and presented more polymorphisms in the substrate binding domain. To avoid the genotype-specific character of bacteriophages, an inducible expression vector was designed to express one of the endolysins in a probiotic bacterium. Altogether these approaches emphasize the need to precisely know the genetic background of pathogenic bacterial strains in order to design tailor-made biocontrol solutions as an alternative to antibiotic treatments.

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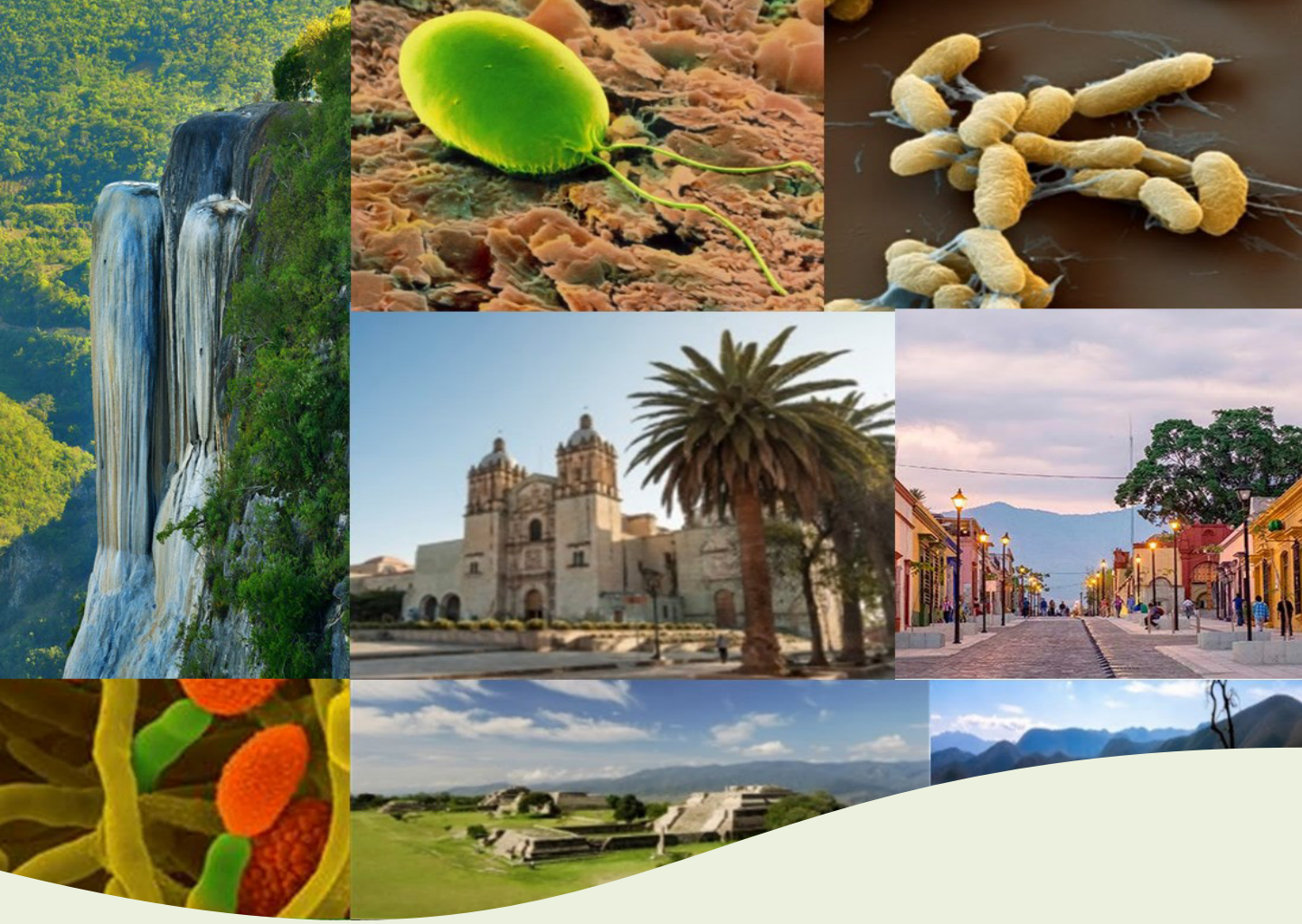

Oral Abstracts

XLI National Meeting of the Mexican Association of Microbiology (AMM)
VI Meeting of Biochemistry and Molecular Biology of Bacteria (BBMB)

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The effect of the number of chambers on the performance of a *MESynC* that produces succinic acid by *A. succinogenes*

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Succinic acid (*H_2Succ*) or butanedioic acid is known to be a "building block" of several synthesis processes; it can be transformed into a wide range of products that can be used in the food, solvents, and plastics/polymer industries, among others. The *H_2Succ* is a value-added product and to some extent its relatively high cost is related to the separation and purification processes that can account for 50% to 80% of the final cost. *H2Succ* is typically produced by petrochemical means, although its microbial production is receiving an increasing attention in recent years. The microbial electrosynthesis cells (*MESynC*) consume electrical energy to boost reducing power in order the biocatalysts to synthesize more chemical compounds of interest. Thus, the objectives of this work were the following: *(i)* to and determine the effect of the membrane type, and *(ii)* to evaluate the effect of the number of chambers, on the performance of *MESynC* producing succinic acid in terms of the production, concentration, and purification of *H_2Succ*. Two anionic membranes were tested to separate the cathodic chamber from the intermediate chamber, the Zirfon ® and the Fumasep ® FAA3-PK-130 membranes, in the 3-chamber *MESynC*. Lab scale *MESynC* with 2 and 3 chambers cell configuration were built and used (2c-cell and 3c-cell, respectively). The 2c-cell was equipped with Nafion membrane as separator. The substrate was a hydrolyzate of the organic fraction of municipal solid wastes with a typical concentration of 21.5 g/L reducing sugars (*RS*); all the cells were inoculated with *Actinobacillus succinogenes*.

The 3-c cell equipped with Zirfon membrane did not transfer the *H_2Succ* to the intermediate chamber (neither transferred concomitant organic products) whereas the 3-cell with Fumasep did transfer up to 0.37 g/L *H_2Succ* at the end of 72 h operation. The 3c-cell with Fumasep exhibited a yield of 0.146 g of *H_2Succ*/g $RS_{consumed}$, the electrical energy consumed in the period was 1.36 kJ; the *H_2Succ* and the concomitant products were transferred to the intermediate chamber, with formic acid, acetic acid and finally succinic acid being favored. For the 2-c cell the yield and the electrical energy consumed were 0.196 g of *H_2Succ*/g $RS_{consumed}$ and 1.59 kJ, respectively; therefore, 3c-cell had 25% lower performance in terms of the yield. The index $\varepsilon_{H2Succ/ee}$ defined as the ratio between mass of *H_2Succ* produced and electrical energy consumed (*ee*) exhibited values $3.60E10^{-7}$ kg *H_2Succ*/J and $4.24E10^{-7}$ kg *H_2Succ*/J for the 3c-cell and 2c-cell, respectively.

In summary, the 2-c cell has better performance and energy use and mass *H2Succ* produced of than the 3-c cell, and the purification of the desired product in the third camera was not achieved as expected.

Analysis of Gp37 function of the coliphage mEp021

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Bacteriophages are of great importance in the enviroment and are recognized as the most abundant biological agent on Earth. Usually we can find them in water, soil, food and human gut. The latter is a good source to find a diversity of phages, also the phage mEp021 that infects *E. coli*, was isolated from human faeces *(Virology, 1999)* and was defined as a non-lambdoid phage due to its regulation and growth that differ from the lambdoid phages. However, it requires Nus factors of the host bacteria as many lambdoid phages need to carry out the antitermination process. In the mEp021 genome, there is a gene annotated as Q-like antiterminator (Gp37) whose product allows the development of lambda phage on *nus* mutant lawns. Despite of the structural similarity between λQ antiterminator and Gp37, this can not restore the mEp021 growth on *nus* mutant and it can not even recognize the *qut* region in the pR' promoter, which is essential for λQ activity. This was observed by expressing Gp37 in an antitermination reporter system (λpR'[qut]-tR'-GFP) to determine the fluorescence (RFU) given by the GFP expression. On the other hand, a probably promoter region (2082 bp) located downstream of gp37 in the mEp021 genome, was cloned in a reporter system (p5x021[tR]-GFP). Analyzing the fluorescence data (RFU), Gp37 possibly recognize at least one promoter within the p5x021 region, which is conserved in most of the phages sequence-related with mEp021. Having this approach, we consider that Gp37 is essential for the production of viral progeny of mEp021 phage. Therefore, we used the recombineering technique *(modif. PNAS, 2000)* for knocking Gp37 in mEp021 genome. We replaced Gp37 gene with kanamycin resistance cassette and tested by PCR and phage production. The mutant could not produce viral particles on a sensitive strain, only in the presence of Gp37 which is expressed in a plasmid (p37) by a tac promoter.

So we conclude that Gp37 is a potential antiterminator and is essential for mEp021 development. However, It is necessary to evaluate the transcripts related to structural genes of the mutant phage and in the presence of p37. Although it shares similarity in 3D structure with λQ, it may needs a specific sequence. For mEp021 phage antitermination, Gp37 may require a sequence located several base pairs downstream of this gene to perform its activity, opposite to λQ which recognize the *qut* sequence located inmediately after λQ gene.

Silencing of unused sectors of the E. coli proteome using CRISPRi and its application in synthetic biology.

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Introduction. The adequate stability and predictability of synthetic circuits within the host organism are some of the main problems of Synthetic Biology. One of the main reasons is the limited availability of cellular resources, for which the genetic circuits and the endogenous machinery of the cell must compete, causing the phenomenon of metabolic overload (1). Microorganism express proteins whose function is to provide protection against negative effects of the eviroment dedicating a considerable part of their proteome to this function (2). A catalytically dead versión of the Cas9 enzyme (dCas9) is used in the CRISPRi system and is used to regulate gene expression at the transcrptional level without affecting the integrity of the DNA sequence (3).

The main objective of our work is to reduce the expression of non associated proteome sectors with the growth of E. coli to improve the integration of synthetic functions.

Methodology. We choose as TF's targets: *marA*, *csgD* and the sigma factor *rpoS*. Plasmid CRISPathBrick from Addgene repository (#65006) was used, which maintains the architecture of a CRISPR array (4). Plasmid pSEVA63-Dual was used, which contains a constitutively expressed GFP and RFP induced by acyl homoserine lactone (AHL). Allowing to quantify the fluorescence ratio of both protein, through the use of isocost lines, which allow to determine the managment of a given budget in an optimal way, in our case the said budget are the cellular resources (5).

Results. The assembly in the vector of the three gRNA's was achieved, and a double combinationof gRNA's was generated, with which it was possible to repress the expression of two TF's simultaneously. During the kinetic experiments the release of cellular resources was checked through an increase in fluorescence levels, compared to the fluorescecnce levels emitted by the wild strain. The double combination of simultaneously repressed TF's maintained fluorescence levels higher tan the rest of the starins with a single repressed TF.

Conclusions. Repressed transciptional factors using CRISPRi system were able to release enough cellular resources to increase fluorescent protein production. The double combination of repressed TF's was able to release a large amount of cellular resources, suggesting that this phenomenon may be additive.

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DEVELOPMENT OF A METHODOLOGY FOR THE GENETIC TRANSFORMATION OF *Agave tequilana* Weber var. Azul MEDIATED BY *Agrobacterium tumefaciens* AND BASED ON ORGANOGENESIS

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The Agave tequilana Weber var. Azul is the most cultivated agave species for being the source of carbohydrates and minor chemical components for tequila production. Due to the traditional way of cultivating the agave by means of suckers and without allowing flowering, its genetic diversity is very limited. This has generated more vulnerable clones to new and more aggressive pathogens, generating uncontrolled diseases in crops of large geographical areas, which, in turn, leads to high economic losses. On the other hand, the study of genes of interest in this genus is very limited, so genetic manipulation is a valuable support for numerous research and applications of both scientific and industrial interest.

Taking these limitations into account, an *in vitro* propagation system was developed via organogenesis of *Agave tequilana* using apical meristems obtained from bulbils as explants. A minimum size of regenerable explant with a high capacity for sprout formation (20 CFB) was obtained from a cross section in bulbil meristems. The explants were exposed in agar medium with Eriksson / Linsmaier-Skoog salts and the best response based on regeneration was found using indole-acetic acid (IAA) as a source of auxin and benzyl-amino-purine (BAP) as source of cytokinins. The presence of buds was observed in the first four weeks; the buds were separated and transferred to rooting medium for elongation, and finally at six months they were taken to the greenhouse with 100% adaptation. On the other hand, a genetic transformation protocol was established through the *Agrobacterium tumefaciens* system and the optimal conditions of transformation were determined: tissue damage, liquid bacterial culture, 16 hours of explant-bacterial exposure, regeneration medium and selection of transformants. The material transformed with the plasmids pXBb751-UBIL and pXBb-7-F-F-UBIL was manipulated for the evaluation of the stable transformation by histochemical analysis and PCR, obtaining transformation efficiencies of 1% and 1.5%, respectively.

This methodology is proposed as the basis for the genetic improvement of agaves. It is intended in the future to achieve the manipulation of genes that improve the growth time of the plant, the concentration of carbohydrates in the stem, resistance to bacteria or fungi and combat to the most frequent diseases in crops.

Phenotypic trait diversity of budding yeast populations associated to Agave fermentation in Mexico

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The budding yeast *Saccharomyces cerevisiae* is a model organism widely used to understand eukaryotic cells thanks to its small genome, short life cycle, and powerful genetic tools. However, its natural history is poorly understood. In the specific case of Mexico, very little is known about the population structure and ecological dynamics of this microorganism, despite of its importance during the fermentation processes required for the production of traditional alcoholic beverages throughout the country. In this study, we have generated a collection of 2400 yeast strains associated to Agave fermentation, isolated specifically from 60 mezcal factories in the States of Colima, Durango, Estado de México, Guanajuato, Guerrero, Jalisco, Michoacán, Oaxaca, Puebla, San Luis Potosí, Sonora, Tamaulipas, and Zacatecas. Yeast strains were identified at the species level by mass spectrometry profiles; 58% corresponded to *S. cerevisiae*. We will present our results of the budding yeast population structure in Mexico, based on the large-scale phenotypic characterization of over 1400 isolates grown under different laboratory conditions. Our study provides insights not only into microorganismic domestication for Agave fermentation, but also into the natural history of budding yeast in the context of a megadiverse country.

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Establishment of a protein concentration gradient in the outer membrane requires two diffusion limiting mechanisms.

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OmpA-like proteins are involved in the stabilization of the outer membrane, resistance to osmotic stress and pathogenesis. In *Caulobacter crescentus* OmpA2 forms a polar concentration gradient in the outer membrane. This pattern is physiologically relevant and establishes by a novel mechanism, in which the gradient orientation depends on the position of the gene locus. This suggests that OmpA2 is synthesized and translocated to the periplasm close to the position of the gene and that the gradient forms by diffusion of the protein from this point. To understand the molecular mechanism that determines the formation of this gradient, we characterized the localization and mobility of the full protein and of its two structural domains, an integral outer membrane β-barrel and a periplasmic peptidoglycan binding domain. We show that OmpA2 does not diffuse and that both domains are required for gradient formation. The C-terminal domain binds tightly to the cell wall and the immobility of the full protein depends on the binding of this domain to the peptidoglycan, in contrast the N-terminal membrane β-barrel diffuses slowly. Our results support a model in which the formation of the OmpA2 gradient occurs in two steps. Once OmpA2 is translocated to the periplasm, the N-terminal membrane β-barrel is required for an initial fast restriction of diffusion, until the position of the protein is stabilized by binding of the C-terminal domain to the cell wall. Elucidation of the mechanisms that limit the OmpA2 diffusion is of special interest because protein concentration gradients are not common in bacteria, but they play a relevant role in cell organization. Additionally, we show that the OmpA2 outer membrane β-barrel can diffuse in contrast to what has been reported previously for several integral outer membrane proteins in *Escherichia coli*, suggesting a different organization of the outer membrane proteins.

Single-cell plasmid dynamics in fluctuating environments

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Plasmids are extra-chromosomal and self-replicating DNA molecules that enable horizontal transmission of genes between bacterial hosts and, therefore, can be important drivers of bacterial evolution. Moreover, recent studies have argued that multicopy plasmids can be more than simple vehicles for genetic interchange, as they can (1) accelerate the rate of adaptation (by increasing the probability of appearance of a beneficial mutation and subsequently amplifying its expression), and (2) alleviate evolutionary trade-offs (by producing a genetically-diverse population where ancestral and mutant alleles co-exist). Here we use high-throughput microfluidics and image processing algorithms to quantify plasmid copy-number distributions with single-cell resolution. In particular, we use a well-characterized system of drug resistance evolution (plasmid-mediated TEM-1 evolution towards Ceftazidime resistance in Escherichia coli) to evaluate the effect of different plasmid configurations in bacterial fitness. Furthermore, we use a computational approach that implements a multi-scale agent-based model to study the impact cell-to-cell variabilities in plasmid copy number have on the evolutionary dynamics of plasmid-bearing populations in fluctuating environments. Both our theoretical and experimental approaches show that multicopy plasmids can maintain genetic diversity in individual cells, suggesting that bacterial communities may use multicopy plasmids as platforms that enable the implementation of bet-hedging strategies to increase the probability of survival in stochastically-switching environments.

The CtrA regulon of *Rhodobacter sphaeroides* favors adaptation to particular life styles.

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CtrA is a response regulator widely distributed among alpha-proteobacteria which regulates the trancription of genes involved in cell division, flagellar biogenesis and chemotaxis. Using RNA-seq, we identified the CtrA regulon in *Rhodobacter sphaeroides*, which comprises 321 genes distributed in several functional categories. From these, 239 were positively controlled and 82 were negatively regulated. Genes encoding for the Fla2 polar flagella, gas vesicles, and pilus are activated by CtrA; as well as genes involved in stress responses, c-di-GMP metabolism, and several transcription factors. In contrast, the photosynthetic and CO_2 fixation genes are repressed by this protein. Potential CtrA-binding sites were bioinformatically identified leading to the proposal that 175 genes could comprise the direct regulon. Aditionally, we identified that 4 sRNAs previously reported in this bacteria are transcriptional targets of this protein.

Further studies on the role of CtrA in the physiology of this bacterium led us to propose that the transcriptional response controlled by CtrA enables a lifestyle in which *R. sphaeroides* will populate the surface layer of a water body enabled by gas vesicles. Simultaneously, fine tuning of photosynthesis and stress responses will reduce the damage caused by heat and high light intensity in this water stratum. Interestingly, under certain conditions CtrA and the quorum sensing system promote biofilm formation.

In summary, in this bacterium CtrA has evolved to control physiological responses that allow its adaptation to particular life styles instead of controlling the cell cycle as occurs in other species.

Phenotypic plasticity by reaction norms in *Bacillus* spp. species from wild environments from Cuatro Ciénegas Coahuila desert facing physical environmental factors

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Adaptation to temperature is an important trait among organisms that strongly determines life-style in microbial world. Since temperature is a physical variable in the environment it can affect a lot of biological functions to expose a great diversity of phenotypes as a signature in species such as molecular features and patterns in growth and because *thermal adaptation* is the outcome of a collective process and some characteristics can also be related and identified at the level of genotype.

A way to understand the influence of genotype coping a specific selective pressure is evaluating a system in near close species with similar genotypes between two species such as *Baciilus subtilis* and *Bacillus cereus*. Both species has been a great model to compare adaptation. So we evaluated difference sin genotype and phenotype concerning thermal adaptation on both species with a wide variety of isolates from natural systems at high temperatures (Hot springs in Michoacán) and medium temperatures (temperate lagoons in Cuatro Ciénegas Coahuila) that have evolved in a close relationship in their original and natural environmental space. We also evaluated genotypic features (mutations) relative to temperature adaptation and reaction norms of the same both species evolving 1000 generations under laboratory experimental evolution (artificial adaptation) submitted to strong selective pressure of different temperatures.

Results in growth patterns, reaction norms and genotypic features reveal that thermal adaptation has reflected a dependence, of tolerance to temperature, with species stronger than with environment isolation as might be expected; *genotype over environment*. It suggest, so far, that evolving history has determined a more stable genotype in a intra-species way, that determines thermal adaptation, despite the comparative differences in temperature in their original two environments and as *B. cereus* seems to be a specialist microorganism, *B. subtilis* appears more a generalist organism in both environments . As well as some common intra-species features in evolving strains under experimental evolution, *B. cereus* had suffered stronger modification in reaction norms after laboratory adaptation.

CreR, an EIL domain-containing protein, positively regulates the expression of the *ecp* fimbrial operon in *Citrobacter rodentium*

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Citrobacter rodentium is a bacterium that causes colitis and transmissible murine crypt hyperplasia, which shares 67% of its genes with enteropathogenic *Escherichia coli* (EPEC) and enterohemorrhagic *E. coli* (EHEC), both causal agents of human diarrheal diseases around the world. These pathogens produce the A/E (attaching and effacing) lesion on the surface of enterocytes, which is mediated by the gene products encoded within the locus of enterocyte effacement (LEE). Surface structures called fimbriae or pili, often mediate adherence of these bacteria to host epithelial cells. The *E. coli* common pilus (ECP), present in commensal and pathogenic *E. coli* has been shown to play a role in pathogenic *E. coli* interactions with environmental reservoirs and host epithelial cells.

As for *E. coli*, the *C. rodentium ecp* operon is a cluster of five genes (*ecpABCDE*) encoding proteins involved in the assembly of the fimbria, which expression is favored in static DMEM cultures at 26°C. Using an ecp-cat transcriptional fusion, mutant strains, and 3XFLAG-tagged derivates, we found that, in contrast to *E. coli*, CreR, a novel protein with a conserved cyclic-di-GMP phosphodiesterase domain, is essential and specific for *ecp* activation. The *creR* gene is located downstream of the ecp operon and co-transcribed as part of it; however, its expression is also directed by a putative *creR* promotor, which responds to the same growth conditions than *ecp*. Single and double mutants carrying the *ecp-cat* fusion and Electrophoretic Mobility Shift Assays showed that the global regulators IHF and H-NS control *ecp* expression positively and negatively, respectively. CreR and IHF were still needed even in the absence of H-NS.

Moreover, a regulatory motif, named Distal Regulatory Element (DRE), is essential for CreR-mediated activation and perhaps the binding site of a positive regulatory protein responding to c-di-GMP levels. Using a synthetic chromogenic substrate, we found that CreR is a functional PDE; however, point mutations in conserved amino acids for PDE activity have only a partial or null effect in the CreR-mediated activation of *ecp* expression. We hypothesized that CreR has an additional novel regulatory function, which is essential to activate *ecp* expression in *C. rodentium*.

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Bacteria and Archaea distribution in subsurface sediments of the Gulf of Mexico

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Marine sediments are considered complex habitats in which microorganisms act as key drivers of biogeochemical cycles. The study of these microbes is of particular interest in understanding how the communities are affected by diverse environmental factors and how they respond at them to maintain a stable ecosystem. The Gulf of Mexico (GoM) has been affected by anthropogenic pollution and several oil seeps, this in combination with its natural history of depositional environments, makes the GoM sediments a crucial ecosystem for microorganisms community composition studies. The diversity of microbial communities in GoM sediments has been studied at different depths and it exhibits an excellent level of uncultured bacterial and archaeal diversity but very few studies contemplate the vertical distribution of the communities in the sediments bellow surface level and its relationship with geochemical variables.

In this study, we sample two regions of the GoM, Perdido region and Campeche knolls, we collected four sediment push cores of approximately 30 cm long (two for each region), then we sectioned the push cores every two cm. Physicochemical parameters: sulfate, nitrate, nitrite, ammonium and metal concentration were determined at every two cm layer. Additionally, to every sectioned layer DNA was extracted and the V3-V4 region of bacterial 16S rRNA the V1-V2-V3 region of archaeal 16S rRNA genes were amplified, these PCR products were sequenced using Illumina MiSeq sequencing technology. Data sets were processed using QIIME2 in combination with Silva 132 ribosomal ARN database.

Diversity analysis show a vertical stratification in the communities of microbes in the sediments, particularly in archaeon groups the order *Nitrosopumilales* dominates the upper layers (2-6 cm) and at the beginning of the 6-8 cm layer abundance decreases considerably in all four samples and other archaeal groups begin to appear according to the depth in the sediment. The diversity levels of bacteria are higher than archaea and the groups also change according to subsurface depth. Most of the assigned groups are related to *Proteobacteria, Planctomycetes* and *Chloroflexi*, which participate in the various geochemical processes like sulfate, nitrate, and carbon cycles.

Archaeal and bacterial diversity combined with geochemical data from each layer gives the possibility to generate beta diversity analysis that elucidates how the communities distribute, in response to electron acceptors, metals, nutrients and depth. Moreover, how these communities participate in geochemical cycles for maintaining a stable ecosystem in the Gulf of Mexico.

Study of enzymatic promiscuity at the enzyme level, family and metabolic pathway, and its role in genomic mining of natural products

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Abstract:

An enzyme is promiscuous when catalyzes more than one chemical reaction. Promiscuity is part of the evolutionary process providing material for metabolic innovation, as it is required in the synthesis of natural products (NPs). Often, this innovation is mediated by gene expansions because of gene duplications and horizontal gene transfer, which in turn leads to new enzyme families. Here we address promiscuity by distinguishing between promiscuous enzymes and promiscuous families. Then we generalize the concept of enzyme promiscuity to a biosynthetic gene cluster (BGC) responsible for the synthesis of natural products. To infer promiscuity in prokaryotic (pan)genomes we aimed at developing a series of bioinformatics tools: (i) Orthocore, which seeks to understand gene families preserved without expansions in a taxonomic lineage; (ii) EvoMining, directed to detect chemical innovation through the divergence of families from conserved metabolism. To do so, EvoMining finds families that do have extra copies and organizes these variations in possible metabolic destinations; and (iii) CORASON, with a level in organizational complexity higher, and seeks to understand the variation of groups of genes (BGCs). Scytonemin and detoxin BGCs, in Cyanobacteria and *Streprtomyces* respectively, are shown as examples of the production of molecular variations by BGC families. In-depth bioinformatics analyses, which in some cases were validated by experimental metabolomics analyses, will be presented. Overall, our results not only provide an state-of-the-art genome mining platform, but they help to decipher the metabolic origin and fate of enzymes through the course of evolution.

Characterization of a *Rhizobium etli* OmpR-type regulator that participates in motility and nitrogen fixation with bean plants.

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Two-component systems (TCS) are signaling modules composed by a sensor histidine Kinase (HK) that activates a specific response regulator (RR) through phosphorylation. The OmpR subfamily of RRs is the most abundant one and includes well characterized transcriptional regulators with a variety of physiological roles including the response to biotic and abiotic stressors and the adaptation to hosts. *Rhizobium etli* CE3, a soil bacterium that establishes an effective symbiosis with common bean plants, has 68 response regulators, 17 of them belonging to the OmpR subfamily. Despite their importance for survival under harsh conditions in multiple organisms, OmpR-type regulators remain poorly characterized in *R. etli*. To begin to understand how these regulators are implicated in the response of *R. etli* to different environmental conditions, we generated mutants and analyzed free-living and symbiotic phenotypes. Our results revealed that compared to the wild-type (WT) strain, a mutant lacking the gene *RHE_PC00057* (*pc57*) negatively affects motility in soft agar, and showed a delayed formation of nodules in bean plant roots resulting in a reduced number of nodules that are more effective in nitrogen fixation compared to WT nodules.

The gene *pc57* is predicted to be in an operon with *pc58* in the megaplasmid p42c. The product of *pc58* is a HK, to assess if PC58 could be the cognate of PC57 we conducted *in vitro* phosphorylation experiments. Our results strongly suggest that PC57 and PC58 form a TCS.

Using genetic reporters, we were able to demonstrate that *pc57-58* as well as the genes located immediately upstream and downstream of this operon can be strongly upregulated by PC57. One of these regulatory targets is *nodTc* (*pc59*) which encodes a nodulation protein. The nodulation kinetics of a mutant lacking *nodTc* were delayed compared to the WT strain but not to the full extent observed in the mutant lacking *pc57*. To further investigate the mechanism by which PC57 may affect nodulation and nitrogen fixation we analyzed the transcription of bacterial genes implicated in the nodulation and nitrogen fixation processes under symbiotic conditions. Together our results suggest that the novel response regulator PC57 plays an important role in processes that could influence the establishment of a symbiosis: motility, nodulation and nitrogen fixation.

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The CRISPR-Cas system is involved in the synthesis of outer membrane proteins in *Salmonella enterica* serovar Typhi

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The CRISPR-Cas cluster is found in many prokaryotic genomes including those of the *Enterobacteriaceae family*. *Salmonella enterica* serovar Typhi (*S*. Typhi) the etiological agent of Typhoid fever in humans presents a CRISPR-Cas Type I-E system organized in an operon regulated by LeuO, H-NS and Lrp. This genetic system contains multiple transcriptional units including antisense RNAs, whose genetic expression depends of minimal medium and basic pH. In this work was determined that CRISPR-Cas is involved in the negative and positive control of outer membrane proteins, since its presence repress partially the synthesis of OmpA and promotes OmpC and OmpF production. Furthermore, the LysR transcriptional regulator LeuO is unable to induce the expression and synthesis of the quiescents, OmpS1 and OmpS2 porins in *S*. Typhi devoid of CRISPR-Cas. Remarkably, the expression of the master porin regulator OmpR was CRISPR-Cas dependent, suggesting that CRISPR-Cas acts hierarchically on these transcriptional factors to control indirectly outer membrane proteins synthesis in *S*. Typhi.

Recognition of human colostrum bacteria by IgA subtypes and their effect on microbiota establishment in the newborn

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Colostrum is the most important source of nutrition, defense and colonizing microbiota for the newborn. In recent years, the characterization of the microorganisms belonging to the microbiota present in human colostrum has become matter of investigation, since it is the main source of intestinal microbiota for the newborn (Ballard et al., 2013).

The mechanism of establishment of certain bacterial genera in the intestine of the newborn is associated with an adequate intestinal function. The microbiota is one of the first stimuli for the development of the lymphoid tissue associated with the mucosa, and for the maintenance of immunological homeostasis (Walker et al., 2010; O'Sullivan et al., 2015). However, the mechanisms that determine which bacterial taxa are excluded and which are tolerated in the intestine are not well characterized (Magri et al., 2017).

Colostrum contains a high concentration of maternal immunoglobulins (Ig), mainly of the secretory IgA isotype (sIgA). This complex provides passive immunity to infants through immunological exclusion (Parra et al. ., 2002; Ganal-Vonarburg et al., 2017). Recent studies have described that some bacterial genera in breast milk and colostrum are associated with sIgA under homeostatic conditions (Días et al., 2017); however, the effect of this association is still controversial. Bunker et al. 2015, by IgAseq technique, determined that IgA is associated with specific species of the local microbiota or potential pathogens depending on whether its origin was a thymus dependent or independent response (Bunker et al., 2015).

The human colostrum presents both subtypes of IgA (IgA1 and IgA2), and these have a great individual variability with respect to their specificity towards microbial antigens. Some of these antigens seem to induce a more pronounced immune response towards one of the two subtypes (Ladjeva et al., 1989).

The actual knowledge about the composition of the human microbiota is due, in large part, to the metagenomics and massive sequencing of 16S rDNA libraries (Fernández et al., 2013) (Jost et al., 2013) (Gómez-Gallego et al., 2016).

Until now, our research team has described that the presence of microbiota in human colostrum. Certain bacteria genera are associated with specific IgA subtypes. The association of bacteria with IgA2 in colostrum allows establishment of this microbiota in the newborn´s intestine. Our results suggest a regulated mechanism by which certain types of bacteria in human colostrum are associated with specific IgA subtype are transported and selected and how this will contribute to build the infantile microbiota.

ZMP dependent activation of response regulators in *Escherichia coli*

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Abstract

Bacterial two component signal transduction systems (TCS) are molecular circuits that allow microorganisms to detect, amplify and respond to diverse stimuli. A typical TCS is comprised by a membrane bound histidine kinase protein (HK) and a cytosolic response regulator protein (RR). Signal perception by the HK stimulates an ATP-dependent autophosphorylation at a conserved histidine residue, which then donates the phosphoryl group to an aspartate residue in the cognate RR. In the absence of the cognate HK, RRs have been shown to autophosphorylate at the expense of the high-energy phosphate compounds acetyl phosphate and carbamoyl phosphate.

In this study we present experiments demonstrating that ZMP (5-amino-4-imidazole carboxamide riboside-5'-monoposphate), an intermediate of the purine synthesis, can also induce the activation of RRs in a HK-independent manner

The quorum sensing system NprR-NprRB contributes to spreading and fitness in biofilms of *Bacillus thuringensis*

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One mechanism that bacteria use to communicate is quorum sensing (QS), which consists on intercellular signaling molecules and their recognition to coordinate bacterial gene expression in response to cell density. In *Bacillus thuringiensis* (Bt), a gram-positive, spore-forming, ubiquitous bacteria, the QS system NprR-NprRB (receptor-autoinducer peptide) regulates the expression of genes related to nutrient scavenging and also modulates the onset of sporulation, both of which occur during pathogenesis and necrotrophism in insects. However, the relevance of QS in free-living stages of Bt is less known. Previous observations suggested that NprR is involved in other specialization processes, and here we addressed the role of this QS system in passive motility (spreading) and fitness in biofilms. For this, Wild type (Wt) Bt strain 8741, its derivate mutant Δ*nprR-nprB* with a deletion in the QS cassette, and complemented strains with *nprR* only and with *nprR-npRB* genes, were spotted in agar media. Spreading and fitness assays were performed by measuring colony radius and CFUs, respectively, in surface biofilms incubated for 7 days at 30 ºC. We used conventional media or artificial soil substrate to simulate natural habitats. Co-inoculations and external addition of synthetic NprRB (the heptapeptide SKPDIVG) were used for assessing the role of extracellular compounds and QS signaling on these phenotypes, respectively. Spreading phenotype of individual strains in co-inoculations was assessed using GFP-expressing Wt and mutant strains by macroscopic imaging of biofilm fluorescence. We found that the presence of both *nprR* and *nprRB* genes is necessary for dispersion, both in conventional or soil media. Co-inoculating the Wt strain and the mutant strain complemented with the NprR receptor, failed to rescue the mutant phenotype. This was corroborated by fluorescence imaging, where we observed that the mutant strain remained localized in the center of the biofilm while the Wt strain spread normally; however, the phenotype was recovered when 500 nM SKPDIVG was externally added. Moreover, peptide addition had no effect when the NprR receptor is absent. Thus, normal spreading requires both the mature signaling peptide and its recognition by the NprR receptor. Subsequently, we show that the spreading phenotype, which requires the NprR-NprRB system, allows an increased fitness of the Wt strain compared to the mutants. These findings show an unanticipated and essential role of the NprR/NprRB QS system for the evolution and ecology of the free-living lifestyle of Bt.

Biosurfactant and/or Bioemulsifier Production by *Gordonia sp.* R4M20CR Utilizing Agro-industrial Waste Products

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Water pollution caused by organic substances is a widespread environmental issue. Removal of contaminants from water is often an expensive, laborious and time-consuming process; therefore there is a need for cheap, effective and environmentally friendly methods. Microbial biosurfactants and/or bioemulsifiers are amphiphilic molecules that reduce the surface tension between water and other immiscible substances or that can generate stable emulsions. These microbial metabolites can be used to remove hydrophobic contaminants from waterbodies. *Gordonia* spp. are soil actinomycetes with a wide potential to degrade heavy hydrocarbons, polymers, PAH compounds and other contaminants, and are among the bacterial species that can produce emulsifiers and/or biosurfactants. The objective of this research was to evaluate the ability of *Gordonia sp.* R4M20CR to consume agro-industrial waste products (including spent coffee grounds, wheat chaff, apple bagasse, pecan shell, sotol bagasse, oregano bagasse, pomegranate seeds and rind) as source of carbon and energy. Also, to determine which of those residues favored the production of biosurfactant and/or bioemulsifier. Microbial growth was determined by inoculation of the *Gordonia* strain in mineral salts medium (M9) added with waste product at a concentration of 0.15% m/v in triplicate. After incubation for one week at 25°C, a sample from each medium was taken to determine the concentration of microbial cells by dilution and plate count. Presence of biosurfactant was assessed by the Drop Collapse method and bioemulsifier production tested with the Emulsification Index method. All the residues supported microbial growth, but it was lower with the spent coffee grounds, and higher with oregano bagasse ($7x10^7$ CFU/ml). Besides, considering the antibacterial capacity known of oregano, the bacterial cultures were not contaminated. Using only waste products as carbon source, Gordonia did not produce extracellular biosurfactant/bioemulsifier. Using glucose as control, however, the cell free medium presented a 85% emulsification index using olive oil. It is necessary to add a hydrophobic compound as an inducer, and to further test the capacity of growth and bioemulsifier production. Nonetheless, the use of waste products for Gordonia growth can be an alternative for production of metabolites that can be used in bioremediation processes.