PROGRAM

1ST MICROBIOME SYMPOSIUM

PR & Caribbean

Community Dynamics in a Changing World

February 28 2026

Courtyard by Marriott Isla Verde Beach Resort
San Juan, Puerto Rico

COBRE Puerto Rico Center for Microbiome Sciences

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NIH National Institute of General Medical Sciences

1ST MICROBIOME SYMPOSIUM

COBRE Puerto Rico Center for Microbiome Sciences

Community Dynamics in a Changing World

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Abstract submissions due Jan 30

Email submission to: cobremicrobiomepr.rcm@upr.edu

subject line: ABSTRACT-your name

Courtyard by Marriott
Isla Verde Beach Resort
San Juan, Puerto Rico

February 28
9:30AM-6:00PM
2026

REGISTER HERE: https://www.surveymonkey.com/r/1st_PR_Microbiome_Symposium

Welcome to the First Microbiome Symposium of Puerto Rico and the Caribbean

Dear colleagues, trainees and distinguished guests,

On behalf of the Puerto Rico Center of Microbiome Sciences, its leadership and staff, I am delighted to welcome you to the *First Microbiome Symposium of Puerto Rico and the Caribbean,* ***"Community Dynamics in a Changing World"*****.**

We are proud to celebrate this Inaugural event organized and hosted by the COBRE Puerto Rico Center for Microbiome Sciences (PR-CMS). This landmark gathering marks an historic moment for our region, uniting microbiome leaders and innovators in microbiome research, to share the latest scientific discoveries, explore community impact, and highlight cutting-edge applications in data analysis and measurable outcomes across health, disease, and the environment.

Held in sunny San Juan, Puerto Rico, this no-cost event offers a unique opportunity to engage directly with internationally recognized microbiome researchers in an intimate and collaborative setting. The symposium features a full day of dynamic scientific exchange, including presentations from leading experts an interactive roundtable discussion and poster sessions showcasing emerging research from students and from Puerto Rican Institutions. We encourage you to engage in meaningful dialogue, collaboration, and network with this community. This program publication commemorates a historic milestone: the establishment of the first microbiome-focused research center in the Caribbean and one of the first microbiome COBRE centers nationally funded by the National Institute of General Medical Sciences (NIGMS) under NIH Award P20 GM156713. As we conclude our first year, we proudly reflect on our progress, including the recruitment of key personnel, the development of core resources, and the organization of seminars and workshops to strengthen microbiome research capacity across Puerto Rico. The mission of PR-CMS is to build a strong and sustainable research infrastructure that empowers investigators across the island to advance microbiome science, translational research, and microbiome-driven innovation. The Center supports early-stage investigators through mentorship, access to core facilities, pilot project funding, and collaborative opportunities designed to strengthen biomedical discoveries with direct relevance to the Puerto Rican population. Stay tuned for new opportunities and calls for pilot and feasibility studies. Thank you to the *Sociedad de Microbiologos de Puerto Rico* (SMPR) and *Applied Microbiome International* (AMI) for their support of student presentation awards, and to the entire COBRE team, administrative and research cores, for their support in organizing this meeting. Microbiome science is transforming our understanding of health and disease. Through this initiative, Puerto Rico is advancing research and strengthening collaborations to address regional and national priorities. Check us out at our web page and social media. Thank you for being part of our inaugural event, and for supporting the future of microbiome science in Puerto Rico and the Caribbean.

Filipa Godoy-Vitorino, Ph.D.
PI Puerto Rico Center for Microbiome Sciences
1st Microbiome Symposium Chair

COBRE
Puerto Rico Center for Microbiome Sciences

Our Philosophy

At the Puerto Rico Center for Microbiome Sciences, we believe that scientific discovery thrives in a culture of collaboration, curiosity, and inclusion. Our philosophy is grounded in the understanding that microbiomes play essential roles in human health, disease, behavior, and environmental resilience—and that advancing this field requires interdisciplinary expertise and shared access to cutting-edge technologies. We are committed to cultivating an environment where researchers at all career stages can innovate, learn, and grow. By fostering strong partnerships across clinical, basic, and computational sciences, we support rigorous, ethical research that expands knowledge and empowers the next generation of scientists. Our Center values diversity of ideas, mentorship, teamwork, and open scientific dialogue as the foundations of transformative microbiome research.

Our Vision

Our vision is to establish Puerto Rico as a leader in microbiome science within the Caribbean and the broader global research community. The PR-CMS aims to drive impactful discoveries, expand research capacity across the UPR system, and strengthen the scientific workforce through integrated training, state-of-the-art core facilities, and support for innovative investigators.

We aspire to create a sustainable, collaborative research ecosystem that accelerates microbiome-driven solutions to pressing biomedical challenges. As members of national microbiome research networks, we envision Puerto Rico as a hub for excellence, shaping the future of microbiome science through rigorous research, technological innovation, and community engagement.

Our Mission

The Puerto Rico Center for Microbiome Sciences is dedicated to advancing microbiome research in the region by establishing itself as a premier resource center, equipped with instrumentation, robust analytical capabilities, and comprehensive training opportunities. By providing essential infrastructure and expert guidance, the Center ensures accessibility to cutting-edge microbiome science for researchers at every career stage across Puerto Rico, promoting a broader participation in scientific discovery. Moreover, through enhancing microbiome literacy and fostering a diverse scientific workforce, the PR-CMS positions Puerto Rico as a pivotal hub for microbiome research, addressing critical questions in health, disease, and industrial innovation.

The PR-CMS is fully aligned with the mission of the University of Puerto Rico and that of the Medical Sciences Campus by advancing education, research, and innovation in microbiome science. Through cutting-edge training programs, the PR-CMS will educate a diverse and competent new generation of physicians, researchers, and biomedical scientists. Advancing equitable, high-impact microbiome research to enhance biomedical science and improve quality of life for all is our ultimate mission.

AGENDA

1st Microbiome Symposium

February 28, 2026

Courtyard by Marriott Isla Verde Beach Resort

San Juan, Puerto Rico

Location: *Salon de Mar Ballroom*

8:30 – 9:30 AM	**REGISTRATION** **Poster mounting opens**
9:30 – 9:50 AM	**WELCOMING REMARKS - 1st PR Microbiome Symposium** • Filipa Godoy-Vitorino, PhD – PI and Program Director, COBRE PR-CMS (5 min) • Zayira Jordán-Conde, PhD - President, University of Puerto Rico (5 min) • Myrna L. Quiñones Feliciano, MD, JD - Chancellor, UPR RCM Campus (5 min) • Debora H Silva, MD, Dean UPR School of Medicine • Victor M. Ramos Otero, MD – Secretary of Health of Puerto Rico (5 min)
9:50 – 10:10 AM	**PLENARY SESSION** Filipa Godoy-Vitorino, PhD, University of Puerto Rico School of Medicine ***Powering Discovery: The Puerto Rico Center for Microbiome Sciences*** (20 min)
10:10 – 11:05 AM	**Keynote Speaker** Dr. María Domínguez-Bello, Rutgers University ***Early Microbiome Disruptions*** (45 min + 10 min Q&A)
11:05 – 11:20 AM	**COFFEE BREAK / Poster mounting** *[Salón del Mar Ballroom Lobby]*
11:20 – 11:55 AM	**SPECIAL INVITED SPEAKER** Dr. Keith Crandall, George Washington University Title: ***Genomic Language Models for Microbiome Characterization, Antibiotic Resistance Detection, and Biosynthetic Gene Cluster Analysis*** (30 min + 5 min Q&A)
11:55 AM – 12:30 PM	**SPECIAL INVITED SPEAKER** Dr. Ana Maldonado-Contreras, University of Massachusetts Title: ***You Are What Your Microbes Eat: Diet and Immune Modulation*** (30 min + 5 min Q&A)
12:30 – 12:55 PM	**YOUNG SCIENTIST ORAL PRESENTATION** Title: ***Microbial Regulation of Viral Therapeutics and Cervical Disease Pathogenesis: Harnessing Microbes for Anti-Cancer Strategies*** Dr. Natalie Meléndez-Vázquez, UPR Medical Sciences Campus (15 min + 5 min Q&A)
1:00 – 2:20 PM	**LUNCH BREAK & GROUP PHOTO** *[Sirena Restaurant Buffet or beach]*

2:20 – 3:20 PM	***STUDENT FORUM – FUTURE OF MICROBIOME SESSION*** **Selected student Lightning Talks** **Flash Talk 1 — 10 min** Speaker: Luis H. Pagán Rivera, UPR Medical Sciences Campus Title: *Gut microbiome modulation by tamoxifen following spinal cord injury in male and female rats* **Talk 2 — 10 min** Speaker: Yilmaz Berk Koru, UPR Rio Piedras Campus Title: *The role of gut microbiota on the development of behavioral circadian rhythm and clock system maturation in honeybees (Apis mellifera)* **Flash Talk 3 — 10 min** Speaker: Edgardo L Rosado Ramos, UPR Mayagüez Campus Title: *Characterization of the gut microbiome in wild Eretmochelys imbricata (Hawksbill Sea Turtle) nesting females and neonates in Mona Island, Puerto Rico* **Flash Talk 4 — 10 min** Speaker: Anelisse Dominicci-Maura, UPR Medical Sciences Campus Title: *Anal microbial signatures associated with concurrent anogenital HPV infection* **Q&A Section** (5 min) **Elevator Pitches – Postdocs, Residents and Grad Students** • Melanie Reinoso Arnaldi, BS UPR Rio Piedras Campus (3 min) • Juliana M. Serrano-Rodríguez UPR Comprehensive Cancer Center (3 min) • Laura S. Bermúdez-Martínez Universidad Central del Caribe School of Medicine (3 min) • Paula Cruz Vázquez, UPR Medical Sciences Campus (3 min)
3:20 – 4:20 PM	**POSTER SESSION & JURY REVIEW**
	COFFEE BREAK *[Salón del Mar Ballroom]*
4:20 – 5:15 PM	**ROUNDTABLE: FUTURE OF MICROBIOME** *[Salón del Mar Ballroom]* *Maria Gloria Dominguez-Bello, Keith Crandall, Ana Maldonado-Contreras, Janet Jansson, Martin J. Blaser* Moderator: Filipa Godoy-Vitorino
5:15 – 6:00 PM	**CLOSE UP, POSTER AWARDS & NETWORKING RECEPTION** *[Salón del Mar Ballroom Exterior]*

1st Microbiome Symposium - Invited Speakers

Dr. Maria Dominguez Bello

Maria Gloria Dominguez-Bello, Ph.D. is a Distinguished Professor and Henry Rutgers Professor of Microbiome and Health at Rutgers University, where she also serves as Professor of Anthropology in the School of Arts and Sciences. Her work bridges microbiology, medicine, anthropology, and urban studies to understand how the human microbiome develops and how modern lifestyles shape microbial ecosystems critical to health. Dr. Dominguez-Bello's research focuses on the development of the human microbiome from birth, its functions for the host, and the consequences of practices that reduce microbial transmission or disrupt microbial communities. She investigates how Cesarean section birth, antibiotic use, sanitation, and other modern interventions alter early-life microbial exposure, potentially influencing immune development and long-term disease risk. A central theme of her work is identifying strategies to restore beneficial microbial functions that may be lost through modernization.

Her recent research includes studies on C-section–associated microbiota and their effects on immune responses. Supported by the Juvenile Diabetes Research Foundation (JDRF), one major project uses the NOD mouse model to determine microbial factors that increase or decrease Type 1 Diabetes outcomes. Another project examines the effects of water disinfection agents and their by-products on the developing microbiome and host physiology, exploring how antimicrobial residuals in urban water systems may contribute to microbiome disruption and urban-associated diseases.

Additionally, Dr. Dominguez-Bello studies the microbiomes of isolated hunter-gatherer societies. Supported by the C&D Fund and Emch Fund, this work investigates microbial community structure and function in populations minimally exposed to antibiotics, C-sections, and industrialized hygienic practices, providing insight into ancestral microbial states and their potential protective effects against modern epidemic diseases. Through interdisciplinary collaboration, her work advances understanding of how restoring microbial diversity may promote health in contemporary societies.

Dr. Keith Crandall

Keith A. Crandall, PhD is the founding Director of the Computational Biology Institute at the George Washington University. Professor Crandall studies the computational biology, population genetics, and bioinformatics of a variety of organisms, from crustaceans to agents of infectious diseases. His lab also focuses on the development and testing of data analytic approaches, especially for Omics and clinical data. He applies these methods and others to the study of the evolution of infectious diseases with particular focus on microbiome studies. Professor Crandall has published more than 300 peer-reviewed publications, as well as three books (The Evolution of HIV, Algorithms in Bioinformatics, and Decapod Crustacean Phylogenetics). Dr. Crandall's research has been funded by both the National Science Foundation and the National Institutes of Health as well as from a variety of other agencies, including American Foundation for AIDS Research, National Geographic, US Forest Service, Pharmaceutical Research Manufacturer's of America Foundation, Alfred P. Sloan Foundation, etc.

He has been a Fulbright Visiting Scholar to Oxford University and an Allen Wilson Centre for Molecular Ecology and Evolution Sabbatical Fellowship at the Bioinformatics Institute at the University of Auckland. Professor Crandall has received a number of awards for research and teaching, including an Alfred P. Sloan Foundation Postdoctoral Fellowship in Molecular Evolution at the University of Texas, the American Naturalist Society Young Investigator Award, an NSF CAREER Award, a PhRMA Foundation Faculty Development Award in Bioinformatics, an NIH James A. Shannon Directors Award, ISI Highly Cited Designation, Honors Professor of the Year award at Brigham Young University, and the Edward O. Wilson Naturalist Award. He was also recently elected a Fellow in the American Association for the Advancement of Science (AAAS) and the Linnean Society of London. Professor Crandall earned his BA degree from Kalamazoo College in Biology and Mathematics, an MA degree from Washington University in Statistics, and a PhD from Washington University in Biology and Biomedical Sciences. He also served as a Peace Corps Volunteer in Puyo, Ecuador.

Dr. Ana Maldonado Contreras

Ana Maldonado-Contreras, PhD is a clinical translational researcher and Assistant Professor in the Department of Microbiology at UMass Chan Medical School. Her research centers on understanding how diet shapes the human microbiome and how these diet–microbiome interactions influence inflammation and disease. Through clinical cohorts, dietary interventions, and multi-omics approaches, Dr. Maldonado-Contreras investigates microbiome-centered precision strategies aimed at reducing inflammation and improving health outcomes.

Originally from Punto Fijo, Venezuela, Dr. Maldonado-Contreras earned her B.S. in Biology from the Universidad del Zulia in 2002. She completed her M.S. in Microbiology at the Instituto Venezolano de Investigaciones Científicas in Caracas and went on to obtain her Ph.D. in Microbiology from the University of Puerto Rico under the mentorship of Dr. Maria Gloria Dominguez-Bello. She then pursued postdoctoral training in mucosal immunology and microbial pathogenesis at UMass Chan Medical School in the laboratory of Dr. Beth McCormick, supported by the prestigious Charles A. King Trust Postdoctoral Research Fellowship Program (2009–2015).

In 2015, Dr. Maldonado-Contreras joined the faculty at UMass Chan as part of the Faculty Diversity Scholar Program. Her research has focused on inflammatory bowel diseases and has more recently expanded to maternal and infant health, exploring how early-life nutrition influences immune development through microbiome modulation. Her work has been supported by The Helmsley Charitable Trust and the American Gastroenterological Association.

In 2020, she was recognized as a Dr. Marcellette G. Williams Distinguished Scholar, an honor awarded to outstanding UMass Chan faculty members. Dr. Maldonado-Contreras also serves on the Diversity Committee of the American Gastroenterological Association, reflecting her commitment to advancing equity and excellence in biomedical research and academic medicine.

Dr. Natalie M. Meléndez-Vázquez

Natalie M. Meléndez-Vázquez is a Puerto Rican microbiologist and postdoctoral fellow within the Center for Collaborative Research in Health Disparities (CCRHD – RCMI) from the University of Puerto Rico-Medical Sciences Campus, where she specializes in microbiome research and its role in cancer therapy and women's health. Her work focuses on integrating multi-omics data to understand how microbial communities influence disease progression and treatment response, particularly in cancers associated with the gut and cervicovaginal microbiome. Natalie earned her bachelor's degree in microbiology with a second concentration in general biology from the University of Puerto Rico at Humacao. She later obtained her Ph.D. in Microbiology under the mentorship of Dr. Godoy-Vitorino, where she received multiple honors for academic excellence, leadership, and research. During her doctoral project she collaborated with Dr. Candelaria Gomez-Manzano at the University of Texas MD Anderson Cancer Center, to assess the role of gut microbial communities in modulating the efficacy of oncolytic viruses against solid tumors. Throughout her career, Dr. Meléndez-Vázquez has contributed with peer-reviewed publications in oncology and microbiology, while also serving as speakers at national and international conferences. Dr. Meléndez-Vázquez has received numerous awards recognizing her scientific excellence and leadership. These include the American Association for Cancer Research (AACR) Minority Scholar in Cancer Research Award, the ASM Peggy Cotter Award, and multiple honors as a graduate student from the University of Puerto Rico-Medical Sciences Campus. She has also been selected in mentorship programs, including the NIH Research Centers in Minority Institutions (RCMI) Targeted Faculty Development Program, reflecting her commitment to advancing biomedical research and her potential as an emerging leader in science. Beyond research, Dr. Meléndez-Vázquez is deeply committed to mentorship, education, and advancing diversity in STEM. She currently serves as a Health Equity Ambassador for the American Cancer Society and as president-elect of the Puerto Rico Society of Microbiologists. She actively mentors students at multiple levels and is passionate about supporting young women in science, helping them develop skills and pursue scientific careers. Through her work, she strives to bridge scientific discovery, education, and community engagement to improve health outcomes and inspire the next generation of scientists.

Meet the Puerto Rico Center for Microbiome Sciences Team

Dr. Filipa Godoy-Vitorino

Principal Investigator, Program Director and Research Core Leader

Filipa Godoy-Vitorino, PhD, is Professor and Chair at the Department of Microbiology and Immunology at the University of Puerto Rico School of Medicine and a Microbial Ecologist by training. Originally from Portugal, she earned her *Licenciatura* in Biology from the University of O'Porto and an ERASMUS fellowship to study Applied Algology at the Universidad de Las Palmas, Canary Islands, Spain. She completed her Ph.D. in Biology (Microbial Ecology) from the University of Puerto Rico in collaboration with the Lawrence Berkeley National Lab, WUSTL and NYU, under the mentorship of Dr Maria Gloria Dominguez-Bello. She earned a prestigious NSF postdoctoral fellowship to obtain training in metagenomics at the DOE Joint Genome Institute with Drs Phil Huggenholtz and Susannah Tringe.

Her career centers on microbial biodiversity, community dynamics, and dysbiosis in human and animal microbiomes, pioneering metagenomic and bioinformatic approaches across the Caribbean. Her research integrates basic laboratory science with translational and clinical microbiome studies. She has led landmark work characterizing cervicovaginal and oral microbiomes in Hispanic and Caribbean populations, identifying microbial features linked to high-risk HPV persistence and cervical cancer. Her group was the first to show the predominance of *Lactobacillus iners* in Puerto Rican vaginal microbiomes and to link high-risk HPV with *Malassezia* yeasts, uncovering microbial and metabolic biomarkers of cervical disease. She has co-discovered bacterial phyla, characterized microbiomes across systems globally, and forged collaborations with institutions in Puerto Rico and worldwide, including in the US, Latin America, and Europe. She has held key roles including PI across multiple NIH and NSF initiatives focused on cancer prevention, health disparities and animal and ecosystem conservation. She contributes as Editorial board member and peer reviewer to multiple journals, is past president of the AAAS Caribbean Division and is an international ambassador for applied and microbial ecology groups, including ISME and AMI. Her projects have been pivotal in advancing microbiome research in Puerto Rico by expanding bioinformatics expertise, strengthening laboratory infrastructure, fostering global collaborations, and mentoring over 100 trainees, while promoting inclusion, scientific rigor, and workforce diversification.

Dr. María A. Sosa

Administrative Core Director

Dr. Sosa is a distinguished neuroscientist at the University of Puerto Rico (UPR) Medical Sciences Campus, where she has led an active and productive research program for over 26 years. She earned her B.S. in Chemistry from the Pontifical Catholic University of Puerto Rico, followed by a Ph.D. in Neuroscience from the University of Florida, and completed postdoctoral training at the UPR Institute of Neurobiology.

Her research focuses on understanding the neural mechanisms that underlie behavior, particularly aggressive interactions and dominance hierarchies, using invertebrate model systems. Dr. Sosa's work has significantly advanced knowledge of synaptic physiology, sensory system development, and biogenic amine signaling. Her laboratory uses the freshwater prawn *Macrobrachium rosenbergii* as a model to examine how neural circuits regulate social behavior and how these mechanisms can be modulated by neurotransmitters and environmental factors. Through an integrative approach, her team combines behavioral analysis, electrophysiology, molecular biology, immunohistochemistry, and advanced imaging techniques to investigate neural function. Her research has also expanded into environmental neuroscience, examining how anthropogenic contaminants affect the nervous system and behavior of aquatic and terrestrial species. This work includes studying polluted urban rivers in Puerto Rico and their impact on neural circuitry and survival in fish and crustaceans.Dr. Sosa has served as Principal Investigator, Co-Investigator, and Subproject PI on multiple NIH and NSF grants, contributing to projects on synaptic mechanisms, environmental neuroscience, and research infrastructure development. In addition to her scientific achievements, she has held key leadership roles, including Interim Associate Dean for Biomedical Sciences and Interim Director of the Institute of Neurobiology.

A dedicated mentor, Dr. Sosa has guided more than 15 faculty researchers and numerous trainees, while also overseeing major laboratory renovations and infrastructure initiatives that have strengthened neuroscience research in Puerto Rico.

Dr. Mark Miller

Director Faculty Development Core

Dr. Mark Miller is a Professor in the Department of Anatomy and Neurobiology at the University of Puerto Rico (UPR) Medical Sciences Campus and an internationally recognized neuroscientist whose career spans more than four decades. He earned his B.A. in Psychology from the University of Pennsylvania and his M.S. and Ph.D. in Neuroscience from the University of Connecticut. He completed postdoctoral training in neurophysiology and animal behavior at leading research institutions in Hawaii, Jerusalem, and UCLA, establishing a strong interdisciplinary foundation in brain and behavior research.

Dr. Miller's research has significantly advanced the understanding of neural circuit structure and function, with a particular focus on neuromodulation, neural plasticity, neuropeptide signaling, and central pattern generator networks. Using both vertebrate and invertebrate model systems, his work explores how neural circuits generate behavior and adapt to internal and environmental changes. His integrative approach combines physiology, behavior, and molecular techniques to uncover fundamental principles of nervous system organization.

Since joining UPR in 1992, Dr. Miller has led and contributed to numerous large-scale research and training initiatives. These include an NSF Undergraduate Research Mentoring program, the NSF CREST Center in Environmental Neuroscience, and an NSF PIRE program focused on neural mechanisms of reward and decision-making. He has also played a central role in the NIGMS-funded Center of Biomedical Research Excellence (COBRE) for Neuroplasticity, serving as Interim Director during Phase I and currently as Director of the Administrative Core.

More recently, Dr. Miller's research has expanded into the intersection of neuroscience and parasitology. His laboratory investigates how infection by *Schistosoma mansoni* alters the nervous system and behavior of its snail host, *Biomphalaria glabrata*, to identify novel strategies to disrupt disease transmission. A dedicated mentor and scientific leader, Dr. Miller continues to support the development of early-career scientists and the advancement of biomedical research at UPR.

Meet the Microbiome Core Lab

Mariam Vázquez, PhD.

Dr. Mariam Vázquez Berríos is Project Coordinator for the RCM-COBRE Microbiome Center. She holds a BA in Psychology from Princeton University, a Master's in Psychopharmacology from Universidad Complutense de Madrid, and a PhD focused on the endocannabinoid system and alcoholism from the same institution. She completed postdoctoral training at the Institute of Neurobiology at Recinto de Ciencias Médicas. As Project Coordinator, she supports microbiome research to advance scientific knowledge and improve public and environmental health.

Zoila Alvarez Aponte, PhD.

Dr. Zoila Alvarez Aponte is an Adjunct Professor of Metagenomics at the COBRE Puerto Rico Center for Microbiome Sciences. She holds a PhD from UC Berkeley, where she studied nutrient-sharing interactions among soil bacteria using genomic analyses and experimental microbial ecology. Her research spans vaginal, gut, plant- associated, and soil microbiomes, focusing on how microbial interactions shape community structure and function. At COBRE-PRCMS, she supports bioinformatics training and contributes data analysis expertise to collaborative research projects serving Puerto Rico and the Caribbean.

Irmarie Cotto Ramos, PhD.

Dr. Irmarie Cotto is an Adjunct Professor in Bioinformatics at the COBRE Puerto Rico Center for Microbiome Sciences. She holds a Ph.D. in Civil and Environmental Engineering from Northeastern University and completed an NSF ASEE Postdoctoral Fellowship at the University of Washington. Her research focuses on environmental microbiology, wastewater treatment, and using metagenomics and bioinformatics to study microbial communities and antimicrobial resistance. She has published in leading journals including Water Research and Environmental Science & Technology. At the COBRE Center, she provides bioinformatics training in metagenomics, data analyses, and leads collaborative research advancing microbiome science in Puerto Rico.

Jaleniz Suárez Pérez, BSc.

Miss Suarez is a research associate and bioinformatician with a Bachelor's Degree in Science with a major in Environmental Sciences, mentored by Dr. Filipa Godoy- Vitorino. Her research focuses on microbial ecology and applied microbiome science across environmental and clinical contexts with a strong interest in data-driven research and translational science. She contributes to projects examining the microbial community structure in a variety of settings across Puerto Rico. In the COBRE Center she supports data generation, bioinformatics analyses, project organization, and interdisciplinary collaborations.

Meet the Administrative Personnel

Kreshlya De la Paz R, MPH.

Program Coordinator

Mrs. Kreshlya De La Paz Rodríguez is a public health professional with 5+ years managing federal health programs over $200M. As a Public Health Analyst at HRSA, she oversees $215M in federal funds for 165 beneficiaries, leads contractor teams, and develops SOPs to improve efficiency. She previously served as a CDC Quarantine Officer and coordinated NIH research programs. She holds master's degrees in Public Health and Forensic Criminal Studies, with certifications in project management and emergency response.

Nydia L. Rivera-Rivera, PhD.

Outreach, Education and Logistics Coordinator

Dr. Nydia L. Rivera-Rivera is a neuroscientist and educator with over 10 years of experience in higher education and research in Puerto Rico. She holds a PhD in Cellular and Molecular Biology from the University of Puerto Rico, Río Piedras, specializing in neuroscience and developmental biology. From 2013 to 2024, she served as Assistant Professor at UPR Bayamón Campus, teaching neuroscience, anatomy, physiology, microbiology, immunology, and developmental biology. She is experienced in curriculum design, laboratory instruction, student mentorship, and research ethics, and has served on IRB and biosafety committees. She currently serves as COBRE Microbiome Sciences Outreach, Education and Logistics Coordinator

Brenda Carrucini González, Bs.

Administrative Support

Microbiology and Immunology Department

Vivian Santos Quiñones, Bs.

Administrative Suppport,

Anatomy and Neurobiology Department

Meet the Professional societies supporting the Scholar presentations

The Puerto Rico Society of Microbiologists (PRSM) is a leading scientific organization dedicated to advancing microbiology in Puerto Rico. Founded in 1957 as a 501(c)(3) non-profit organization, tracing its roots to early scientific efforts of the University of Puerto Rico. Today, PRSM serves as the official branch of the American Society for Microbiology (ASM) in Puerto Rico, connecting local scientists with a global network committed to promoting microbial sciences. PRSM's mission is to advance microbiological research, education, and practice while ensuring equitable opportunities for all individuals in Puerto Rico to contribute to the field. Its vision recognizes microbiology as a cornerstone of educational excellence and scientific progress on the island. Through its programs and activities, PRSM promotes scientific discovery, supports professional development, and fosters an inclusive and diverse community of microbiologists at all career stages. As an ASM Branch, PRSM plays a critical role in strengthening scientific engagement across Puerto Rico. PRSM has also been instrumental in recognizing excellence in science and encouraging student participation. A notable example is the Américo Pomales-Lebrón Award, established in honor of one of the society's founding members. Dr. Pomales-Lebrón (1904–1984) was a pioneering microbiologist and Chair of the Microbiology Department of the UPR School of Medicine. His work spanned infectious diseases such as hemolytic streptococci, brucellosis, and enteropathogenic *Escherichia coli*. He held leadership roles nationally and internationally, including serving as president of the Latin American Society for Microbiology, and contributed significantly to the development of graduate education at the University of Puerto Rico Medical Sciences Campus. The award that bears his name continues to recognize outstanding student research reflecting commitment to emerging scientists.

Dr. Pomales-Lebrón

Applied Microbiology International (AMI), formerly known as the Society for Applied Microbiology (SfAM), is the oldest microbiology society in the United Kingdom, founded in 1931. With more than half of its membership based outside the UK, AMI is a truly global organization, bringing together microbiologists from universities, research institutes, healthcare, agriculture, and industry. Its overarching mission is to advance the science of microbiology for the benefit of society, with applications spanning environmental sustainability, human and animal health, food security, and industrial innovation. As a professional membership organization, AMI supports individuals at all stages of their careers, from undergraduate and doctoral students to early-career scientists and established professionals. Through networking opportunities, training programs, and access to resources, AMI fosters professional development and collaboration across disciplines. Many of its members are internationally recognized leaders in applied microbiology, serving as ambassadors for the field worldwide. AMI is actively engaged in scientific communication and dissemination of research through its portfolio of respected publications, including the *Journal of Applied Microbiology*, *Letters in Applied Microbiology*, and *Sustainable Microbiology*, as well as its digital magazine, *The Microbiologist*. The organization also hosts scientific meetings, conferences, and specialized symposia, including events dedicated to early-career researchers, promoting knowledge exchange and innovation. The society further supports its members through an extensive range of grants and awards. Among these, the Horizon Awards recognize excellence and impact across key areas such as public health, environmental conservation, food security, policy, and diversity in science. Through its global reach, commitment to excellence, and focus on real-world applications, AMI continues to play a leading role in advancing microbiology to address pressing global challenges.

Oral Presentations

Human Microbiome

Abstract: 20260228_055

Title: Anal Microbial Signatures Associated With Concurrent Anogenital HPV Infection

Authors: Anelisse Dominicci-Maura[1], Jaleniz Suárez-Pérez[1], Natalie M. Meléndez-Vázquez[1], Natalia Pagán-Zayas[1], Andrea Cortés-Nazario[1], Josefina Romaguera[2], Filipa Godoy-Vitorino[1]

Institution(s): [1]Department of Microbiology and Immunology, University of Puerto Rico School of Medicine, Medical Sciences Campus, San Juan, Puerto Rico; [2]Department of Obstetrics and Gynecology, University of Puerto Rico School of Medicine, Medical Sciences Campus, San Juan, Puerto Rico.

Background: Human papillomavirus (HPV) is a common sexually transmitted infection that can infect multiple anogenital sites, including the cervix and anus. While cervical HPV has been extensively studied, the role of the anal microbiome in HPV infection remains poorly characterized. Although anal and cervical microbiomes differ by body site, it remains unclear whether the anal microbiome varies between single-site versus concurrent anogenital HPV infection.

Methods: Anal swab samples were collected from 192 non-pregnant, non-menopausal women under IRB protocol 1050114. Anal bacterial communities were characterized using 16S rRNA gene amplicon sequencing, and quality control was performed using DADA2. Samples were rarefied to 1,600 reads prior to downstream analyses. HPV status was analyzed as overall HPV detection (including low- and high-risk serotypes). Participants were stratified by anal HPV status alone, followed by a combined anogenital infection variable (HPV-negative, HPV on at least one site, and concurrent anal–cervical infection). Single-site infections were further stratified into cervical-only and anal-only HPV groups.

Results: Community structure differences in anal samples were observed between women with concurrent anal–cervical HPV infection and those with HPV detected at only one site, either cervical or anal ($p=0.008$). After stratifying single-site infections, anal microbial community structure differed significantly across infection groups, with the strongest separation observed between women with concurrent anal–cervical HPV infection and those with only cervical HPV ($p=0.007$). Alpha diversity also differed across infection groups, with higher diversity observed in women with concurrent anal–cervical HPV compared to those with cervical HPV only ($p=0.035$) and anal HPV only ($p=0.041$), while microbial richness did not differ significantly across groups. Taxonomic profiling at phylum level revealed that cervical HPV was associated with a higher relative abundance of Pseudomonadota and Fusobacteriota, whereas anal HPV and co-infection showed increased representation of Bacillota subclasses. At the genus level, cervical HPV was characterized by a higher relative abundance of *Bifidobacterium*, whereas anal HPV was associated with enrichment of *Streptococcus* and *Peptoniphilus* with reduced *Blautia*. Lastly, patients with co-infection were marked by a higher concentration of *Fenollaria*.

Conclusion: The anal microbiome differed more significantly according to concurrent anogenital HPV infection (anal and cervical) than to anal HPV status alone. Concurrent detection of HPV at anal and cervical sites was associated with increased anal microbial diversity and distinct community structure compared to single-site infections, suggesting that multi-site HPV detection reflects a unique microbial state within the anal niche.

Keywords: Human papillomavirus; Anal microbiome; Anogenital infection

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Animal

Abstract: 20260228_014

Title: The role of gut microbiota on the development of behavioral circadian rhythm and clock system maturation in honeybees (Apis mellifera)

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Background Gut microbiota plays an important role in brain development and behavior, in addition to its effects on metabolism and the immune system. It has also been shown to influence circadian rhythms at both physiological and behavioral levels. However, the role of gut microbiota in the development of circadian rhythms and maturation of the clock system is still understudied. We hypothesize that gut microbiota affects the development of circadian rhythms and the maturation of the clock mechanism, similarly to its effects on other neural processes.

Methods-To test this hypothesis, we used honey bees (Apis mellifera) as a model organism, which shares conserved features with humans. Gut microbiota was manipulated using three approaches: (1) antibiotic treatment, (2) interaction with nurse bees to augment microbial acquisition, and (3) brood cap depletion to reduce gut microbial load. The development of behavioral circadian rhythms was assessed using Locomotor Activity Monitors (LAMs). To evaluate clock neuron maturation, we performed immunostaining and quantified pigment-dispersing factor (PDF) expressing pacemaker neurons by counting their somata. In addition, RNA-seq analysis was performed on antibiotic-treated bees to identify candidate genes, followed by validation using qPCR.

Results Our results show that disruption of gut microbiota impairs the development of behavioral circadian rhythms, with fewer bees displaying rhythmic activity. Gut microbiota disruption also affects the maturation of PDF-expressing neurons, which were fewer in bees with disrupted microbiota.RNA seq analysis identified IGFALS as a candidate gene affected by antibiotic treatment. qPCR results showed increased IGFALS expression at early ages in antibiotic-treated bees, suggesting altered insulin-like growth factor (IGF) bioavailability.

Conclusion In conclusion, gut microbiota dysbiosis affects circadian clock maturation and behavioral rhythmicity, potentially through modulation of IGF signaling.

Keywords: Gut microbiota, Development of circadian rhythm, Honey bee

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Environment

Abstract: 20260228_004

Title: Gut Microbiome Modulation by Tamoxifen Following Spinal Cord Injury in Male and Female Rats

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Spinal cord injury (SCI) induces profound and sustained alterations in the gut microbiome, leading to systemic inflammation and impaired recovery. Emerging evidence suggests that microbiome dysbiosis following SCI exacerbates immune dysfunction through gut-brain axis signaling, highlighting the gut microbiome as a possible therapeutic agent. Tamoxifen (TAM), a selective estrogen receptor modulator with known neuroprotective and immunomodulatory properties, has been shown to improve outcomes after SCI, however, the mechanisms behind these beneficial properties remain unknown. We hypothesized that TAM treatment promotes favorable remodeling of the gut microbiome following SCI, shifting microbial communities toward an anti-inflammatory profile in both male and female rats. Understanding how TAM modulates host-microbiome interactions after SCI may reveal novel microbiome related mechanisms underlaying its therapeutic effects and identify sex-specific therapies for SCI. The objective of our study was to determine whether TAM treatment modulates gut microbiome composition and dynamics after SCI in a sex-dependent manner. For this, we used adult male and female Sprague–Dawley rats were subjected to a moderate contusion injury at the T10 spinal level using a vehicle control. Fecal samples were collected longitudinally at five timepoints: day 0 (prior to injury), and days 7, 14, 21, and 28 post-injury. Microbial DNA was extracted and subjected to 16S rRNA gene sequencing. Bioinformatics analyses were conducted to evaluate alpha and beta diversity, identify differentially abundant taxa, and examine temporal shifts in microbial community structure. Comparisons were made across sex, timepoint, and treatment groups to determine the specific impact of TAM on gut microbial dynamics following SCI. Results revealed rats treated with TAM displayed a significant increase in bacterial genera associated with anti-inflammatory cytokine production, particularly Bifidobacterium. This population shift became evident at day 14 post-injury and persisted through later time points, suggesting a sustained microbiome-mediated anti inflammatory effect. These findings suggest that TAM administration modulates the gut microbiome and enhances the abundance of anti-inflammatory bacterial genera following SCI. This supports the potential role of TAM as a therapeutic modulator of the gut–brain axis to improve post-injury outcomes.

Keywords: Gut microbiome, spinal cord injury, neurotrauma

Abstract: 20260228_083

Title: Characterization of the Gut Microbiome in Wild *Eretmochelys imbricata* (Hawksbill Sea Turtle) Nesting Females and Neonates in Mona Island, Puerto Rico

Authors: Edgardo L. Rosado-Ramos, Derick Gil- Hernandez, Carlos Diez and Timothy J. Colston

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Background: The Hawksbill sea turtle (*Eretmochelys imbricata*) is a Critically Endangered spongivore with a specialized role in Caribbean reef ecology. While adults rely on a complex gut microbiome to digest toxic demosponges, the acquisition of this community in hatchlings remains unknown. We investigated whether neonates inherit this functional microbiome vertically from the mother or acquire it horizontally from the environment, and whether hatchlings exhibit the site-specific differentiation characteristic of adults.

Methods- We collected deep cloacal swabs (~7.6 cm), oral, and skin samples from nesting females (n=14) and recent hatchlings (n=11) on Mona Island, Puerto Rico. DNA was extracted (ZYMObiomics) and the 16S rRNA V4 region was sequenced (Illumina MiSeq). Data were processed in QIIME 2 with rigorous decontamination. We analyzed Alpha diversity (Shannon), Beta diversity (Bray-Curtis), and core microbiome overlap to assess transmission and niche specialization.

Results- Our analysis revealed a stark contrast in microbiome maturity. While adults exhibited highly specialized, site-specific communities (Oral ≠ Cloacal, PERMANOVA $p=0.001$), differentiation was not detected among neonate body sites ($p > 0.05$), suggesting a homogenous community during early development. Despite achieving adult-like alpha diversity (Shannon ~6.2 vs 7.0, $p=0.10$), neonates shared only 3.3% of core ASVs with the maternal deep-cloacal community. Instead of maternal inheritance, neonate microbiome structure was significantly driven by nesting beach (PERMANOVA, $p=0.008$), indicating rapid colonization by local environmental taxa rather than vertical transmission.

Conclusion- Hawksbill neonates hatch with a diverse but undifferentiated "blank slate" microbiome that is distinct from the specialized "spongivore" gut of adults. The lack of direct maternal transmission and the strong signal of site-specificity suggest that the nest environment is the primary inoculum for hatchlings. Niche differentiation and functional specialization are likely acquired traits that develop post-hatching, highlighting the critical importance of nesting beach quality for early microbiome development.

Keywords: *Eretmochelys imbricata*, Microbiome, Environmental Acquisition

Funding: NSF

Elevator Pitches

Animal Microbiomes

Abstract: 20260228_027

Title: Characterization of Metabolomic and Behavioral Changes in Young and Old Drosophila Adults Mono-Associated with Probiotic Lactiplantibacillus plantarum
Authors: Melanie Reinoso Arnaldi Caroline Casiano Charles Pfeiffer Josue Rodriguez-Cordero Alfredo Ghezzi Jose Agosto Imilce A. Rodriguez-Fernandez
Institution: College of Natural Sciences, Department of Biology, University of Puerto Rico Rio Piedras

The gut microbiota-brain axis is a bidirectional communication between the resident microbes, the gut, and the brain; it plays a pivotal role in aging and age-related diseases. Probiotics have emerged as a promising avenue for interventions targeting age-related diseases by modulating this axis. In this study, we explore the effects of the commensal bacteria and probiotic Lactiplantibacillus plantarum (formerly Lactobacillus plantarum) on the gut-brain axis in the fruit fly Drosophila melanogaster by using an untargeted metabolomics approach.

Flies are a genetically amenable model, display age-related phenotypes, and have a simple microbiota that is easy to manipulate. These traits allow discoveries made in flies translatable to mammals. To understand how L. plantarum can provide a benefit to the health of animals we supplemented young and old flies with or without L. plantarum. These flies were flash-frozen and separated by heads (brain) and bodies (gut) and collected separately. This approach allowed us to identify changes in metabolites that are age-, tissue- and treatment-specific. Our results show a total of 855 biochemicals: 798 known biochemicals and 57 unknown biochemicals. Our findings revealed substantial metabolomic disparities linked to age and body section, emphasizing the dynamic nature of the gut-brain axis in the context of aging. Notably, the influence of L. plantarum supplementation on the metabolome appeared relatively modest. However, there were significant differences in neurotransmitters of interest, specifically acetylcholine which is increased in the bodies of old flies treated with L. plantarum.

Next, we explored the effects of L. plantarum in locomotion and sleep in conventional and Antibiotic-induced microbiome depletion (AIMD)-raised flies. Flies were treated for 3 days with either a 5% sucrose solution as a mock control, one of two L.plantarum strains (wild-type fly-derived LpWF or cabbage-derived Lp39), or E.coli as a negative control in 5% sucrose. Locomotor and sleep behaviors were assessed using the Trikinetics DAM2 monitoring system. Results indicated that AIMD flies treated with L. plantarum exhibited a decrease in sleep latency and an increase in overall sleep duration. In terms of locomotion, L.plantarum seems to rescue a hyperactive phenotype exhibited by AIMD flies. Data obtained from this project will help us characterize the molecular mechanisms used by L. plantarum to influence the gut-brain axis.

Human Microbiome

Abstract: 20260228_066

Title: Oral Microbiome Dysbiosis and Inflammatory Profiles Associated with Periodontal Disease in People with HIV

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Background-People with HIV (PWH) are at a higher risk of developing oropharyngeal cancers. Periodontal disease (PD) is a chronic inflammatory disease highly prevalent in PWH that is associated with increased risk for oropharyngeal cancers. Chronic inflammation, a hallmark for HIV, PD and cancer, can lead to dysbiosis of the human microbiome that can result in breached oral epithelial barrier contributing to oncogenesis. However, these factors have not been evaluated altogether in PWH, especially in Puerto Rico. In this study, we reconstructed the oral metagenome in PWH with and without PD and its association with inflammation.

Methods- We collected saliva samples and evaluated PD status from 75 virologically suppressed PWH. Among the 75 participants 84% had PD. We performed shotgun metagenomics (Illumina NovaSeq 2x150bp), quan fied short chain fa y acids acetate, butyrate and propionate (GC-MS) and measured inflamma on markers levels Il-1β, Il-4 and TNF-α (ELLA). Sta s cal analyses were performed in R-sta s cal soware.

Results- PD was significantly associated with higher bacterial (p=0.038) and viral (p=0.015) richness. Bacterial richness in PD was characterized by higher levels of Anaeroglobus micronuciformis (p=0.014) and Prevotella jejuni (p=0.030). In addition, 27% of participants with PD had Prevotella nanceiensis and 13% had Prevotella intermedia. In addition, PD was significantly associated with increased levels SCFAs acetate, butyrate and propionate (p<0.001) and higher levels of Il-1β and Il-4 and lower levels for TNF-α (p=0.056, p=0.018 and 0.029, respectively).

Conclusion Oral microbiome dysbiosis and elevated inflammation linked to PD may drive oral tissue damage and increase cancer risk in Puerto Rican PWH. Moreover, significantly higher abundance of A. micronuciformis, P. jejuni, P. nanceiensis and P. intermedia is associated with oral infections and increased inflammation. This could lead to alterations in host immune responses, promoting immune and oncogenic pathways activation, thus these pathogens may play a key role cancer development and progression in PWH. PD related tissue damage may also promote pathogen colonization, reactivation of endogenous viruses and increased susceptibility to subsequent viral infections. Understanding these interactions is critical for identifying early biomarkers, guiding personalized treatments, and improving prevention strategies for oropharyngeal cancer.

Keywords: Periodontal disease, microbiome, inflammation

Fundings: This project was supported by the National Cancer Institute: R21CA264606 and diversity supplement, National Institute of General Medical Sciences (Center for the Promotion of Cancer Health Research: P20GM148324, the National Institute on Minority Health and Health Disparities: RCMI Program U54MD007600.

Abstract: 20260228_074

Title: Pregnancy as a potential protective Factor Against CST-IV and Cervical dyspasia Risk

Authors: Paula M. Cruz Vázquez, MD[1]; Alexia N. Torres-Negron BS,MS[2]; Josefina Romaguera MPH, MD[1]; Filipa Godoy-Vitorino, Ph.D[1]

Institutions: [1]University of Puerto Rico-Medical Sciences Campus, San Juan Puerto Rico; [2]University of Puerto Rico Comprehensive Cancer Center

Introduction: Puerto Rican women experience disproportionately high rates of cervical cancer associated with HPV infection. Cervicovaginal microbiota composition has been linked to HPV persistence and cervical disease. Community State Types (CSTs) classify vaginal microbiota by dominant bacteria; CST-IV is associated with inflammation and HPV persistence. In Puerto Rico the prevalence of CST-III and IV (unstable microbiomes) are predominant in non-pregnant women. Pregnancy induces hormonal and mucosal changes that may alter microbial communities, yet its impact on CST-IV prevalence and cervical disease remains unclear. We hypothesized that pregnancy is associated with a reduced prevalence of the common CST-IV, reflecting a protective effect on the cervicovaginal microbiome.

Methods: This ongoing study uses a publicly available dataset (Godoy Lab) of 251 women samples from a clinic in Puerto Rico that underwent 16S rRNA deep sequencing and CST characterization using VALENCIA bioinformatics clustering. Variables include CST classification, pregnancy status, HPV infection, age, BMI, and cervical disease. Fisher's Exact Tests were used to compare CST-IV and high-grade squamous intraepithelial lesion (HGSIL) rates between pregnant and non-pregnant women, reporting risk ratios (RR) with 95% confidence intervals (CI). Poisson regression models with robust standard errors were used to estimate adjusted risk ratios (aRR) controlling for age and BMI. Power analyses assessed sample adequacy and informed future work.

Results: CST-IV prevalence was lower among pregnant women (17.1%) than non-pregnant women (37.0%) (unadjusted RR=0.46, 95% CI=0.22–0.98, p=0.015, one-sided). After adjustment, pregnancy remained associated with reduced CST-IV prevalence (aRR=0.49, 95% CI=0.22–1.06, p=0.071). HGSIL prevalence was higher in pregnant women (25.7%) compared to non-pregnant women (13.9%) (unadjusted RR=1.85, 95% CI=0.96–3.56, p=0.082, two-sided), though adjusted models showed a weaker and non-significant association (aRR=1.48, 95% CI=0.76–2.88, p=0.247). Power analysis confirmed adequate power for CST-IV differences but insufficient power to robustly test HGSIL without larger samples.

Discussion: These preliminary findings suggest pregnancy may protect against CST-IV, while associations with HGSIL remain inconclusive. The results also highlight possible unaccounted risk factors underlying the high burden of cervical disease among Puerto Rican women. Future work will integrate multivariable models and larger cohorts to confirm associations and clarify pregnancy's role in shaping cervicovaginal health.

Abstract: 20260228_084

Title: Stability of the Gut Microbiome Across Genetic and Behavioral Risk Factors in Hispanic Adults With MASLD

Authors: Laura S. Bermúdez-Martínez, BS[6], Andrea Pi-Rivera, BS[1], Carolina I González-Frontera, MS[7], Jaleniz Suárez-Pérez, BS[2], Carlos F. Ríos-Bedoya, M.P.H., Sc.D.[5], Filipa Godoy-Vitorino, Ph.D.[2], José F Rodríguez-Orengo, Ph.D., M.P.H.[3, 4]

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Background & Objectives: Metabolic Dysfunction-Associated Steatotic Liver Disease (MASLD), formerly known as “non-alcoholic fatty liver”, is defined by excessive hepatic fat accumulation (>5% of liver weight) in individuals without significant alcohol intake. Its pathophysiology reflects the overlap of metabolic stressors, genetic susceptibility, and gut microbial imbalance, yet how these factors interact remains unclear. In this IRB-approved study (Pro00078051), we focused on a Hispanic population in Puerto Rico to investigate the composition of gut microbiota associated with the PNPLA3 rs738409 C>G polymorphism, a genetic variant linked to MASLD susceptibility and progression. We additionally evaluated the effects of percent body fat, diet quality, and alcohol consumption patterns on microbial composition.

Methods: This study recruited 104 Hispanic adults with MASLD. We used TaqMan-based genotyping and 16S rRNA V4 sequencing of fecal samples to characterize participants' genetic and microbial landscapes, respectively. To describe metabolic risk, a validated questionnaire was used to gather additional data on anthropometric measurements, diet, and lifestyle. Random Forest classification, differential abundance evaluations, and alpha and beta diversity metrics were used to analyze microbial data.

Results: There was no discernible difference in the overall microbial community structure between PNPLA3 genotypes. Likewise, percent body fat, diet quality, and alcohol use showed no significant effects on microbial diversity or community structure. Alpha diversity remained largely stable, with a modest but significant richness difference (Chao1) between heterozygous and wild-type individuals ($p = 0.0139$). Random Forest identified Lachnospira, Faecalibacterium, and Blautia taxa associated with genotype status. However, analyses showed only minor taxonomic variation across groups. This pattern is consistent with known small effect sizes of host genetics on the human microbiome.

Conclusions: Our results suggest a generally stable gut microbial community across PNPLA3 genotypes and specific metabolic factors in this cohort.

Keywords: MASLD, PNPLA3 Polymorphism, Gut Microbiome.

Funding: This research was supported by Fundacion De Investigacion De Diego Science And Education.

Poster Presentations
Animal microbiomes, basic and applied science topics

Abstract: 20260228_019

Title: The impact of dietary composition on aggression in *Astyanax mexicanus*.

Authors: Luis Pérez Fabregat[1,2], Paola K. Figueroa Colón[1,2], Alexander Figueroa Negrón[1,2,] Roberto Rodríguez Morales, PhD[1,2]

Institutions: Department of Anatomy and Neurobiology[1], UPR-Medical Sciences Campus[1], Molecular Science Research Center[2]

Aggression is ubiquitous across the animal kingdom and are often dependent on resource acquisition and availability. We asked whether dietary variation could modulate aggression through changing diversity of the gut microbiota in the blind Mexican cavefish, Astyanax mexicanus, a species of fish that exists as two versions: a highly aggressive surface fish and a blind, non-aggressive cavefish. We conducted a dietary experiment in which we fed three diets—vegetable pellet, standard commercial zebrafish pellets, and a natural feed, bloodworms—to both surface fish and the Pachón cavefish for 4 weeks. To determine the effects of dietary variation on aggression, we conducted a resident/intruder assay in which we measured striking behavior, freezing, and zone-specific freezing in both the middle and corner areas of the tank. Our preliminary data suggests that surface fish were consistently more aggressive than Pachón cavefish across all diets. Notably, the surface fish on the vegetable diet were more aggressive than those on the other diets, suggesting that diet composition may affect aggression. Cavefish were completely non reactive during the assay, displaying no attacks regardless of diet manipulations. Our preliminary data suggest that diet can influence the adaptation of complex behaviors like aggression, and future work will determine whether these changes are occurring through variability of gut microbiota.

Keywords: aggression, dietary variation, gut microbiome

Funding: (NIGMS-NIH) P20 GM156713, RCMI U54 grant MD007600, 5R16EY037336 02

Abstract: 20260228_026

Title: Initial characterization of the microbial communities across multiple kingdoms associated with coffee beans under varying degrees of CBB infestation.

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Background- Coffee is one of the most important commodities worldwide. In recent years, a highly damaging coffee pest has arrived in the Caribbean: *Hypothenemus hampei* Ferrari, 1867 (Coleoptera: Curculionidae) (coffee berry borer, CBB). This pest bores into the coffee endosperm, reducing coffee quality and yield. Several studies have shown that this pest's microbiome is detrimental to its development and can vary across locations. However, no studies have examined the effect of CBB infestation on the coffee endosperm microbiome.

Methods- In our study, we analyzed coffee beans under three infestation levels: not infested, initial infestation, and advanced infestation, at two different locations, Utuado and Adjuntas. Berries were collected, separated into infested and non-infested groups, and kept refrigerated until arrival. In the lab, they were frozen at -80℃ until processed. The outer layers were removed, and only the endosperm was retained. We removed all insects and cleaned all beans prior to DNA extraction to minimize environmental contamination. We used 16S rRNA and ITS-targeted sequencing to characterize bacterial and fungal communities, respectively. We replicated each infestation group for each location five times.

Results- Our results showed that, at the phylum level, *Bacteroidota* and *Pseudomonadota* were the most abundant, with *Pseudomonadota* increasing with increasing infestation levels. At a higher taxonomic level, we observed a relatively stable community, with the family *Mariniliabiliaceae* as the most abundant taxon (JC017, an unclassified bacterial genus). Furthermore, as infestation increased, we observed greater taxonomic diversity. As for the fungal community, *Ascomycota* and *Basidiomycota* were the most abundant phyla, and *Nectriaceae* was the most abundant genus at most locations in infested beans. Nonetheless, our observations indicate a higher taxonomic diversity in healthy, non-infested beans, whereas a reduction in taxonomic diversity is evident in infested berries. Furthermore, it was observed that four bacterial and fifteen fungal taxa were common among beans at varying levels of infestation.

Conclusion- We conclude that there is compelling evidence of microbial dysbiosis in infested beans, characterized by increased bacterial and decreased fungal taxa. Further an analysis is necessary to assess the effect of these microorganisms on fermentation outcomes and flavor profiles.

Keywords: Microbiota, multi-kingdom, food security.

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Abstract: 20260228_048

Title: Optimizing Tissue Lysis and DNA Extraction Protocols to Enhance Bacterial Diversity Profiling in the Drosophila melanogaster Gut Microbiome

Authors: Carlos L. Quiñones Sánchez, Jan L. Bilbao Del Valle, Miguel Urdaneta Colón, Imilce A. Rodríguez Fernández

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The gut microbiota is a dynamic community that influences host metabolism, immunity, and overall health. Accurate characterization of this community requires robust and reproducible DNA extraction methods; however, technical biases introduced during tissue lysis and DNA isolation remain major challenges in microbiome research, particularly in animal model systems. In this study, we compared two commercial DNA extraction kits (Qiagen and Zymo) and two lysis methods (manual pestle homogenization and bead-beating) to evaluate their impact on microbiota profiling in a microbial community standard (MCS) and Drosophila melanogaster gut samples, a tractable model for host–microbe interactions. Full-length 16S rRNA sequencing was performed using Oxford Nanopore Technologies, followed by bioinformatic analysis using EPI2ME for taxonomic classification and standard diversity pipelines. Our data revealed that extraction and lysis methods significantly influence microbial composition, with some protocols resulting in inflated richness in MCS samples. Pestle homogenization with the Qiagen kit yielded the highest bacterial species richness while maintaining consistent representation of both Gram-positive and Gram-negative taxa. These findings demonstrate that extraction methodology strongly affects microbial diversity estimates and emphasize the need for standardized protocols to ensure reproducibility across microbiome studies, particularly those using model systems.

Keywords: Gut microbiome, gDNA extraction, 16S rRNA sequencing

Funding: We acknowledge funding support from the NIH-funded Increasing Diversity in Genomics for the Next Generation (IDGeNe) program (1R25HG012702) for supporting J.L.B.-D.V. Additional support was provided by start-up funds from the University of Puerto Rico, Río Piedras Campus, the NIH–NIGMS COBRE (5P20GM103642 and 5P30GM149367), and the Catalyzer Research Grant (#2023-00056) from the Puerto Rico Science, Technology & Research Trust, awarded to I.A.R.-F.

Abstract: 20260228_050

Title: Collecting tissue for assessing microbiota diversity in surface and cave populations of Astyanax mexicanus

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Institutions: [1]Department of Biology, UPR-Bayamón Campus, [2]Department of Anatomy and Neurobiology, UPR-Medical Sciences Campus, [3]UPR Molecular Sciences Research Center

Background: Diet is an essential regulator of gastrointestinal microbiota composition and diversity. However, its influence on neural structures that ultimately translate into circadian cycles, feeding strategies, and complex social behaviors, through modulation of the gut-brain axis remains understudied. We are interested in uncovering whether changes in diet have an impact on aggression, sleep, and feeding. To answer this question, we use a vertebrate fish model, Astyanax mexicanus, composed of two morphotypes: highly social surface fish and non social, blind cavefish, to test whether diet correlates with the plasticity of aggression among these populations.
Methods: To test this, we exposed both Astyanax morphs for 21 days under three distinct dietary conditions: a standard pellet diet (balanced), a natural, protein-skewed feed (bloodworms), and a lower value diet (vegetable pellets). Next, we performed behavioral tests for aggression, sleep, and feeding, after which we collected tissue samples for metabolomic and transcriptomic profiling, to examine the molecular changes associated with diet-induced behavioral differences.
Results: Here, we present an atlas of tissue dissections and samples collected for analysis of microbiota diversity. We characterized differences in standard length between all organs collected from surface fish and cavefish morphotypes.
Conclusion: Our study aims to unravel how diet shapes the gut microbiome, and how the latter is associated with neural circuits governing aggression. These findings will advance understanding of microbiome–brain interactions and provide insight into how particular bacterial strains contribute to behavioral evolution.

Keywords: Astyanax mexicanus, Aggression, Gut-microbiota

Funding: COBRE Puerto Rico Center for Microbiome Sciences (NIGMS-NIH) P20 GM156713

Abstract: 20260228_062

Title: Effects of a High-Fat Diet and gut-microbiome disruption on acute alcohol tolerance development in *Drosophila melanogaster*

Authors: Enrique Rodríguez Borrero, Astrid N. Reyes Torres, and Tayshira M. Vazquez Rivera
Institution: University of Puerto Rico – Cayey

Excessive alcohol consumption is a significant global health issue, contributing to the development of Alcohol Use Disorder (AUD). Alcohol tolerance, a key factor in the progression of AUD, can be influenced by dietary factors and the composition of the gut microbiome. This study investigates the effects of a High-Fat Diet (HFD) and antibiotic-induced microbiome disruption on acute ethanol (EtOH) tolerance in *Drosophila melanogaster*. Flies aged 2 to 5 days were maintained on diets supplemented with 15% and 30% coconut oil for 7 days to induce high-fat conditions, with parallel groups receiving or excluding an antibiotic cocktail of Rifampicin (200ug/ml), Tetracycline(50ug/ml), and Ampicillin (0.1ng/ml). An acute alcohol tolerance assay was conducted over two consecutive days using 50% and 75% EtOH concentrations to assess behavioral adaptation and tolerance acquisition. Following the assay, flies were dissected to isolate and culture their intestinal microbiome on Nutrient Rich Agar, MRS agar, Acetobacter-selective and Enterobacter-selective culture medium. We also performed some biochemical testing of our bacteria isolated from the gut. Our preliminary findings demonstrated different CFU on specific medium and on biochemical testing Mannitol Salt Agar (MSA) was the most significant differential culture medium showing more diversity. Our results also demonstrated that flies on 30% coconut oil developed enhanced acute tolerance to ethanol, with a significant reduction in recovery time. Furthermore, a 75% EtOH concentration induced more robust sedation compared to 50% EtOH, suggesting that alcohol concentration plays a role in shaping tolerance development. These findings suggest that dietary and antibiotic-induced alterations to the gut microbiome influence the development of alcohol tolerance in *D. melanogaster*, providing valuable insights into the complex interplay between diet, microbiome, and neurobehavioral responses to alcohol. Further studies on 16S sequencing will provide more specific data on changes induced by both the gut disruption and alcohol exposure.
Funding: Pilot Project to Enrique Rodríguez Borrero PRINBRE-IDeA Network 5P20GM103475

Abstract: 20260228_073

Title: Curcumin preserves intestinal barrier integrity and remodels the gut microbiome during aging in Drosophila

Authors: Naomi Z. Serrano-Colón, Linoshka Nieves-González, Imilce A. Rodríguez Fernández
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Background: The world's population is aging, presenting an urgent public health challenge. Aging is the primary risk factor for many chronic diseases and is accompanied by progressive alterations in host–microbe interactions in the intestine. The intestinal epithelium serves as a critical interface between the host and its microbiota, and age-associated intestinal barrier dysfunction (or 'leaky gut') is strongly linked to microbial dysbiosis and systemic decline. In both flies and mice models, interventions that preserve intestinal barrier integrity and modulate the gut microbiome have been shown to improve organismal health and, in some cases, extend lifespan. Thus, finding therapeutic interventions that improve or restore intestinal barrier function is a promising approach to extend the healthspan (the disease-free period of life) and lifespan (maximum longevity) of organisms. Natural products represent a rich reservoir of compounds with the potential to promote longevity and healthspan by modulating host–microbiome interactions. Curcumin, a polyphenolic compound extracted from the turmeric root, has been reported to extend the lifespan in adult Drosophila. Our preliminary data suggest that curcumin improves age-related intestinal barrier integrity. However, the mechanisms underlying this effect during aging remain poorly understood. We hypothesize that curcumin preserves gut barrier function by modulating the gut microbiota.
Methods: To do this, we are using an aging-accelerated model, Sod1 heterozygous null flies (Sod1n1,red1/+), which are prone to oxidative stress and shortened lifespan. Female flies were aged to 18 days old and treated with curcumin at 0 µM, 62.5 µM, 125 µM, and 500 µM in 0.147% DMSO for 3 – 4 weeks. Validation experiments were performed using normally aging flies. The Smurf assay was performed using blue dye No. 1 to assess gut barrier dysfunction. Immunohistochemistry of dissected guts was used to detect proliferation of mitotic cells in the gut as a proxy for gut regeneration status. Detection of changes in gut bacteria was done using colony-forming unit (CFU) counts, and full-length 16S rRNA.
Results: Preliminary data show that curcumin ameliorates age-related gut barrier dysfunction and extends lifespan in both an accelerated-aging model Drosophila models and in normal aging flies in a dose-specific manner. In the aging-accelerated model, curcumin induces dose-dependent remodeling of the gut microbiome and modulates intestinal regeneration relative to control.
Conclusion: These findings provide insight into the protective effects of curcumin in the context of aging and suggest that modulation of the gut microbiome contributes to its beneficial effects on intestinal barrier function.

Keywords: aging, microbiome, natural products

Abstract: 20260228_077

Title: Genotype Specific Differences in Antibiotic Induced Microbiome Depletion in Drosophila melanogaster

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Antibiotic treatment is a common strategy to experimentally deplete the gut microbiome in many model organisms including the fruit fly Drosophila melanogaster, to test host-microbe interactions. However, accumulating evidence suggests that many of the gut-associated bacteria are resistant to antibiotics, and that even when antibiotic cocktails are administered, microbial depletion is often incomplete. The extent to which host genotype influences depletion efficiency and subsequent microbial rebound remains unresolved. Understanding these interactions is essential for designing reproducible manipulation protocols and for accurately interpreting microbiomedependent phenotypes. In this study we examined whether two widely used laboratory strains, wild-type CantonS (CS) and white gene-null mutant (w^{1118}), differ in their susceptibility to antibioticinduced microbiome reduction, with particular attention to genotypespecific effects and microbial resilience. These strains differ by a mutation in the white gene, which encodes an ATP-binding cassette (ABC) transporter with known pleiotropic effects beyond eye pigmentation, providing a relevant framework to assess host genetic contributions to microbiome depletion and recovery.

Methods: Conventionally raised (with intact microbiome) mated female flies (CS and w^{1118}) were aged to 7 days old and then assigned to either an antibiotic-treated or conventional diet. The antibiotic cocktail consisted of 100 µg/ml vancomycin, 200 µg/ml neomycin, 200 µg/ml ampicillin, and 200 µg/ml metronidazole and was administered for 5 days, followed by three days of conventional food. During the +/- antibiotic period, flies were further subdivided into two groups that were either transferred daily to fresh food or maintained on the same food. Thus, four treatment conditions were analyzed per genotype: antibiotic food flipped daily (A-F), antibiotic food not flipped (A-NF), conventional food flipped daily (C-F), and conventional food not flipped (C-NF). At the selected timepoints, five whole guts per sample were dissected, homogenized in sterile PBS and plates on selective media to quantify Acetobacter, Lactobacillus and Enterobacter species via Colonyforming unit (CFU). Three biological replicates were performed for each condition.

Results- We found that antibiotic treatment substantially reduced, but did not completely deplete, gut bacterial load in both genotypes. Notably, this reduction was transient, with bacterial levels rebounding shortly after treatment ended. Across all replicates and treatment conditions, w^{1118} consistently retained higher bacterial loads than CS following antibiotic exposure, suggesting a robust genotypedependent difference in depletion efficiency.

Conclusion The persistent differences between CS and w^{1118} may reflect genotype-dependent colonization resistance/resilience, differences in baseline microbiota between conventionally raised strains or both. Because these fly strains were not outcrossed, the observed differences are best interpreted as host strain-specific and may reflect genetic variation beyond the white locus. Ongoing work using germ-free and gnotobiotic flies will disentangle host-genotype effects from initial community composition and identify taxa that drive differential depletion and reassembly.

Keywords: Drosophila melanogaster; microbiome; host genotype

Funding: Support was provided by start-up funds from the University of Puerto Rico, Río Piedras Campus to I.A.R.F.

Abstract: 20260228_081

Title: Evaluating the effects of Different Concentrations of the probiotic Lactiplantibacillus plantarum on the locomotion of young and old Drosophila

Authors: Camila S. Marco-Colón, Karina Y. Torres Santiago, Geraldine M. Ortiz-Sosa, Dr. Imilce A. Rodriguez Fernandez

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Aging is characterized by a gradual decline in tissue functionality and is considered the main risk factor for multiple chronic diseases, including cardiovascular, neurodegenerative, and metabolic disorders. At the molecular level, aging is accompanied by changes in several pathways, including alterations in gut microbiota composition that often lead to dysbiosis. A central question in the field is whether probiotics could represent a new intervention to promote healthy aging. Probiotics are defined by the World Health Organization as live microorganisms that, when administered in adequate amounts, confer health benefits to the host. Beyond their classical role in digestive health, probiotics can also modulate metabolism, immunity, and even brain function, although the mechanisms remain under investigation. Among them, Lactiplantibacillus plantarum has emerged as a promising candidate due to its natural presence in fermented foods and the gastrointestinal tract. Previous studies in animal models have linked it to improved memory, locomotion, and lifespan, making it an excellent model to explore its role in healthy aging. To test the impact of probiotic supplementation in aging, we used Drosophila melanogaster as a model due to its short lifespan, genetic tractability, and well-described aging-related phenotypes such as reduced locomotion and intestinal dysfunction. Our study evaluated the effects of L. plantarum strains LpWF and Lp39 at three concentrations (10^8, 10^9, and 10^{10} CFU/mL) on the climbing ability of young (15-day-old) and aged (35-day-old) flies at 3 and 24 hours post-treatment. This design allowed us to directly compare locomotion across ages, strains, and doses, providing insight into potential age-dependent effects of probiotic supplementation. Preliminary results show that probiotic supplementation does not significantly affect locomotion in young flies, while in aged flies, Lp39 at all doses and LpWF at 10^{10} CFU/mL appear to negatively impact climbing ability at 24 hours. These findings suggest that probiotic effects are context-dependent and highlight the importance of age when evaluating microbiome-based interventions. Importantly, we also observed unexpected differences in the control group, which suggest that the vehicle (5% sucrose solution) itself may influence locomotion and should be examined in future experiments. Future experiments will explore whether these effects are conserved across different genetic backgrounds, assess the long-term impact of probiotic supplementation, and determine whether early-life exposure can promote lifespan extension or healthy aging. Additionally, we aim to clarify the role of dosage in modulating these outcomes, which could provide critical insights for designing microbiome-based strategies to improve functional capacity and quality of life in aged organisms.

Key Words: Aging, Probiotics, Drosophila melanogaster

Funding: National Institutes of Health

Abstract: 20260228_002

Title: I've Gut a Feeling: Early Life Stress Shifts Behavior, Microbiota & Permeability in Both Sexes

Authors: Melanie Ortiz Alvarez de la Campa, B.S. [1, & 2], Peter Belenky, PhD [2]

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Background: Anxiety disorders, affecting over 40 million adults (19.1% of total adults) in the U.S., represent a prevalent mental health challenge. Among those is Generalized Anxiety Disorder, of which 50% of patients will not respond to treatment. Advances in gut-brain axis research have uncovered intriguing connections between the microbiome and anxiety. However, the intricacies of this relationship remain elusive. Moreover, the influence of early life stress (ELS) on both the microbiome and anxiety has yet to be fully understood.

Methods: In this work, we used a limited bedding and nesting murine model of ELS to study the relationship between anxiety-like behavior and microbiome composition. We induced ELS from postnatal days 4-11 and treated with antibiotics after weaning. Later, at 4-8 weeks old, mice underwent anxiety-like behavior tests, including the open field, elevated-plus-maze, and marble burying tests. Microbiome composition was assessed throughout the entire gastrointestinal tract using 16S rRNA sequencing.

Results: We found significant differences between male and female mice in both behavior and microbiome composition. ELS exposure resulted in a significant increase in both inflammatory & protective bacteria, as well as an increase in fear and repetitive behavior, particularly in males. Microbiome variation was also influenced by the gastrointestinal location, with upper and lower tracts showing distinct microbial community shifts. Additionally, antibiotic modulation improved anxiety-like behavior symptoms in a sex-dependent manner. Interestingly, ELS serum led to a protective effect on the blood-brain barrier *in vitro*.

Conclusion: Overall, this work shows that sex, microbiome composition and ELS exposure all have significant impacts on the development of anxiety-like behavior in mice. These results have implications for the future implementation of personalized anxiety treatments and underscore the importance of microbiome-inclusive biobehavioral research.

Keywords: gut microbiome, anxiety, gastrointestinal tract, sex differences, early life stress

Funding/ Acknowledgements: National Science Foundation Graduate Research Program Fellowship [#2040433], Carney Innovation Award 2025 (Zimmerman #GR500231), National Institute of Diabetes and Digestive and Kidney Diseases [R01 #DK125382]

Abstract: 20260228_003

Title: Dissecting Biofilm-Associated Genes in Lactiplantibacillus plantarum and Their Potential Role in Host Nrf2/CncC Activation

Authors: Joseph E. Cancel Lozada[1], Karla M. Casillas Pagán[1], Imilce A. Rodríguez Fernández[1]
Institution: [1]Department of Biology, College of Natural Sciences, University of Puerto Rico, Río Piedras, San Juan, PR

The gut microbiota plays essential roles in host nutrition, immunity, and epithelial homeostasis, and its successful colonization often depends on the ability of bacteria to form biofilms. Biofilms are structured communities stabilized by extracellular polysaccharides (EPS) that promote adherence and persistence within the gut environment. Biofilm formation is, therefore, a key mechanism by which commensal microbes establish long-term associations with their hosts. In the host, the probiotic and commensal bacterium Lactiplantibacillus plantarum (Lp) can activate the conserved Nrf2/CncC transcription factor pathway, thereby enhancing the cellular antioxidant response. However, it remains unknown which genes in Lp are responsible for activating Nrf2/CncC in the host. We hypothesized that the capacity of Lp to form biofilms could be part of the mechanism used to activate Nrf2/CncC. To investigate this, we generated a collection of 300 Lp mutants using EZ-Tn5 transposon–mediated mutagenesis. The EZ-Tn5 transposon carries the Kan-2 gene, which confers kanamycin resistance and integrates randomly into the genome. Our goal is to evaluate the phenotypic characteristics of biofilm formation and growth in these L. plantarum mutants. Biofilm formation was quantified using the crystal violet microtiter-plate assay. Briefly, Lp mutants (n = 32) were inoculated into 96-well plates with MRS medium and 800 µg/ml kanamycin. Biofilms were fixed with 99% methanol, stained with crystal violet for 30 minutes, and destained with 33% glacial acetic acid. Absorbance was measured at 24 and 48 hours. Biofilm formation was classified as weak, moderate, or strong. To determine how each mutation affected growth dynamics under selective and non-selective conditions, growth curves were generated by inoculating strains into fresh MRS medium with and without kanamycin and measuring OD600 over 24 hours. Preliminary data (n = 32) show that at 24 hours, 14% of mutants exhibited weak biofilm formation, 17% moderate, and 68% strong; at 48 hours, 5% were weak, 17% moderate, and 74% strong. Growth curves revealed a decrease in growth rate in mutants compared to the control. In future work, we will select mutants with weak and strong biofilm phenotypes to test their ability to activate Nrf2/CncC in larvae carrying an Nrf2/CncC genetic reporter. Identifying Lp genes involved in biofilm formation will help elucidate microbial factors that shape host–microbe interactions and contribute to beneficial host responses.

Abstract: 20260228_005

Title: Characterization of Outer Membrane Vesicles (OMVs) from *pks*+ NC101 and *pks*- DH10B *E. coli* strands

Authors: Lissette Pérez-Rovira [1,2], Jeremy J Colon-Morales[2,3], Grace Vélez-Crespo [2], Luis Prieto-Costas [2], Abel Baerga-Ortiz[1,2,3]

Institution: [1]Comprehensive Cancer Center of Puerto Rico, [2]UPR Molecular Research Center, [3]Medical Science Campus of Puerto Rico

Background & Objectives: Colibactin is a genotoxin encoded by the *pks* genomic island in pathogenic Gram-negative bacteria and has been implicated in colorectal cancer. Colibactin synthesis and activation occur in a two-step process in which pre-colibactin is produced in the bacterial cytoplasm and subsequently activated into colibactin within the periplasmic space. However, the mechanism by which *pks*$^+$ bacteria export colibactin to host cells remains unclear. We hypothesize that outer membrane vesicles (OMVs), nanosized proteoliposomes released by Gram-negative bacteria capable of transporting diverse biomolecules, serve as a delivery system for this toxin to host cells.

Methods: To investigate this, OMVs were isolated from *pks*$^+$ NC101 and *pks*- DH10B *E. coli* strains using the Qiagen exoEasy Maxi Kit (#1) and the Exobacteria OMV Isolation Kit (#2) and quantified with a BCA protein assay to compare yields and determine the method providing the highest recovery. The stability and morphological characteristics of the extracted OMVs have been evaluated using dynamic light scattering (DLS).

Results: OMVs concentrations with Kit #1 was approximately 200 µg/mL, whereas kit #2 produced substantially higher concentrations of approximately 1,400 µg/mL. Results from DLS analysis showed a consistent OMV size distribution typical of bacterial OMVs, ranging from 110 nm to 170 nm. Additionally, metabolites extracted from OMVs will be examined via mass spectrometry to confirm the presence of known colibactin-related intermediates. Finally, OMVs will undergo proteomic analysis to identify proteins involved in OMV–host interaction mechanisms.

Conclusion: Ultimately, this research seeks to clarify how OMVs mediate colibactin transport and cytotoxicity, providing new insights into bacterial factors that promote colorectal carcinogenesis.

Acknowledgements: This research was funded by the National Institute of Allergy and Infectious Diseases (NIAID) Grant #5R25AI183304-02.

Abstract: 20260228_008

Title: More Than Just a Legume: How Microbial Communities Shape the Survival of Puerto Rico's Endangered *Chamaecrista glandulosa* var. *mirabilis*.

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Leguminous plants are crucial for ecosystem sustainability through organic matter enrichment, nutrient cycling, water retention, and nitrogen fixation. This study explores the microbial communities associated with root nodules, leaves, and surrounding soils of *Chamaecrista glandulosa* var. *mirabilis*, an endangered legume endemic to Puerto Rico. Confined to fragmented habitats of acidic, nutrient-poor siliceous sands, this species faces environmental pressures that likely influence its microbiome. Understanding these microbial communities is essential for developing effective conservation strategies. We collected 32 samples from leaves (n=10), soil (n=11), and root nodules (n=11) from 11 individuals at the Reserva Natural Laguna Tortuguero, Puerto Rico, in spring 2024. Metagenomic DNA was extracted using the DNeasy PowerSoil Pro Kit (Qiagen), quantified with a NanoDrop 2000, and amplified for the 16S rDNA gene. Sequencing was conducted on an Illumina MiSeq (300 x 300 bp). Data analysis using QIIME2 included alpha and beta diversity, taxonomy distribution, and differential abundance, with visualizations created using GraphPad Prism (Version 10.4.1). Taxonomy was assigned using the silva-138.1 taxonomic database. Rarefaction was performed to 20,511. Samples showed significant differences in alpha diversity indices (Observed Species, Shannon Entropy, Faith PD) among groups ($p < 0.05$). Beta diversity (Bray-Curtis and Weighted UniFrac) indicated distinct community compositions across leaves, nodules, and soil samples ($p < 0.05$). Differential abundance analysis identified key taxa: *Nitrosocomiscus* in soil, *Bradyrhizobium* in nodules, and *Methylobacterium* in leaves, all significant with $p < 0.05$ and fold change of |2. This study reveals distinct microbial communities associated with different plant structures of *Chamaecrista glandulosa var. mirabilis*, highlighting their potential roles in nutrient cycling and environmental adaptation. *Nitrosocomiscus* enrichment in soil suggests involvement in nitrogen cycling, enhancing soil fertility under nutrient-poor conditions. *Bradyrhizobium* dominance in nodules confirms its role in nitrogen fixation, supporting plant growth in challenging soils. *Methylobacterium* presence on leaves indicates possible roles in methanol utilization and growth promotion. These findings demonstrate that *C. glandulosa* var. *mirabilis* relies on specific microbial partnerships for nutrient acquisition and stress tolerance, crucial for survival in fragmented habitats. The study underscores the importance of considering plant-microbiome interactions in conservation strategies, as maintaining these microbial networks is vital for the species' resilience. This research not only advances understanding of plant-microbiome dynamics but also offers insights for ecological restoration and the conservation of endangered species

Keywords: Nodule, legume, endemic, endangered, leave, soil

Funding: Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health under grant number P20 GM103475-21 (PRINBRE).

Abstract: 20260228_009

Title: Identification of Microbial Diversity and Toxin Secretions of Invasive Cuban Tree Frogs (Osteopilus septentrionalis)

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The Cuban tree frog (Osteopilus septentrionalis) is an invasive species introduced to Puerto Rico in the early 1960s and possesses defensive mucous secretions containing noxious, toxic compounds. Despite frequent reports of irritation and toxicity, the biochemical composition of these secretions remains poorly characterized and may vary across individuals. This variability suggests that external factors such as the skin microbiome may influence toxin production, presenting a relevant but understudied host-microbe interaction within amphibian chemical defense systems. To investigate this potential relationship, we conducted a comparative analysis of microbial communities and toxin-associated metabolites from multiple O. septentrionalis from western Puerto Rico. Skin mucus and glandular secretions were collected from wild individuals. Bacterial diversity was assessed using 16S rRNA metabarcode sequencing, and toxin metabolites were characterized using UPLC-MS to evaluate chemical variation and potential microbial contributions. Preliminary analyses reveal a highly diverse skin microbiome, comprising > 500 bacterial genera across 50 sampled frogs from five localities. Metabolomic profiles show substantial variation in toxin composition among individuals, with several metabolites co-occurring alongside bacterial taxa known to produce bioactive compounds. These findings support the hypothesis that skin-associated microbes may contribute to or modulate the chemical defenses of O. septentrionalis. Understanding this potential symbiosis may provide insight into how microbial communities enhance the ecological success of invasive amphibians.

Keywords Skin-microbiome; Host-microbiome interactions; amphibian defenses

Abstract: 20260228_010

Title: Functional Host Cell Responses to a Microbiome-Derived Fungal Polysaccharide Peptide in an In Vitro Model

Authors: Geraldine Cintrón-Vélez, B.S. Student [1]; Glamaris Rosario-Sanfiorenzo, B.S. Student [2]; Giovanni Alicea-Perez, B.S. Student [2]; Naiara Hernández-Santisteban, B.S. Student [3]; Amanda Rivera-Payán, B.S. Student [3]; Jeshua Colón-Fernández, B.S. Student [3], Ashlin Álvarez-Flores, B.S. Student [4]; Carolina Nieves-Moreno, B.S. Student [4]; Yariselis Cardona-Maldonado, B.S. Student [2]; Samuel Caldero-Reyes, B.S. Student [2]; Natalia Sánchez-Otero, B.S. Student [3]; Fabiola Colón-Santiago, MD Student [5]; Perla Rivera-Soto, B.S. Student [6]; Genesis Matos-Morales, B.S. Student [3]; Andrea Rodríguez-De La Rosa, B.S. Student [3]; Fabiola Guevarez-Russe, B.S. Student [2]; Julieness Correa-Haifa, B.S. Student [2]; Carolina Felix-Rosario, B.S. Student [2]; Gabriela Arvelo-Colón, B.S. Student [4]; Carla Toledo-Tejada, B.S. Student [4]; Alanis Pagan-Santisteban, B.S. Student [3]; Eduardo Álvarez-Rivera, PhD [5].

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Background: Microbiome-derived metabolites are increasingly recognized as important modulators of host cellular physiology beyond immune-specific contexts. Fungal components of microbiomes, including bioactive polysaccharides, can influence host cell viability, stress responses, and long-term cellular adaptation. Polysaccharide-peptide (PSP), isolated from the medicinal mushroom *Coriolus versicolor*, has demonstrated biological activity across multiple host systems; however, its direct functional effects on host cellular viability over extended exposure periods remain underexplored. This study evaluates a dose- and time-dependent host cellular response to a fungal-derived microbiome metabolite using an in vitro model. Methods: Human A172 cells were cultured and exposed to increasing concentrations of PSP (500-4000 µg/mL) for 6 and 9 days to assess functional cellular responses to prolonged metabolite exposure. Cell viability was quantified using MTT assays to evaluate dose-dependent and time-dependent effects. All experiments were performed under controlled conditions to ensure reproducibility and objective data collection. Results: Exposure to PSP resulted in a progressive reduction in cellular viability in a concentration- and time-dependent manner. Higher PSP concentrations (3500–4000 µg/mL) reduced cell viability to approximately 48% after 6 days and to 30% by day 9, while lower concentrations produced milder effects. These findings demonstrate a clear exposure-dependent host cellular response to sustained treatment with a fungal-derived microbiome metabolite. Conclusion: This study demonstrates that prolonged exposure to a microbiome-derived fungal polysaccharide peptide induces measurable, dose- and time-dependent changes in host cellular viability. These findings contribute to a growing understanding of how fungal-derived metabolites influence host cellular physiology and highlight the importance of characterizing functional host responses to microbiome-associated bioactive compounds. Further studies are warranted to investigate the underlying mechanisms driving these responses and their broader biological relevance, including comparisons of survival and cell-mediated death across a broader range of microbiological systems.

Keywords: Microbiome-derived metabolites; fungal bioactives; host cellular responses

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Abstract: 20260228_011

Title: Microbiome-Derived Immunomodulation of Adaptive Antiviral Signaling Through TLR4-PKR Pathways

Authors: B.S. Student [1]; Glamaris Rosario-Sanfiorenzo, B.S. Student [2]; Giovanni Alicea-Perez, B.S. Student [2]; Naiara Hernández-Santisteban, B.S. Student [1]; Amanda Rivera-Payan, B.S. Student [1]; Jeshua Colón-Fernández, B.S. Student [1]; Ashlin Álvarez-Flores, B.S. Student [3]; Carolina Nieves-Moreno, B.S. Student [3]; Yariselis Cardona-Maldonado, B.S. Student [2]; Samuel Caldero-Reyes, B.S. Student [2]; Natalia Sánchez-Otero, B.S. Student [1]; Fabiola Colón-Santiago, MD Student [4]; Perla Rivera-Soto, B.S. Student [5]; Genesis Matos-Morales, B.S. Student [1]; Andrea Rodríguez-De La Rosa, B.S. Student [1]; Fabiola Guevarez-Russe, B.S. Student [2]; Julieness Correa-Haifa, B.S. Student [2]; Carolina Felix-Rosario, B.S. Student [2]; Gabriela Arvelo-Colón, B.S. Student [3]; Carla Toledo-Tejada, B.S. Student [3]; Geraldine Cintron-Velez [6]; Eduardo Álvarez-Rivera, PhD [4].

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Background: Microbiome-derived bioactive compounds play a critical role in shaping host immune responses and maintaining immune homeostasis. Fungal metabolites, in particular, have emerged as potent immunomodulators that influence both innate and adaptive immune signaling pathways. Polysaccharide peptide (PSP), isolated from the medicinal mushroom *Coriolus versicolor*, has been shown to enhance innate antiviral defenses through pattern recognition receptor signaling. However, its role in modulating adaptive immune signaling remains poorly understood. This study investigates whether a fungal-derived immunomodulator can reprogram adaptive immune pathways associated with antiviral restriction, highlighting the relevance of host-microbiome immune interactions. Methods: Jurkat T-helper cells were treated with PSP (50-1,000 µg/mL) for 3 and 6 days to evaluate adaptive immune signaling responses. Protein expression of Toll-like receptor 4 (TLR4), protein kinase R (PKR), signal transducer and activator of transcription 1 and 2 (STAT1/2), and cofilin-1/phosphorylated cofilin (pCofilin) was assessed by immunoblotting. PKR transcript levels were quantified using RT-qPCR. Cellular viability was evaluated via MTT assays. To assess functional antiviral outcomes, HIV viral restriction assays were performed in THP-1 monocytic cells as a complementary model. Results: PSP treatment induced a dose-dependent upregulation of TLR4, PKR, STAT1, STAT2, and phosphorylated cofilin, accompanied by a reduction in total cofilin-1 expression. RT-qPCR analysis confirmed increased transcriptional expression of PKR, STAT1, and STAT2 following PSP exposure. Functional assays demonstrated a 73% reduction in viral particle levels in PSP-treated THP-1 cells. No cytotoxic effects were observed across all concentrations and time points tested. Conclusion: These findings demonstrate that a microbiome-derived fungal polysaccharide peptide can modulate adaptive immune signaling pathways associated with antiviral restriction. By activating TLR4-dependent signaling and downstream PKR-STAT pathways, PSP promotes cytoskeletal and antiviral responses that may enhance immune resilience. This study highlights the immunological relevance of fungal-derived metabolites within the microbiome and supports their potential role in shaping adaptive immune function.

Keywords: Microbiome immunology, adaptive immunity, Viral restriction

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Abstract: 20260228_012

Title: Exercise-Induced Remodeling of Gut Microbiota Enhances Microbial Tryptophan Metabolism

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Introduction: Various microbial metabolites derived from tryptophan have been implicated in influencing gut-brain axis. Running exercise has been shown to influence gut microbiota composition and function, but its specific impact on tryptophan metabolism in the gut remains unclear. In our study, we aimed to investigate the impact of running exercise on microbial tryptophan metabolism using a mouse model.

Methods: Fecal samples were collected from sedentary (SED) and running (RUN) groups of mice after 6 weeks of exercise. Microbiome analysis was performed using high-throughput sequencing of the 16S rRNA gene. Additionally, we measured the levels of tryptophan in the gut using GC/MS analysis and tryptophan metabolites in the gut using LC/MS analysis. Taxon-function analysis was used to predict the association between specific microbial taxa and functional activities in TRP metabolic pathways within the SED and RUN groups.

Results: Microbiome analysis revealed significant differences in the composition of the gut microbiota between the SED and RUN groups. We observed alterations in the relative abundances of specific microbial taxa, including an increased presence of *Romboutsia* and *Akkermansia muciniphila* in the RUN group. The running exercise was associated with a shift in the tryptophan metabolizing capabilities of bacterial groups, leading to changes in the production of tryptophan derivatives along the kynurenine and indole pathways.

Conclusion: We observed an enhanced symbiotic interplay between *Akkermansia muciniphila* and *Romboutsia* as a result of running exercise. This symbiotic relationship increased the availability of tryptophan for transport to the brain, resulting in enhanced serotonin synthesis, a key metabolite derived from tryptophan. These findings provide valuable insights into the intricate relationship between exercise, the gut microbiome, and tryptophan metabolism and provide the basis for the development of exercise-based interventions targeting gut health, metabolic function, and brain health, offering non-pharmaceutical approaches for improvement.

Funding: This work was supported by the NIH/NIGMS-PRINBRE Grant 5P20GM103475.

Abstract: 20260228_013

Title: Environmental Exposures Associated with the Human Gut Resistome in Ecuadorian Households

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Background: Antimicrobial resistance (AMR) is a major global public health threat, particularly in low- and middle-income countries (LMICs), where household-level animal husbandry, inadequate WASH (water, sanitation, and hygiene), and unregulated antimicrobial use may contribute to its spread. While the effects of large-scale animal production are well documented, the role of household-level animal exposure is less understood. This study investigated how household animal husbandry and WASH conditions shape the gut resistome in children and pregnant women in Ecuador. Because traditional AMR studies rely on culture-based methods, we used metagenomic sequencing to provide a culture-independent and comprehensive view of antimicrobial resistance genes (ARGs). Methods: We conducted short-read shotgun metagenomic sequencing on 206 stool samples from individuals across various age groups: pregnant women at 37 weeks gestation (*n=53*), children aged 1 week (*n=53*), 3 months (*n=20*), 6 months (*n=20*), and 18 months (*n=60*). We evaluated the number of clinically relevant ARGs, ARG abundance, and prevalence of ESKAPEE pathogens across households with varying levels of animal exposure, sanitation facilities, and drinking water sources. We utilized linear models to evaluate the association between these environmental factors and microbiological outcomes. Results: The number of clinically relevant ARGs was significantly higher in mothers with high household animal exposure exposure, suggesting that close contact with domestic animals may influence the adult gut resistome. ARG abundance was lower among mothers with access to piped drinking water, and the relative abundance of *Klebsiella pneumoniae* was reduced in households with improved water and sanitation, highlighting the potential protective role of WASH infrastructure. In contrast, ARG abundance and the number of clinically relevant ARGs in children were highly variable and not associated with animal husbandry or water and sanitation conditions, indicating that additional factors, such as age, diet, antibiotic exposure, and broader environmental inputs, may play a larger role in shaping the early-life resistome. These findings suggest that household animal exposure and WASH conditions are associated with the maternal gut resistome. Conclusions: Improving drinking water and sanitation facilities could reduce the human gut resistome in adults, offering public health officials an additional strategy to combat AMR beyond traditional stewardship efforts. Furthermore, regulating the use of antibiotics in livestock, educating antimicrobial resellers, and strengthening veterinary care in rural communities could help mitigate the AMR burden associated with animal ownership.

Keywords: Antimicrobial resistance genes, shotgun metagenomic sequencing, gut microbiome

Funding: This project was supported by: UW Microbial Interactions & Microbiome Center, ASEE e-fellows program Federal Award 2127509, P30 ES007033, R01AI137679 and R01AI162867.

Abstract: 20260228_015

Title: Microbiome-derived neuroactive/immunomodulatory metabolites regulating host cytoskeletal dynamics

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Background: Microbiome-derived metabolites play an essential role in regulating host cellular processes beyond classical immune signaling, including cytoskeletal organization and cellular adaptability. Fungal components of the microbiome produce bioactive compounds capable of influencing host cell structure and function. Erinacines, a class of secondary metabolites isolated from the medicinal mushroom *Hericium erinaceus*, have been reported to exhibit neuroactive and immunomodulatory properties; however, their effects on host cytoskeletal regulation remain poorly characterized. This study examines the impact of a fungal-derived microbiome metabolite on host actin dynamics through modulation of the actin-regulatory protein cofilin-1. Methods: Jurkat T cells were treated with erinacines (50-1000 µg/mL) for up to 6 days to evaluate host cellular responses to metabolite exposure. Cofilin-1 expression and phosphorylation status were analyzed by Western blot, and transcript levels were quantified by RT-qPCR. Statistical analyses were performed using one-way ANOVA with post hoc testing to evaluate dose-dependent effects. Results: Erinacine treatment induced a significant dose-dependent increase in total and phosphorylated cofilin-1 expression. These changes were most pronounced at extended exposure time points and were consistent with enhanced actin remodeling activity. Transcriptional analysis supported increased cofilin-1 regulation in response to fungal metabolite exposure, indicating coordinated modulation at both protein and mRNA levels. Conclusion: These findings demonstrate that a microbiome-derived fungal metabolite can modulate host cytoskeletal dynamics by regulating cofilin-1 activity in a cellular model. This work highlights a previously underexplored role of fungal-derived bioactive compounds in shaping fundamental host cellular processes and underscores the importance of investigating microbiome-associated metabolites beyond immune-specific contexts.

Keywords: Microbiome metabolites; fungal bioactives; cytoskeletal regulation

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Abstract: 20260228_017

Title: Bioactive Antimicrobial Potential of the Puerto Rican Wetland Microbiome

Authors: Alanis N. Saéz-Ferrer[1] and Rafael Maldonado-Hernández[1,2]

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Wetland ecosystems support highly complex and diverse microbiomes, many components of which remain insufficiently characterized. These environments represent promising reservoirs for the discovery of novel antimicrobial compounds, particularly in the context of increasing global antibiotic resistance. In this study, bacterial isolates were obtained from sediment and water samples collected in the Sabana Seca wetlands of Puerto Rico. Samples were serially diluted and cultured on general and selective media to isolate morphologically distinct colonies, which were subsequently purified and subjected to phenotypic and biochemical characterization, including Gram staining, catalase testing, and potassium hydroxide string assays. Two pigmented isolates were further taxonomically identified by 16S rRNA gene sequencing: a red-pigmented strain corresponding to Serratia marcescens and a violet-pigmented strain corresponding to Chromobacterium violaceum. Both strains demonstrated antimicrobial activity on TSA plates, producing clear zones of inhibition against Escherichia coli and Staphylococcus aureus. Untargeted metabolomic analysis using high-resolution QTOF-MS/MS revealed the presence of secondary metabolites associated with antimicrobial function. Bioactive compounds were recovered through organic solvent extraction, with prodigiosin and violacein confirmed as the primary antimicrobial agents. Minimum inhibitory concentration (MIC) assays indicated potent activity of prodigiosin against E. coli (94 µg/mL) and violacein against S. aureus (50 µg/mL). Collectively, these findings underscore the Puerto Rican wetland microbiome as an underexplored source of bioactive metabolites with significant clinical potential. Ongoing and future studies will focus on cytocompatibility evaluation and mechanistic characterization to advance the translational applicability of these native microbial derived compounds.

Keywords: Antimicrobial Resistance; 16S rRNA; MIC

Abstract: 20260228_018

Title: Building Microbiome Research Capacity Through a Financial, Academic, and SocioEmotional Support Ecosystem for Talented Low-Income Students

Authors: Cafaro, MJ; Alfaro, M; Bellido, C; Delgado, BM; Lopez Del Puerto, C

Institution: University of Puerto Rico at Mayaguez

Puerto Rico faces an urgent need to develop a robust STEM workforce capable of advancing microbiome research and related life-science and chemical sectors, while simultaneously addressing long-standing inequities affecting low-income students. This work describes an integrated support ecosystem designed to build microbiome-relevant research capacity by investing in talented undergraduate students in Biology and Chemistry at the University of Puerto Rico at Mayagüez. Grounded in an evidence-based program model, the initiative combines three tightly coupled components: (1) targeted financial support to reduce economic barriers and allow sustained academic focus; (2) structured academic mentoring and research engagement to strengthen disciplinary foundations in biology, chemistry, and microbiology; and (3) intentional socio-emotional support to promote resilience, belonging, and persistence in demanding STEM pathways.

The ecosystem, funded by a grant by the National Science Foundation (NSF), prioritizes early exposure to research skills central to microbiome science—including experimental design, data interpretation, and interdisciplinary thinking—thereby aligning student training with current and emerging workforce needs in biomedical, environmental, and industrial microbiology. Program outcomes demonstrate measurable gains in academic performance and retention, particularly among Biology and Chemistry majors, and increased participation in research experiences that function as gateways to graduate education and scientific careers.

A key workforce development milestone has been the placement of four students in competitive summer research internships within the State University of New York (SUNY) system—at SUNY Upstate Medical University and Stony Brook University—providing high-impact training in biomedical and chemical research environments beyond Puerto Rico. These external placements expanded professional networks, reinforced research identity, and accelerated students' readiness for advanced study and employment. Collectively, this model demonstrates that an integrated financial, academic, and socio-emotional support ecosystem can effectively cultivate microbiome-relevant talent among low-income students, strengthening the local and national STEM workforce while offering a scalable framework for other institutions serving historically underrepresented populations.

Abstract: 20260228_020

Title: Initial characterization of the microbial communities across multiple kingdoms associated with coffee beans under varying degrees of CBB infestation.

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Background- Coffee is one of the most important commodities worldwide. In recent years, a highly damaging coffee pest has arrived in the Caribbean: *Hypothenemus hampei* Ferrari, 1867 (Coleoptera: Curculionidae) (coffee berry borer, CBB). This pest bores into the coffee endosperm, reducing coffee quality and yield. Several studies have shown that this pest's microbiome is detrimental to its development and can vary across locations. However, no studies have examined the effect of CBB infestation on the coffee endosperm microbiome.

Methods- In our study, we analyzed coffee beans under three infestation levels: not infested, initial infestation, and advanced infestation, at two different locations, Utuado and Adjuntas. Berries were collected, separated into infested and non-infested groups, and kept refrigerated until arrival. In the lab, they were frozen at -80℃ until processed. The outer layers were removed, and only the endosperm was retained. We removed all insects and cleaned all beans prior to DNA extraction to minimize environmental contamination. We used 16S rRNA and ITS-targeted sequencing to characterize bacterial and fungal communities, respectively. We replicated each infestation group for each location five times.

Results- Our results showed that, at the phylum level, *Bacteroidota* and *Pseudomonadota* were the most abundant, with *Pseudomonadota* increasing with increasing infestation levels. At a higher taxonomic level, we observed a relatively stable community, with the family *Mariniliabiliaceae* as the most abundant taxon (JC017, an unclassified bacterial genus). Furthermore, as infestation increased, we observed greater taxonomic diversity. As for the fungal Community *Ascomycota* and *Basidiomycota* were the most abundant phyla, and *Nectriaceae* was the most abundant genus at most locations in infested beans. Nonetheless, our observations indicate a higher taxonomic diversity in healthy, non-infested beans, whereas a reduction in taxonomic diversity is evident in infested berries. Furthermore, it was observed that four bacterial and fifteen fungal taxa were common among beans at varying levels of infestation.

Conclusion- We conclude that there is compelling evidence of microbial dysbiosis in infested beans, characterized by increased bacterial and decreased fungal taxa. Further an analysis is necessary to assess the effect of these microorganisms on fermentation outcomes and flavor profiles.

Keywords: Microbiota, multi-kingdom, food security.

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Abstract: 20260228_023

Title: Expression and Purification of the Uropathogenic Specific Protein

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Institution: University of Puerto Rico, Molecular Science Research Center. University of Puerto Rico, Medical Sciences Campus.

Background: The Uropathogenic Specific Protein (USP) is a multi-domain protein produced by various strains of uropathogenic E. coli. The protein domains consist in an HNHc nuclease, a Pyocin S like domain and a Hemolysin coregulated protein domain (Hcp). While these individual domains have been studied previously, the mechanisms of action of the full-length protein have yet to be elucidated. The USP protein has shown to possess low solubility, and its purification has been difficult. Methods: The USP gene was integrated into a pUC19 plasmid with a histidine tag at the amino terminal of the protein sequence and an ampicillin resistance gene to aid in the selection of the transformed cells. A strain of E. coli denominated BL21 was transformed and grown on LB media containing IPTG and ampicillin. These cells were then pelleted and lysed by sonication under denaturing conditions with 8M Urea for an hour at 37˚ C. The lysis suspension was filtered and loaded to the FPLC coupled with a His-Trap affinity column that binds to the histidine residues of the protein, after which the protein was eluted with a high imidazole buffer. The resulting protein is then concentrated and loaded once more in the FPLC, this time to separate using a size exclusion column to ensure proper purification. Each fraction is loaded into an SDS-PAGE and stained with Coomassie to determine the protein presence and size of the proteins in each fraction. Further confirmation is obtained via a western blot of the fractions using a monoclonal antibody that detects the Pyocin domain of USP. Results: We have been able to purify the protein using this method in two forms, the wild type USP and the USPΔHNHc both confirmed by Coomassie stain and western blots. Conclusion: While the presence of both proteins has been determined using the same starting volume of cell culture, the amount of pure protein obtained by liter of culture are 0.43 mg for the wild type USP and 66.7 mg for the USPΔHNHc. DNase activity assays will be performed to assess the catalytic activity for these enzymes.

Keywords: Microbiome, Protein purification, FPLC

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Abstract: 20260228_025

Title: Uncovering the Biological Complexity of Thalassia testudinum through Multi-Omics Profiling Landscape

Authors: Abner J. Colón Colón, Gerardo Laureano Rosario, Dariel A. Vázquez Fuentes, Rosalinda Aybar Batista, Christopher A. Sambolín Pérez, Ramón E. Rivera Vicéns, and Ángel R. Núñez Marrero*
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Seagrass meadows are vital members of coastal systems and essential for sediment stabilization, nutrient cycling, and coastal biodiversity. A predominant species in the Caribbean ecosystem is the native tropical seagrass Thalassia testudinum. Given its environmental abundance, most reported studies have been focused on the morphological traits for taxonomical classification. Conversely, studies addressing seagrass microbiome composition are limited. Seagrass-microbe interaction is pivotal for seagrass growth, health, and functioning. In this study, the bacterial community of T. testudinum from southwest Puerto Rico was analyzed by full 16S rRNA sequencing using the MinION platform. In addition, the chloroplast genome for T. testudinum was sequenced to evaluate evolutionary distance relative to the publicly available Thalassia spp. chloroplast genomes. However, the bacterial community profile was largely composed of members of the phylum Pseudomonadota. At the genus level, Alteromonas was among the most abundant taxa detected, and it is commonly known to be a potential plant growth-promoting bacterium (PGPB). Additionally, the microbiome composition included bacterial taxa previously reported to be associated with disease suppression and biological nitrogen fixation. Interestingly, the phyla Bacteroidota, Cyanobacteriota, and Bacillota, present at low abundance, likely play key functional roles in carbon degradation, nitrogen cycling, and stress resilience within the seagrass microbiome. At the cp genome level, T. testudinum measured 179,257 bp and showed overall structural conservation across Thalassia spp., with pronounced differences in gene annotation, ranging from 89 genes in Puerto Rico to 112 in Florida and 112–160 in Chinese T. hemprichii. Therefore, this study brings insight into the bacterial composition and initial evolutionary analysis of the important Caribbean seagrass, T. testudinum.

Keywords: Thalassia testudinum, seagrass microbiome, chloroplast genome

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Abstract: 20260228_030

Title: Cobamides as Model Nutrients for the Study of Soil Bacterial Interactions

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Background- Microbial communities in soil impact numerous global processes, from nutrient cycling to agriculture. The global effects of microbes are greatly dependent on metabolic interactions that affect community composition and function. However, microbial interaction studies are challenging due to the physicochemical and taxonomic complexity of soil. By focusing on cobamides (the vitamin B12 family of cofactors) as model shared nutrients, we aim to study metabolic interactions among soil microbes in a mechanistic manner.

Methods- Here, we studied interactions among bacteria that were previously isolated from soil and characterized as cobamide producers (synthesize cobamides de novo) or dependents (require cobamides but cannot synthesize them). We combined a culture-based approach with whole genome sequence analysis to predict and test the outcome of interactions in co-cultures and tri cultures of corrinoid dependents and corrinoid producers.

Results -The outcome of competition between pairs of dependents was predictable based on monoculture growth characteristics. We observed that the dominant microbe was determined by its adaptation to a specific cobamide concentration range. Cobamide producers supported the growth of dependents in co-culture and influenced the outcome of competition between dependents in tri-cultures. Whole genome sequence analysis confirmed metabolic capabilities and revealed that cobamides are likely the main shared nutrient in our co- and tri-cultures.

Conclusion-This work highlights the utility of the model nutrient approach for generating accurate predictions of microbial interactions in consortia of increasing complexity. The knowledge acquired through this approach can be applied in efforts to decode interactions in complex microbial communities.

Keywords: Soil microbiome, cobamide, interactions

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Abstract: 20260228_033

Title: Translational Potential of Antimicrobial Metabolites Derived from the Eleutherodactylus spp. Microbiome

Authors: Luis Perez-Dieppa[1], Valerie Ortiz-Gómez [2], Luis A. Prieto-Costas[3] and Rafael Maldonado-Hernández[1]

Institution: [1]Department of Biology, University of Puerto Rico Cayey Campus, Cayey, Puerto Rico, United States; [2]Department of Natural Sciences and Technology, Ana G. Méndez University, Gurabo Campus, Puerto Rico, United States, and [3]Center for Tropical Biodiversity at the Puerto Rico Science Trust, San Juan, Puerto Rico, United States.

Widespread declines have positioned amphibians among the most threatened vertebrate groups worldwide, largely driven by habitat loss, climate change, and emerging infectious diseases. Despite this global vulnerability, the critically endangered Puerto Rican endemic frog Eleutherodactylus spp. demonstrates notable resistance to microbial infections. We hypothesized that its egg gelatin matrix harbors microbial communities capable of producing antimicrobial compounds that protect developing embryos. The objective of this study was to characterize these microbial populations and their secreted metabolites using integrated molecular and metabolomic techniques. Microbial diversity was assessed via 16S rRNA sequencing, and untargeted metabolomic profiling using high-resolution mass spectrometry enabled identification of key secondary metabolites. Several antimicrobial compounds were detected, including Prodigiosin, Violacein, and bioactive lipopeptides. Minimum Inhibitory Concentration (MIC) assays showed that egg gelatin extracts inhibited Staphylococcus aureus growth at 700 µg/mL, while Prodigiosin and Violacein inhibited Escherichia coli with MIC values of 94 µg/mL and 50 µg/mL, respectively. These findings highlight the role of host-associated microbiomes and chemical defenses in amphibian survival and suggest potential applications of these natural products as templates for novel antimicrobials. Future directions include functional validation, conservation-based bioprospecting, and exploring their potential use against multidrug-resistant pathogens.

Keywords: Eleutherodactylus spp., microbial interaction, untargeted metabolomics, lipopeptides, antimicrobial activity

Abstract: 20260228_034

Title: Concentrations of Fecal and Total Coliforms in Northern Puerto Rico Beaches

Authors: Alejandra Ortiz Forti, Samuel Perez Gross & Sandra Barroso Lorenzo

Institutions: Universidad Ana G. Méndez, Recinto de Carolina, P.R.

Monitoring bacterial indicators in recreational waters is essential for protecting public health and maintaining environmental quality. Fecal indicator bacteria such as coliforms and enterococci are commonly used to assess water quality because their presence suggests contamination from human or animal waste. Exposure to contaminated waters has been associated with gastrointestinal illness, ear and skin infections. This study evaluated bacterial growth in coastal waters of Puerto Rico, where seasonal rainfall and temperature changes may influence bacterial presence. From a microbiome perspective, these indicators provide insight into changes in coastal water quality over time. Coastal water samples were collected from a public recreational site during two sampling periods (September and December). Environmental parameters were recorded, including temperature and pH. Samples were diluted, then filtered through membrane filters, and placed on selective and differential media, including Eosin Methylene Blue agar (EMB) and Brilliant Green Agar (BGA). Plates were incubated for 48 hours at 37 °C. Bacterial growth was assessed by colony presence, colony-forming units (CFU), and pigmentation. Gram staining supported basic cellular characterization. Analysis included quantitative comparison of colony counts and qualitative comparison of growth patterns between sampling periods. Bacterial growth occurred in both sampling periods. In September (30 °C; pH 8.0), EMB plates showed colonies too numerous to count (TNTC). BGA counts averaged 157 CFU. In December (28.9 °C; pH 7.06), EMB showed TNTC growth, while BGA averaged 166 CFU. Corrected for dilution, values corresponded to approximately 1,540–1,660 CFU. Colonies displayed diverse morphology and pigmentation, indicating multiple bacterial groups. Differences in CFU counts and colony density suggest environmental and seasonal influences on bacterial prevalence. These findings demonstrate elevated bacterial levels in recreational coastal waters of Puerto Rico. Observed patterns suggest environmental and seasonal conditions may influence bacterial variability. Results highlight culture-based monitoring as a practical approach for tracking changes in environmental bacterial communities over time. This emphasizes the importance of monitoring bacterial indicators to provide baseline data, support public health protection, and improve understanding of microbial communities in Puerto Rico’s coastal waters.

Keywords: Microbiology | Environmental | Monitoring

Funding: UAGM, Recinto de Carolina: B02-049-24

Abstract: 20260228_036

Title: Colony PCR for validation of an Tn5 Transposon mutant library in Lactiplantibacillus plantarum

Author: Nicole M. Ruiz-Cardona, Karla M. Casillas Pagán, María V. Mendoza-Dasilva, Merliz Pérez Vázquez, Yadiel Benítez Colón, Imilce A. Rodriguez-Fernández

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Background: The gut microbiota plays a critical role in the gut-brain axis, but its balance shifts during aging, increasing inflammation and oxidative stress. *Lactiplantibacillus plantarum* (*Lp*), a gram-positive commensal bacterium, exhibits probiotic properties in mammals and flies. Previous studies show that *Lp* promotes cytoprotection by activating the transcription factor Nrf2/CncC in flies and mice. However, the mechanism and bacterial genes responsible for this activation remain unknown.

Method: *Lp* was isolated from *Drosophila* wild fly gut, transformed with a Tn5 transposon carrying kanamycin resistance gene (Kan2), and selected on MRS agar with 800µl/ml of Kan2. Colony PCR using Kan2 and 16S rRNA primers confirmed transposon insertion, with products visualized on agarose gels.

Results: Our results showed, more than 300 mutants were selected by growing the bacteria in agar media with 800µl/ml of Kan. Also, we were able to confirm that the transposon was inserted using colony PCR.

Conclusion: In conclusion, this work establishes the basis for generating an *Lp* mutant library using Tn5 transposon mutagenesis. Given its 3.3 Mb genome, approximately 3,300 mutants are needed to cover 0.1% of the total genome. Future work will sequence positive hits to identify insertion sites.

Funding: This project is supported by UPRRP Start-up funds, NIH-NIGMS COBRE (5P20GM103642 and 5P30GM149367), the Catalyzer Research Grant (2023-00056), Puerto Rico Science, Technology & Research Trust (PRST), and the NIH-RISE Grant 1T32GM152384-0. Thanks to W. Ludington (Carnegie Science) for proving the LpWF strain.

Abstract: 20260228_038

Title: Early Outcomes of a Student–Faculty Co-Created, Systems-Based Microbiome Curriculum Using UDL-Informed Microcapsules

Authors: Julián F. Bayron, BSc, MS[2], Ricardo J. Laboy, BSc, MS[2]; Sebastián A. Hernández, BSc, MS[2]; José G. Tormos BSc, MS[2]; Andrea Cortés BSc, MS[2], Martha García, MD, MSc

Institutions: San Juan Bautista School of Medicine, Caguas, PR.; Universidad Central del Caribe, Bayamón, PR; Florida State University, Fl, US.

Background- Microbiome science is reshaping understanding of inflammation, immune regulation, and chronic disease, yet many health professions curricula lack a coherent structure to integrate microbiota–immune principles across organ systems.

Methods- Student–faculty teams developed standardized Microcapsules (brief micro-lecture, infographic/concept map, guided inquiry, and synthesis activity) for flipped-classroom active learning. Universal Design for Learning (UDL) principles were embedded through multiple means of engagement, representation, and action/expression. A completed curriculum mapping process aligned capsule objectives with organ-system block outcomes and competency frameworks, including Lifestyle Medicine competencies and the 36 Nutrition Competencies for Medical Education. Design was also informed by proposed curricular elements for public health and medicine in microbiota (diet, antibiotics, breastfeeding as anchor topics). Implementation included an Introductory module plus integration within lymphohematopoietic/immune, cardiovascular, respiratory, and urinary systems.

Results- Forty-five learners participated across four sessions, completing 12 Microcapsules with a 100% participation rate. Faculty adoption included four faculty facilitators. Mean knowledge scores improved from 50.0% (pre) to 89.6% (post). Learner ratings were highly satisfactory across evaluated domains. Focus group themes emphasized significant learning gains, contemporary and engaging content, and improved ability to maintain focus and integrate concepts across systems, linking microbiota–immune mechanisms to clinical concepts.

Conclusion- A student–faculty co-created, competency-mapped, UDL-informed microbiome curriculum delivered via Microcapsules demonstrated strong feasibility, meaningful faculty adoption, substantial short-term knowledge gains, and high learner satisfaction. Following this pilot, the team is prepared to expand development and implementation across additional organ systems and to evaluate retention and transfer to clinical reasoning.

Keywords: Microbiome education; Systems-based curriculum; Medical education innovation

Abstract: 20260228_039

Title: Your Diet Dominates the Unknown World of the Gut and Predicts Inflammation and Immunologic Health

Author: Jose G. Tormos BSc, MS[2], Ricardo Laboy, BSc, MS[2]; Julián Bayron, BSc, MS[2]; Sebastián Hernández, BSc, MS[2]; Andrea Cortes BSc, MS[2], Martha García, MD, MSc

Institutions: San Juan Bautista School of Medicine, Caguas, PR.; Universidad Central del Caribe, PR; Florida State University, Fl, US.

Background: Diet strongly shapes gut microbiome composition and function, linking nutrition with immune regulation and chronic disease risk. The rise of cardiometabolic, inflammatory, and neurodegenerative diseases parallels the adoption of industrialized, low-fiber diets associated with reduced microbial diversity and increased inflammation. This integrative review examines how dietary patterns influence microbiome diversity, inflammatory balance, and disease risk across modern, ancestral, and migration contexts.

Methods: A qualitative systematic review was conducted following PRISMA guidelines. Literature from PubMed, ScienceDirect, and Google Scholar (2010–2024) was analyzed, focusing on human studies linking dietary patterns, gut microbiome diversity, inflammation, and chronic disease outcomes. Included studies examined ancestral populations, dietary interventions, and immigrant cohorts using validated microbiome sequencing methods. Key findings were synthesized thematically. Meta-analysis was not performed due to heterogeneity.

Results: Across contexts, dietary patterns consistently influenced gut microbiome structure and function. Plant-forward, high-fiber, and polyphenol-rich diets—including Mediterranean, MIND, NiMe, and traditional African diets—were associated with increased microbial richness and enrichment of SCFA-producing taxa such as Faecalibacterium prausnitzii, Roseburia, Akkermansia muciniphila, Prevotella, Bifidobacterium, and Lactobacillus. Ancestral populations exhibited high microbiome diversity, whereas Western diets were linked to microbial depletion and pro inflammatory signatures. Migration studies showed rapid loss of microbiome diversity following dietary acculturation. Beneficial diets were associated with lower inflammatory markers (CRP, TNF-α, IL-6, IL-17) and improved metabolic and immune profiles, while Western diets showed opposite trends.

Conclusions: Diet is a modifiable determinant of gut microbial resilience and inflammation. Traditional, plant forward dietary patterns support microbiome health and lower chronic disease risk. Integrating ancestral dietary principles into modern nutrition strategies may enhance precision nutrition. As a next step, this evidence synthesis is being used to inform educational initiatives in health professions training, aiming to integrate contemporary microbiome science, dietary patterns.

Keywords: Gut microbiome; dietary patterns; inflammation

Abstract: 20260228_040

Title: Seasonal Variation in Soil Microbiome Composition and Diversity in the Coastal Wetlands of Las Cabezas de San Juan, Puerto Rico

Author: Gabriela P. Román Vázquez, Amanda L. Martínez Santos, Genesis Maldonado Concepción, Gabriela D. García Reyes, Jesus D. Quiñones Llopiz, Clarivel Lasalde De La Cruz

Institutions: Department of Biology, University of Puerto Rico at Bayamón, Puerto Rico

Background. Coastal wetlands are among the most productive ecosystems globally, providing essential ecological services including water purification, flood mitigation, and carbon sequestration. Microbial communities play a central role in biogeochemical processes. However, seasonal variation in soil microbiomes within Caribbean coastal wetlands remains poorly characterized. This study examines changes in soil microbial composition and diversity in relation to precipitation patterns at Las Cabezas de San Juan Natural Reserve in Fajardo, Puerto Rico.

Methods. Soil samples were collected from Las Cabezas de San Juan coastal wetland during periods of low precipitation (March 2025) and high precipitation (September 2025). Environmental parameters, including pH, temperature, and moisture were measured. Total DNA was extracted from soil samples, and the bacterial 16S rRNA gene was amplified and sequenced using Taxonomic classification and diversity analyses were conducted using Epi2Me software.

Results. Alpha diversity indices showed higher microbial richness and Shannon diversity during the high precipitation period across all sampled soils. September samples exhibited 150–200 genera per sample compared to 80–120 genera per sample observed in March. The wet season was characterized by increased relative abundances of halophilic and methylotrophic genera, including Halobacillus, Paenibacillus, and Methyloceanibacter, suggesting enhanced functional diversity associated with nutrient cycling processes.

Conclusion. Seasonal precipitation strongly influences soil microbiome structure and diversity in coastal wetlands. Increased soil moisture during high rainfall was associated with increased microbial richness, which may enhance ecosystem resilience and biogeochemical processes. These findings underscore the importance of temporal monitoring of microbially driven ecosystems to assess and predict wetland ecological health.

Keywords: soil microbiome, coastal wetlands, precipitation

Abstract: 20260228_041

Title: Hexanoate Reduces Oncogenic Phenotypes in Triple-Negative Breast Cancer and Oral Squamous Cell Carcinoma

Author: Nahara Yupe-Muñiz[1], Oscar A. Loperena-González[1], Ariana S. García-López[1,2], Samira B.F. Abdullah Vargas[1,2], Gabriel Borges-Vélez[1], and Josué Pérez-Santiago[1,3]

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Background: Microbiota-derived metabolites have been associated with cancer development and advancement. However, the molecular mechanisms in which microbial metabolites impact different cancer types remain largely undefined. Particularly, medium-chain fatty acids (MCFA) are microbially derived metabolites whose altered levels have shown to mechanistically contribute to cancer progression. Among these, hexanoate represents an understudied MCFA whose effect on oncogenic processes warrants further investigation. For this reason, we evaluated the impact of hexanoate on cell viability and proliferation, two key oncogenic phenotypes using in vitro models of triple-negative breast cancer (TNBC) and oral squamous cell carcinoma (OSCC): MDA MB-231 and OECM-1, respectively.

Methods: MDA-MB-231 and OECM-1 cells were cultured at 37˚C, 5% CO2 in RPMI-media with 10% fetal bovine serum. Cell viability was measured using AlamarBlue assay, and hexanoate treatment was given in serial dilutions (1:2) starting at 800 mM for 24, 48, and 72 hours (h). The half-minimal inhibitory values (IC50) were assessed via fluorescence (590nm). Cell proliferation was evaluated by seeding 150,000 cells per well in 6-well plate and treating cells with 5 mM hexanoate. Cells were quantified at 24h, 48h, and 72h post-treatment using a TC20 automated cell counter.

Results: Hexanoate decreased cell viability in both TNBC and OSCC models across all time points tested. TNBC cells had a consistent IC50 of 29mM through all-time points, while OSCC cells displayed a time-dependent reduction in IC50 values (IC50 = 80 - 50 mM). Furthermore, hexanoate significantly decreased cell proliferation at 72h in TNBC ($p = 0.004$) and OSCC ($p = 0.004$) compared to the control. Conclusions: Our results show that hexanoate can reduce cell viability and proliferation in TNBC and OSCC in vitro models, suggesting a potential role in modulating oncogenic phenotypes. The reduction of oncogenic behavior in both cell lines provides support for hexanoate as a potential therapeutic candidate for aggressive cancer types. Further studies will evaluate the mechanisms through which hexanoate may regulate cancer development and advancement.

Keywords: Medium-chain fatty acids, Oncogenic phenotypes, In vitro models

Funding: This project was funded by the National Institute of Allergy and Infectious Diseases (NIAID) Grant #5R25AI183304-02, National Human Genome Research Institute: 1R25HG012702-01 and diversity supplement, National Cancer Institute: R21 CA264606, the National Institute on Minority Health and Health Disparities: RCMI Program U54 MD007600, and the Federal Department of Education's Developing Hispanic-Serving Institutions Program – Title V (PO31S200104).

Abstract: 20260228_042

Title: Salinity-driven shifts in soil microbiota associated with *Annona glabra* in the Punta Tuna Wetland, Puerto Rico

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Background. Climate change-related flooding and saltwater intrusion are posing a growing threat to Puerto Rico's coastal wetlands, potentially changing the composition of the soil microbiota. At the Punta Tuna Wetland Nature Reserve, limited natural recruitment of *Annona glabra*—a native wetland tree species tolerant to flooding and salinity—has been observed in certain areas, suggesting that shifts in soil microbial communities may be influencing seedling establishment and survival. This study examines the effects of salinity on bacterial and fungal communities in soils associated with *A. glabra*.

Methods. Soil samples and *A. glabra* seedlings were collected from Punta Tuna Wetland Nature Reserve. Seedlings were transplanted into Punta Tuna soils at the UPR-Bayamón Greenhouse and exposed to salinity treatments of 15%, 20%, 25% and 30% NaCl for six weeks. Following salinity exposure, total DNA was extracted from soil samples, and the bacterial 16S rRNA gene and fungal ITS region was amplified and sequenced. Sequence data was processed and taxonomically assigned using Geneious Prime software. Relative abundance and diversity analyses were conducted in RStudio, and comparative analyses were performed between controlled salinity treatments and natural field conditions.

Results. Soil samples exposed to salinity treatments show an increase in microbial diversity with increasing salinity. Bacterial communities in high-salinity treatments were characterized by the presence of archaeal and bacterial taxa adapted to anaerobic and saline environments. Higher salinity was associated with increased relative abundances of families such as Hyphomicrobium and Methanobacteriaceae. Fungal community composition was also influenced by salinity, including Pleosporales, Saitozyma, and Trichocomaceae becoming more prevalent under higher saline conditions.

Conclusion. This study demonstrates that the composition and diversity of soil microbiota in the Punta Tuna wetland are significantly influenced by salinity. Salinity-induced shifts in microbial communities may have important implications for the recruitment and survival of *A. glabra*, as well as for overall ecosystem functioning. Improved understanding of microbiome–environment interactions is fundamental to advancing research on wetland resilience and to support the development of effective conservation strategies aimed at safeguarding coastal vegetation under ongoing and projected climate change scenarios.

Keywords: Salinity, Soil microbiome, *Annona glabra*

Abstract: 20260228_044

Title: Exploring the mechanisms around vanishing meadows: adaptation and resilience of seagrasses, microbial communities, and biodiversity shifts

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Seagrass are marine flowering plants that share key biological traits with terrestrial plants, including their resilience to complex microbial associations. Like land plants, increasing evidence suggests that seagrasses host diverse microbiomes that play essential roles in seagrasses resilience by mediating nutrient cycling, stress tolerance and plant health under environmental change. However, microbiomes associated with seagrasses remain largely unexplored. In the Caribbean, the native sea turtle seagrass, Thalassia testudinum, has been displaced by the invasive species, Halophila stipulacea, which can dominate up to 80% of invaded meadows. This shift highlights a key knowledge gap of whether microbiomes associated with native T. testudinum contribute to resistance against invasion and help maintain ecosystem resilience. Differences in microbial communities between T. testudinum and H. stipulacea suggest that microbial composition, rather than diversity alone, may influence host resilience and competitive outcomes. Therefore, how does T. testudinum's microbiome shift when exposed to different species? To address this question, we conducted a unidirectional competition transplant with four treatments: the control- T. testudinum in monoculture, T. testudinum within mixed seagrasses, T. testudinum surrounded by H. stipulacea, and bare sediment/no seagrass. Roots and sediment samples were collected and sequenced using Illumina MiSeq 16s rRNA (V3- V4). We hypothesized that T. testudinum in monoculture will exhibit a more stable and diverse microbiome with conserved mutualisms. While, in mixed habitats are expected to exhibit an intermediate, transitional microbiome state and proximity to invasive species will present an alteration to the composition, reducing its diversity and causing the displacement of many mutualistic bacteria. Understanding these microbiome shifts will improve our knowledge of how native seagrass respond to invasion, informing strategies to preserve marine ecosystem resilience and essential coastal services in a changing environment.

Keywords: seagrasses, resilience, microbiome

Funding: This study was funded by the Puerto Rico Catalyzer Research Grant-CRG-2024-UPRRP

Abstract: 20260228_045

Title: Mapping Transposon Insertions and Screening Lactiplantibacillus plantarum mutants for Nrf2/CncC Activation

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Background: Lactiplantibacillus plantarum (Lp) is a gram-positive probiotic and commensal bacterium that resides in the guts of mammals and flies. Lp promotes cytoprotection by activating the transcription factor Nrf2/CncC, but bacterial genes responsible for the mechanisms remain unknown. For this, Lp mutants were generated using EZ-Tn5 transposon mutagenesis and over 300 were confirmed by Colony PCR. The goal of this project is to develop a fast and affordable method to map EZ-Tn5 insertion sites in Lp genome and to screen Lp mutants that activate Nrf2/CncC using an in vitro assay.
Methods: Touchdown and inverse PCR were used to identify EZ-Tn5 insertion sites. Amplicons are visualized in 1% agarose gel and unique bands are extracted and sent for Sanger sequencing. For the screening, in vitro Dual-Luciferase assay in Drosophila S2 cells to detect Nrf2/CncC activation. Both ARE and mutant ARE constructs (negative control) will be cloned into pNL1.1 using Gibson Assembly, while Actin (Ac5) in pGL4.10 (internal reference). Reporter constructs will be co-transfected into S2 cells and measure luciferase activity.

Results: Preliminary data suggest that Touchdown PCR and iPCR can amplify mutant-specific products and PCR products were able to send to sequence. For the screening assay, we extracted and purified gDNA from transgenic Drosophila, amplified ARE/mRE sequences.

Conclusion: Understanding the genetic basis Lp-mediated Nrf2/CncC activation will provide mechanistic insights into the antioxidant properties of this probiotic and a potential therapeutic for oxidative stress-related diseases and inflammation. The next steps involve cloning these sequences into vectors and optimizing the screening assay.

Keywords: Lactiplantibacillus plantarum, transposon mutagenesis, Nrf2/CncC activation

Funding: This project is supported by UPRRP Start-up funds, NIH-NIGMS COBRE (5P20GM103642 and 5P30GM149367), the Catalyzer Research Grant (#2023-00056), Puerto Rico Science, Technology & Research Trust (PRST), and the NIH-RISE Grant 1T32GM152384 0. Thanks to W. Ludington (Carnegie Science) for proving the LpWF strain.

Abstract: 20260228_047

Title: Role of antibiotic-induced gut microbiota dysbiosis on avoidance and anxiety- related behaviors in female vs. male rats

Author: Gabriela Morales Rivera1, Hector Haddock1; Natasha Jimenez Rivera Laura Mendez1; Demetrio Sierra-Mercado1; Osmarie Martínez-Guzmán1.

Institutions: University of Puerto Rico (UPR) Medical Sciences Campus.

Background: Antibiotics are essential for treating infectious diseases but can disrupt the gut microbiota, leading to behavioral and neurological alterations. The gut–brain axis mediates communication between the gut microbiota and the central nervous system, influencing emotional regulation and behavior. Broad-spectrum antibiotics can alter gut microbial communities, potentially affecting anxiety- and fear-related behaviors. According to the 2020 National Survey on Drug Use and Health (NSDUH), many Hispanic/Latino adults report mental health conditions, highlighting the need to identify biological and environmental contributors to vulnerability in underserved populations. While microbiota dysbiosis has been linked to changes in fear learning and extinction, its role in active avoidance behaviors and sex-dependent vulnerability remains unclear. This study also proposes to examine correlations between reductions in Lactobacillus, Bifidobacterium, Ruminococcaceae, and Lachnospiraceae and altered behaviors following antibiotic exposure, expanding microbiota-brain-behavior research to include avoidance-related behaviors.

Methods: This study uses a rat model to examine how antibiotic-induced dysbiosis of the gut microbiota influences avoidance and anxiety-related behaviors in a sex-dependent manner. Male and female rats are exposed to a broad-spectrum antibiotic cocktail administered orally for 21 days. Behavioral outcomes are assessed using platform-mediated active avoidance, open field, and elevated plus maze. Neural activation in brain regions implicated in avoidance and anxiety, including the basolateral amygdala and nucleus accumbens, is evaluated following avoidance extinction. Gut microbiota composition will be characterized using 16S rRNA gene sequencing and microbial changes will be examined in relation to behavioral and neural outcomes.

Results: Preliminary findings indicate that antibiotic exposure produces sex-dependent behavioral effects. Female antibiotic-exposed rats showed increased platform time ($p = 0.0402$), reduced open-field center time ($p = 0.0190$), and higher elevated-plus-maze anxiety ($p = 0.0266$).This pattern reflects increased avoidance and anxiety-like behaviors, along with enhanced neuronal activation in limbic regions associated with threat processing and motivational relevance. In contrast, male rats display minimal behavioral and neural changes following antibiotic exposure. These observations suggest that disruption of the gut microbiota may differentially influence avoidance-related responses by sex.

Conclusion: Together, these findings highlight sex-dependent effects of antibiotic-induced gut microbiota dysbiosis on avoidance- and anxiety-related behaviors, particularly in females. This pattern underscores the importance of considering biological sex when evaluating the neurobehavioral consequences of microbiota dysbiosis and its potential contribution to anxiety related disorders, with potential implications for understanding how antibiotic exposure impacts mental health.

Keywords: gut microbiota, avoidance on rats, sex-dependent.

Funding: RCMI Grant U54 MD007600 NIMHD-NIH

Abstract: 20260228_049

Title: Immune Responses in Hispanic Women with Cervical Disease Progression following Antibiotic Treatment.

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Background: Human papillomavirus (HPV) is a highly prevalent infection; yet, only approximately 10% of infected individuals develop persistent HPV cervical lesions, including dysplasia or cancer. In the United States, Hispanic women experience a 45% higher incidence of HPV-associated cervical cancer and a 15% higher mortality rate compared to other racial groups. Differences in microbiome diversity associated with antibiotic use may contribute to these disparities and poorer responses to cancer treatment. Recent studies suggest that alterations in the vaginal microbiome are related to HPV progression and cervical carcinogenesis. Although the effects of antibiotics on the gut microbiome are well understood, the impact of systemic antibiotic use on immune responses and the cervicovaginal microenvironment remains elusive. Our objective is to characterize systemic and cervicovaginal immune responses in Hispanic women with recent antibiotic exposure.

Methods: The study recruits patients from San Juan, Puerto Rico, to collect cervical cytobrush and blood samples. Participants included healthy individuals with no cervical lesions and those with HPV-related dysplasia. Samples were processed to isolate immune cells and phenotyped by flow cytometry to quantify innate immune cells, B cells, and T cell subsets. Immune subset frequencies were compared and stratified according to cervical disease stage and antibiotic use within the last 90 days (recent) or more than 90 days (not recent).

Results: Among 61 participants, 20% reported using antibiotics within 90 days of sampling. The most commonly reported antibiotics were Penicillin-class agents and fluoroquinolones such as Ciprofloxacin. The analysis detected an increased frequency of cytotoxic granzyme B-expressing Natural Killer T (NKT) cells in the blood and cervix from individuals without dysplasia who received recent antibiotic treatment before sampling. This group also exhibited an increased frequency of CD8+ T cells expressing the exhaustion marker Programmed death-1 (PD-1).

Conclusions: Our preliminary results suggest that antibiotic use impacts innate and adaptive immune responses, potentially through the release of microbial antigens, especially in individuals who do not have an ongoing HPV infection. The association of these immune phenotypes with the cervicovaginal microbiome will help us identify the impact of antibiotics on immune and vaginal microbial populations.

Keywords: HPV cervical disease, Antibiotics, and Immune phenotypes

Funding: This study was partially funded by the Institutional National Institute of General Medical Sciences of the National Institutes of Health (NIGMS-NIH) COBRE Puerto Rico Center for Microbiome Sciences 1P20GM156713-01. This study was also partially supported by the National Cancer Institute (U54CA96300) and the National Institute on Minority Health and Health Disparities (R25MD007607).

Abstract: 20260228_052

Title: Global public health impact of CDC- developed molecular tests for the diagnosis and surveillance of arboviral infections

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Institutions: Centers for Disease Control and Prevention (CDC), San Juan, Puerto Rico

Background: Dengue virus (DENV), Chikungunya virus (CHIKV), and Zika virus (ZIKV) are mosquito-borne arboviruses of major global public health importance, causing an estimated 450 million infections annually across more than 140 countries. Public health events such as the CHIKV epidemic in 2014, the ZIKV epidemic in 2016, and the DENV epidemic in 2024 have contributed to the recent surge in travel associated and locally acquired arboviral infections in the United States and globally. Events like these highlight the need for standardized, sensitive, and scalable molecular diagnostics to support clinical management and inform effective public health response.

Methods: The Centers for Disease Control and Prevention (CDC), Dengue Branch located in Puerto Rico developed two Real-Time RT-PCR tests: the DENV-1–4 Real-Time RT-PCR Assay, for detection and differentiation of the four DENV serotypes, and the Trioplex Real-Time RT-PCR Assay, for the simultaneous detection of DENV, CHIKV, and ZIKV. Both assays apply primers and dual-labeled hydrolysis (TaqMan®) probes specifically designed for detection of viruses in contemporary circulation and epidemiological relevance. Test validation included evaluating multiplexing formats, multiple clinical specimen types obtained during the acute phase of infection, internal controls, use of automation for high-throughput testing, and compatibility with legacy and modern Real-Time PCR instruments. Final assay development was completed in Puerto Rico, whereas reagent kits are manufactured and distributed by CDC in Atlanta. Both test kits are currently approved by the US Food and Drug Administration (FDA) for in vitro diagnostic use.

Results: From 2022 to 2025, the CDC distributed 783 DENV-1–4 assay kits, accounting for more than 156,000 dengue tests, supporting public health laboratories in 64 countries including 33 in the US. Similarly, 566 Trioplex kits, accounting for 283,000 tests, were distributed from 2020 to 2025 to 73 countries supporting more than 128 public health laboratories, including 55 in the US.

Conclusion: The development and distribution of these molecular assay kits, in addition to the scientific expertise and technical support provided by the Dengue Branch Laboratory have strengthened public health laboratory capacity and improved arboviral surveillance globally.

Keywords: dengue, chikungunya, Zika, PCR, surveillance, Trioplex

Funding: Centers for Disease Control and Prevention

Abstract: 20260228_058

Title: Bioprospecting of Coastal Fungi for the Degradation of Synthetic Dyes

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Background & Objectives: Synthetic dyes are used in a wide variety of textiles, posing a threat to fragile ecosystems like mangroves. Their resistance to degradation warrants sustainable biotechnological solutions. Fungi, due to their enzymatic versatility and adaptability, are promising candidates for bioremediation. This study explores the bioprospecting of fungi isolated from sediments, wood, leaves, and plastics during a mangrove survey in Cabo Rojo, Puerto Rico.

Methods: Sixty-four strains were isolated, and 22 filamentous fungi were selected for characterization. The strains were cultured in basal liquid medium with 10 mg of Congo Red as the sole carbon source at 28 °C and 120 rpm for 10 days to assess the potential degradation of this dye.

Results: Genera such as Aspergillus, Trichoderma, Cystobasidium, and Penicillium were identified. Several strains decolorized Congo Red from the fourth day on, indicating early enzymatic activity. Aspergillus luchuensis [P05] reached 60.8 mg of biomass, followed by Aspergillus sp. [H02A] and Trichoderma sp. [H1] with 54.4 mg and 54.2 mg, respectively. The most efficient strains came from plastic and leaf litter, suggesting adaptation to recalcitrant substrates.

Conclusions: Mangrove fungi show high efficiency in the absorbance and transformation of industrial effluents. Their environmental origin predicts their degradative performance and provides evidence of ecological adaptation. Acknowledgments: This work was supported by NASA, the Symbiosis Laboratory and the Department of Biology at UPR-Mayagüez, as well as the DRNA Cabo Rojo Reserve and the undergraduate students who collaborated on the project.

Keywords: Bioprospecting, Synthetic dyes, Bioremediation

Abstract: 20260228_061

Title: Mangrove fungi: Agents for Petrochemical Degradation

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Institutions: Background & Objectives: Petroleum-derived pollutants, such as used motor oil and single-use plastics, pose a persistent threat to fragile coastal ecosystems, particularly mangroves. Their resistance to environmental degradation necessitates warrants the development of sustainable biotechnological strategies. Filamentous fungi, due to their metabolic versatility, oxidative enzymatic capacity, and adaptation to recalcitrant substrates, represent promising candidates for bioremediation processes. This study aimed to characterize fungal strains isolated from mangroves in Cabo Rojo, Puerto Rico, evaluating their potential for the transformation of petrochemical pollutants. Methods: Strains H1 and P5 were cultured in basal liquid medium supplemented with 10 mg of Congo Red as the sole carbon source and incubated at 28 °C and 120 rpm for 10 days as proxy to assess their capacity to degrade aromatic compounds. Subsequently, biodegradation assays were performed using used motor oil and LDPE for periods of 21 and 30 days. Degradative activity was evaluated by biomass production and spectroscopic analysis. Molecular identification of strains was performed by sequencing the ITS region. Results: Two effective strains were identified as Trichoderma sp. (H1) and Aspergillus luchuensis (P5). In motor oil degradation tests, A. luchuensis P5 achieved a biomass production of 60.8 mg, while Trichoderma sp. H1 reached 54.4 mg. These strains were isolated from plastic waste and leaf litter, suggesting an ecological adaptation to highly recalcitrant substrates. Spectroscopic analysis revealed chemical modifications in hydrocarbons and polymers, evidenced by characteristic signals near 1374 cm^{-1}. Conclusions: Fungi isolated from mangrove ecosystems exhibit high efficiency in the transformation of petrochemical pollutants and synthetic polymers. The environmental origin of the strains correlates with their functional degradative performance, providing evidence of adaptation to persistent pollutants. Spectroscopic results support their potential as sustainable tools for bioremediation strategies in tropical environments. Acknowledgments: This work was partially funded by NASA, NOAA and supported by the Symbiosis Laboratory and the Department of Biology at the University of Puerto Rico at Mayagüez, as well as the Cabo Rojo Reserve of the Department of Natural and Environmental Resources and the undergraduate students who collaborated on the project.

Keywords: Biodegradation, Fungi, Mangroves

Abstract: 20260228_065

Title: Antimicrobial Screening of Fire Ant–Associated Actinobacteria

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Actinobacteria are Gram-positive bacteria known for producing a wide range of secondary metabolites with antimicrobial and antifungal properties which are crucial for pharmaceutical and biotechnological applications. Symbiotic Actinobacteria associated with invertebrates have recently gained attention due to their role in host defense against pathogens. We hypothesized that Actinobacteria isolated from fire ants (Solenopsis invicta) would exhibit antimicrobial activity against selected microorganisms, as these insects are continuously exposed to pathogenic microorganisms in their environment. To achieve this, ten bacterial isolates were obtained from S. invicta ants collected along the coastal area in Cabo Rojo, Puerto Rico. Actinobacteria were isolated from whole fire ant workers and plated in ISP2 medium under enrichment conditions to favor the selective growth of Actinobacteria. These isolates would be tested in confrontation assays against the opportunistic fungus Penicillium chrysogenum, known to cause respiratory allergies in humans and other infections. Inhibition zones measurement will be performed using ImageJ once the confrontation assays are completed to verify and compare the antimicrobial strength between the isolates. Confrontation assays are still in progress. Preliminary screening indicates several isolates with potential antimicrobial activity. Quantitative data will be added once available. These findings may guide the selection of strains for molecular analyses aiming at the detecting genes associated with antimicrobial production. Overall, the results attempts to highlight S. invicta as a valuable source for isolating Actinobacteria with high potential for future biomedical applications. Research is conducted at the Symbiosis Laboratory, University of Puerto Rico at Mayagüez. Partially funded by Department of Biology, NASA and PR Sea Grant.

Keywords: actinobacteria, symbiosis, fungi

Abstract: 20260228_067

Title: Evaluating different methods to identify changes in the gut microbiota – lessons from alcohol-exposed *Drosophila melanogaster*

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The microbiome, a complex community of microorganisms including bacteria, fungi, viruses, archaea, and eukaryotes, plays key roles in maintaining homeostasis, stimulating the immune system, and providing defense against pathogens. However, age, diet, infections, antibiotics, and alcohol consumption can disrupt the gut microbiota, leading to dysplasia. Understanding how these factors, particularly alcohol exposure, affect the microbiome is crucial for comprehending such disruptions. This study evaluated three methods—Colony Forming Units (CFUs), Nanopore sequencing, and Biolog® Ecoplates—to identify the most informative approach for assessing gut microbiome changes of *Drosophila melanogaster* following ethanol exposure. Wild-type (Canton-S) young flies (7 days old) were exposed to water (control) or 50% ethanol vapor. CFUs quantified *Lactobacilli*, *Acetobacter*, and *Enterobacter* spp.,while Biolog® EcoPlates, which test bacteria utilization of 31 carbon sources, were used on whole *Drosophila* flies. Nanopore sequencing involved the DNA extraction of the intestines and whole 16s rRNA gene (~1500 bp) amplification via PCR. Ethanol exposure significantly increased CFUs of *Lactobacilli*, *Acetobacter*, and *Enterobacteria* in fly intestines, findings corroborated by Nanopore sequencing, showing alcohol-induced changes in bacterial populations and detecting age- and treatment-specific variations in bacterial species. In contrast, Biolog® EcoPlates failed to detect significant bacterial changes in the whole *Drosophila* compared to a positive control. CFUs and Nanopore sequencing were the most informative methods for detecting and assessing alcohol-induced changes in the *Drosophila* gut microbiome. Both methods confirmed an increase in *Acetobacter* species in the alcohol-exposed gut. Importantly, 16s sequencing allowed us to demonstrate changes in bacterial abundance and diversity. Alpha diversity analysis revealed shifts in species richness in response to ethanol exposure, while beta diversity highlighted differences in microbial community structures between ethanol-exposed and control flies in an age-dependent manner. Future experiments will characterize the specific bacterial species affected by alcohol exposure and age-related changes, providing insights into the microbiome's response to ethanol.

Abstract: 20260228_069

Title: How does darkness affect morphology and microbiota diversity in populations of the Mexican tetra?

Author: Sofia Cuevas- Rivera[1,3], Carlos Gonzales- Gerena[4,3], Fabiola D. Pagan- Torres[2,3,4,] Roberto E. Rodríguez- Morales[2,4,3],

Institutions: University of Puerto Rico, Bayamon Campus[1] , Department of Anatomy and Neurobiology, University of Puerto Rico, Medical Sciences Campus[2] , Molecular Research Center[3] , University of Puerto Rico, Rio Piedras Campus[4]

Background: Recent evidence has established the bidirectional relationship that exists between the gut microbiome and the central nervous system, also known as the microbiota gut–brain axis. Astyanax mexicanus has two distinct morphotypes: the river-dwelling surface fish ancestor and various blind cavefish populations that have evolved in darkness. Our goal is to explore how darkness influences the gut-brain axis. Our first approach will be characterizing morphological differences between dark-reared populations. Here, we set out to examine the phenotypic changes darkness can create in an organism before exploring its microbiome.

Methods: We used a total of 20 dwelling surface fish raised in complete darkness for eight and ten months. We measured standard body length from the snout to the caudal peduncle using images taken with a dissecting microscope. Eye axial length was measured from the anterior cornea to the retinal pigment epithelium using lateral images and analyzed in Fiji. Results: Our preliminary findings suggest that fish raised for a longer time in complete darkness have a longer eye axis and are growing slower.

Conclusion: These morphological differences may suggest changes in the brain-gut axis, as the gut produces important biomolecules that may be protective against neurodegenerative diseases. More work is needed to understand how the environment shapes animal physiology and how that modulates its microbiome.

Keywords: Dark-reared, gut-brain axis, neurodegenerative diseases

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Abstract: 20260228_078

Title: Impact of Smoking and Alcohol Use on Oral Microbial Communities Across Diverse Populations

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Background: Various exogenous and endogenous factors – including smoking and alcohol consumption – can alter the oral microbiome. Although oral dysbiosis has been linked to a variety of diseases, the extent to which lifestyle practices shape bacterial communities across different populations remains vaguely understood. Hence, a matched meta-analysis approach was conducted to evaluate data across multiple studies and identify microbial patterns associated with these lifestyle factors.

Methods: Publicly available bacterial amplicon sequences from oral samples were identified across four studies and integrated using a meta-analysis approach on QIITA (PMID:38390467, PMID:35585074, PMID:32034250, and EBI:ERP185631). The dataset included 723 patients, with representation from both females (n=497) and males (n=225). Trimming of sequences was performed at 150 base pairs and followed a deblur pipeline. Associated variables, including body mass index (BMI), smoking status, and alcohol consumption, were filtered and merged across datasets, with samples matched based on an age range of 21–49 years old. Microbial assessment will be conducted downstream using the Greengenes2 extended reference database on QIIME2 and R.

Results: Regardless of sex, most samples fell within the 21–30 age group (43.29%). BMI categories across the cohort included underweight (3.32%), normal weight (44.12%), overweight (21.30%), and obese (26.83%). Among non-smokers, 69.44% were females, whereas only 30.39% were men. On a similar note, among non-alcohol consumers, 69.60% were females and 20.00% were male. When combining both smoking and alcohol consumption variables, 91 participants (12.58%) were positive for both practices. Across the studied lifestyle practices, alcohol consumption was the most prevalent (51.87%).

Conclusion: Future directions for this project include assessing the impact between alcohol consumption and smoking with oral microbial dysbiosis. We aim to identify shifts in key oral taxa linked to these lifestyle practices in addition to elucidating distinct mechanisms of microbiome disruption.

Keywords: lifestyle practices, oral microbiome, BMI

Abstract: 20260228_086

Title: Effect of Glyphosate Salts on the Viability and Growth of Bacteria Representative of the Intestinal Microbiota

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Glyphosate is one of the most widely applied herbicides worldwide, and growing evidence raises concerns regarding its potential effects on human health through alterations of the gut microbiota. Understanding how intestinal microorganisms respond to glyphosate exposure is essential for evaluating potential risks and bacterial adaptation mechanisms. This study assesses the effects of glyphosate salts at different concentrations on representative microbial species of the intestinal environment. Saccharomyces cerevisiae, Streptococcus spp., Enterococcus faecalis, Escherichia coli, and Lactococcus lactis were cultured under standard laboratory conditions and exposed to glyphosate salts at concentrations ranging from 100 to 600 µg. Experiments were performed in triplicate, and bacterial growth and viability were evaluated by monitoring colony development and culture turbidity over time. Preliminary results indicate that all tested species were able to grow in the presence of glyphosate salts across the evaluated concentrations, with no marked growth inhibition observed. However, minor differences in growth patterns among species suggest variable sensitivity to glyphosate exposure. These findings suggest that selected microorganisms representative of the gut microbiota can tolerate glyphosate salts at the tested concentrations, indicating the possible presence of tolerance or adaptation mechanisms. Further studies are needed to characterize the molecular basis of this tolerance, evaluate long-term effects, and determine broader implications for intestinal microbial balance and host health.

Keywords: Gut microbiota; Glyphosate; Bacterial tolerance

Funding: This work was supported by a TriBeta Undergraduate Research Grant and institutional research funds.

Abstract: 20260228_088

Title: Dissecting Biofilm-Associated Genes in Lactiplantibacillus plantarum and Their Potential Role in Host Nrf2/CncC Activation

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The gut microbiota plays essential roles in host nutrition, immunity, and epithelial homeostasis, and its successful colonization often depends on the ability of bacteria to form biofilms. Biofilms are structured communities stabilized by extracellular polysaccharides (EPS) that promote adherence and persistence within the gut environment. Biofilm formation is, therefore, a key mechanism by which commensal microbes establish long-term associations with their hosts. In the host, the probiotic and commensal bacterium Lactiplantibacillus plantarum (Lp) can activate the conserved Nrf2/CncC transcription factor pathway, thereby enhancing the cellular antioxidant response. However, it remains unknown which genes in Lp are responsible for activating Nrf2/CncC in the host. We hypothesized that the capacity of Lp to form biofilms could be part of the mechanism used to activate Nrf2/CncC. To investigate this, we generated a collection of 300 Lp mutants using EZ-Tn5 transposon–mediated mutagenesis. The EZ-Tn5 transposon carries the Kan-2 gene, which confers kanamycin resistance and integrates randomly into the genome. Our goal is to evaluate the phenotypic characteristics of biofilm formation and growth in these L. plantarum mutants. Biofilm formation was quantified using the crystal violet microtiter-plate assay. Briefly, Lp mutants (n = 32) were inoculated into 96-well plates with MRS medium and 800 µg/ml kanamycin. Biofilms were fixed with 99% methanol, stained with crystal violet for 30 minutes, and destained with 33% glacial acetic acid. Absorbance was measured at 24 and 48 hours. Biofilm formation was classified as weak, moderate, or strong. To determine how each mutation affected growth dynamics under selective and non-selective conditions, growth curves were generated by inoculating strains into fresh MRS medium with and without kanamycin and measuring OD600 over 24 hours.

Preliminary data (n = 32) show that at 24 hours, 14% of mutants exhibited weak biofilm formation, 17% moderate, and 68% strong; at 48 hours, 5% were weak, 17% moderate, and 74% strong. Growth curves revealed a decrease in growth rate in mutants compared to the control. In future work, we will select mutants with weak and strong biofilm phenotypes to test their ability to activate Nrf2/CncC in larvae carrying an Nrf2/CncC genetic reporter. Identifying Lp genes involved in biofilm formation will help elucidate microbial factors that shape host–microbe interactions and contribute to beneficial host responses.

Abstract: 20260228_090

Title: Impact of the Humacao Landfill on the Microbiological Air Quality of Bordering Communities: Focus on Fungal Spores

Author: Leira G. Torres Rivera[1] and Denny Fernández del Viso[1]

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Background: Landfills contain organic waste that facilitates the proliferation of fungi, many of which threaten public health and the environment because of their allergenic and pathogenic potential. The Humacao municipal landfill is surrounded by several communities, whose microbiological air quality is potentially affected by their location with respect to the landfill. The objective of this research is to characterize the airborne fungal microbiome of a residential area near the Humacao landfill to evaluate the possibility of air quality deterioration and associated health risks.

Methods: An Allergenco MK3 volumetric air sampler was used to collect air samples in two areas in Humacao, Puerto Rico: one windward-exposed to the landfill and another not exposed to the landfill. Fungal spores observed in air samples are being identified and quantified through light microscopy and image analysis of microphotographies.

Results: Preliminary results indicate that the microbiome in the exposed area exhibits lesser evenness and greater species dominance compared to the non-exposed area. Some of the fungal genera of allergenic/pathogenic relevance that were identified at both study areas are Aspergillus/Penicillium, Fusarium, Curvularia, Cladosporium, and Alternaria. Ongoing analyses aim to compare the allergenic and/or pathogenic potential of the microbiome in both areas.

Conclusion: Preliminary findings suggest that the microbiome of the windward-exposed area may be influenced by fungal spores produced by the Humacao landfill. Future directions include completing the identification of fungal taxa observed, the characterization of each taxon's allergenic and pathogenic potential, and reperforming statistical analyses. This study brings attention to the importance of monitoring the air microbiome near landfills to assess possible air quality deterioration and public health risks.

Keywords: airborne, fungal

Funding: Analítica Fundación, INC

Public Health

Abstract: 20260228_043

Title: Use of Antibiotics in a Cohort of Women Living in Puerto Rico

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Background: Antibiotic resistance has become a significant global health concern as it limits treatment options and increases patient complication risk. Thus, we aimed to describe antibiotic use practices amongst a cohort of women in Puerto Rico (PR).

Methods: This was a secondary data analysis from a cross-sectional, population-based, study of human papillomavirus infection in women. Descriptive statistics were employed to summarize findings.

Results: A total of 1127 cases were exported from the dataset. The sample had a mean age of 39 years (range 21-70), with a higher concentration of participants at 27 years old (4.2%). Most participants (90.4%) reported having used antibiotics at some point in their lives. Many participants (42.6%) were still undergoing treatment at the time of the survey. While 79.2% of participants reported using antibiotics with a physician's prescription, 20.8% reported non-prescribed antibiotic use. Throat infection (3.5%), unspecified upper respiratory infection (1.3%) and COVID-19 (1.1%) were the most prevalent indications for antibiotic use reported in this sample. Regarding probiotics, 62.1% of participants did not consume any type of natural probiotic or supplement in the last three months.

Conclusion: These results emphasize the need for targeted educational interventions and stricter antimicrobial stewardship e`orts in PR to mitigate the global threat of antimicrobial resistance and promote microbiome health.

Keywords: Antibiotics, Women's Health, Antimicrobial Resistance

Abstract: 20260228_051

Title: Strengthening entomo-virological surveillance of arboviruses with scalable molecular systems

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Institution: Centers for Disease Control and Prevention (CDC), San Juan, Puerto Rico

Background: Over the past decades, the Americas have experienced a substantial increase in dengue virus (DENV) transmission, including approximately 13 million cases reported to the Pan American Health Organization in 2024. Puerto Rico was also notably affected, experiencing a dengue epidemic with 6,291 confirmed cases, predominantly caused by serotype 3 (DENV-3). Because most dengue infections are asymptomatic or mild, the true burden of disease is usually underreported, underscoring the limitations of traditional dengue surveillance systems. Entomo-virological surveillance could complement case surveillance systems using molecular methods for viral detection in mosquito collections. This study reports the development and validation of a workflow for molecular testing of arboviruses suitable for viral surveillance in entomology laboratories.

Methods: CDC-developed molecular assays originally designed for the diagnosis of (DENV), chikungunya virus (CHIKV), and Zika virus (ZIKV) were adapted for viral detection in macerates from *Aedes aegypti* mosquito collections. Performance characteristics of the adapted assays—the Mosquito Dengue Serotyping Assay (MDSA) and Mosquito Arbovirus PCR Assay (MAPA)—were initially determined using an automated high-throughput molecular diagnostic workflow for clinical diagnosis. We then validated a molecular testing workflow designed for entomological use, comprising manual methods for viral RNA extraction and the Quantabio Q qPCR cycler, a semi-portable and scalable instrument. Performance of this workflow and instrument was compared with the Thermo Fisher ABI 7500 reference system using DENV-1–4 contrived mosquito macerates and *Ae. aegypti* mosquitoes infected in the laboratory with DENV-1-4 or ZIKV.

Results: Overall performance of the entomological workflow using the MDSA and MAPA assays on the Quantabio Q qPCR cycler was comparable to that of the reference clinical diagnostic workflow. Assay cutoff was confirmed to remain the same as the clinical assays. Sensitivity ($1x10^3$-$1x10^4$ copies/mL) and specificity (100%) of both platforms were equivalent for DENV and ZIKV detection in contrived samples and laboratory-infected *Ae. aegypti* mosquitoes.

Conclusions: Effective entomo-virological surveillance is achievable using validated molecular tools with performance comparable to clinical diagnostic systems. Validation of CHIKV detection and field verification of the system remain to be determined.

Keywords: dengue, chikungunya, Zika, virus, PCR, mosquito, vector, surveillance

Funding: Centers for Disease Control and Prevention

Abstract: 20260228_053

Title: Evaluating Diagnostic Accuracy of Rapid Diagnostic Tests for Acute Dengue Virus Infection: A Retrospective Study

Author: Frances Vila-Hereter[1*], Jessica Carrion[1*], Hans Desale[1], Forrest K Jones[1], Manuela Beltran[1], Candimar Colon-Sanchez[1], Cindia Diaz[1], Genesis Cintron-De Leon[1], Camille Rivera Avilés[1], Maria Burgos-Garay[2], Carolynn DeByle[3], Roxana M. Rodríguez Stewart[2], Angel J. Rivera[2], Eliezer Rovira-Diaz[1], Laura Adams[1], Gabriela Paz-Bailey[1], Gilberto A. Santiago[1], Freddy A. Medina[1]

Institution: Centers for Disease Control and Prevention (CDC), San Juan, Puerto Rico[1], Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA[2], Centers for Disease Control and Prevention (CDC), Anchorage, AK, USA[3]

Background: Dengue is the most prevalent mosquito-borne viral illness worldwide, causing up to 400 million infections annually. Early and accurate diagnosis is crucial for effective clinical management. Currently, no dengue rapid diagnostic tests (RDTs) are cleared by the U.S. Food and Drug Administration (FDA) for diagnostic use in the United States. We evaluated the diagnostic performance and Zika virus cross-reactivity of dengue RDTs available on the U.S. market to prioritize candidates for field validation and regulatory consideration.

Methods: We assessed archived serum samples collected within seven days of symptom onset from patients with acute febrile illnesses in Puerto Rico during 2011–2024. We tested 197 samples from 99 acute dengue cases, 88 samples from patients negative for dengue and Zika, and 10 samples from acute Zika cases to assess cross-reactivity. Dengue positivity was defined using a composite reference standard consisting of RT-PCR, NS1 ELISA, and IgM ELISA assays. Nine RDTs (three NS1-only and six NS1/IgM combination tests) were evaluated by laboratory technicians blinded to reference test results. Sensitivity was calculated as the proportion of reference-positive samples that tested RDT-positive, specificity as the proportion of reference-negative samples that tested RDT-negative, and Zika cross-reactivity as any false-positive dengue RDT result among Zika-positive samples.

Results: Dengue RDT performance varied by manufacturer. Sensitivity ranged from 36% to 82%, and specificity ranged from 78% to 100%. The tests with the highest sensitivity were Artron (82% sensitivity; 78% specificity) and CTK Biotech (80%; 98%). Moderate sensitivity with high specificity was observed for LumiQuick (62%; 97%), Cortez (57%; 97%), Biopanda (57%; 92%), and InBios (56%; 94%). Lower sensitivity but very high specificity was observed for Abbexa (49%; 100%), Creative Diagnostics (45%; 100%), and MP Diagnostics (36%; 99%). Zika cross-reactivity ranged from 0% to 20%: Artron (20%); CTK Biotech, LumiQuick, Cortez, Creative Diagnostics, and MP Diagnostics (10% each); and NS1-only tests (0%; Abbexa, Biopanda, and InBios).

Conclusions: Commercially available dengue RDTs demonstrated wide variability in diagnostic performance. CTK Biotech showed the most balanced performance profile, with high sensitivity, high specificity, and low Zika cross-reactivity, supporting further evaluation using whole blood specimens and under prospective field conditions.

Keywords: dengue, diagnostics, rapid test

Funding: Centers for Disease Control and Prevention

Abstract: 20260228_054

Title: An Early-Illness Dengue Test That Identifies Prior Infection and Infecting Serotype

Author: Jarline Encarnación-Medina, Eliezer Rovira-Diaz, Genesis Cintron-De Leon, Frances Vila-Hereter, Jessica Carrion, Camille Rivera Avilés, Cindia Diaz, Manuela Beltran, Candimar Colon-Sanchez, Forrest K Jones, Laura E. Adams, Gabriela Paz-Bailey, Gilberto A. Santiago, Freddy A. Medina

Institution: Centers for Disease Control and Prevention (CDC), San Juan, Puerto Rico

Background: Structural similarity among the four dengue virus serotypes (DENV-1–4) causes serologic cross-reactivity, limiting serotype discrimination, especially where DENV and related arboviruses such as Zika virus (ZIKV) co-circulate. We previously validated a microsphere-based assay targeting envelope domain III (EDIII) epitopes of DENV and ZIKV to assess past exposure. Here, we calibrated this assay to discriminate ZIKV from DENV serotypes during the acute phase of illness and to distinguish primary from secondary DENV infections.

Methods: Patients with acute febrile illness enrolled in the Sentinel Enhanced Dengue Surveillance System (SEDSS) were included if they had acute RT-PCR confirmed DENV infection with at least two specimens collected 0–14 days after symptom onset. Unexposed controls were obtained from a non-endemic region. IgG binding to DENV-1–4 EDIII and virus-like particle (VLP) antigens was measured as median fluorescence intensity (MFI) using the microsphere immunoassay (MIA) with antigen-coupled beads. Seropositivity was defined using a previously established cutoff derived from a cross-sectional serological survey. Primary infections were defined as no detectable binding to any EDIII or VLP antigen, whereas secondary infections were defined as binding to at least one EDIII or VLP antigen. During initial development, DENV-1 RT-PCR–positive acute samples and paired convalescent specimens were tested to assess IgG binding to DENV-1–4 EDIII antigens.

Results: Seventeen acute DENV-1 cases were analyzed and classified as primary (9/17, 53%) or secondary (8/17, 47%). Among secondary cases, 5/8 (63%) exhibited EDIII IgG binding consistent with prior exposure to a single heterologous DENV serotype (DENV-2–4), whereas 3/8 (37%) showed broad reactivity to multiple DENV-2–4 serotypes, and the number of prior infections could not be determined. Paired t-tests comparing acute and convalescent MFI values showed a significant increase in DENV-1 EDIII IgG binding ($p < 0.001$), indicating rising antibody responses.

Conclusion: These findings support the feasibility of an EDIII-based Luminex IgG MIA as proof of principle for characterizing flavivirus infection history and distinguishing primary from secondary dengue during acute illness. Although limited to DENV-1–confirmed cases, the observed EDIII IgG binding patterns warrant evaluation in larger cohorts and across additional DENV serotypes to assess serotype-specific classification in endemic settings.

Keywords: dengue, diagnostics, antibody

Funding: Centers for Disease Control and Prevention

Human Microbiome

Abstract: 20260228_006

Title: Penile Squamous Cell Carcinoma in Puerto Rico: Integration of HPV, p16, survival, and microbiome data

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Background/Objectives- Penile squamous cell carcinoma (PSCC) is a rare but aggressive malignancy with substantial morbidity and mortality. Puerto Rico exhibits one of the highest PSCC incidence and mortality rates worldwide. Human papillomavirus (HPV) infection and p16INK4a expression are potential prognostic biomarkers, but their roles in survival remain unclear. In addition, the tumor-associated microbiome may influence HPV-driven oncogenesis. This study aimed to investigate the relationship between HPV prevalence, p16 expression, tumor microbiome composition, and clinical outcomes to identify prognostic factors in PSCC.

Methods- A retrospective cohort of 100 PSCC patients diagnosed between 2009 and 2023 was analyzed. HPV genotyping was performed using the InnoLipa and LBP DNA ELISA HPV-SPF10/RHA kits. p16 immunohistochemistry and clinicopathologic variables (tumor grade, stage, recurrence, survival) were recorded. Survival analyses used Kaplan-Meier and Cox regression. A subcohort of 54 patients tumors underwent 16S rRNA sequencing (Illumina MiSeq). QIIME2 and R were used for alpha/beta diversity and taxonomic analyses to assess associations with HPV status and histopathology.

Results- HPV DNA was detected in 56% of tumors, with HPV-16 being most frequent (58.9%). High-risk genotypes were present in 80.4% of HPV-positive cases, and p16 expression was observed in 27.8%. Recurrence occurred exclusively among HPV-positive patients ($p = 0.002$). Although HPV-positive tumors showed a nonsignificant trend toward longer mean survival (6.22 vs 4.55 years, $p = 0.095$), tumor grade was significantly associated with prognosis ($p = 0.009$). In the 54-patient microbiome subcohort, HPV-positive and high-grade tumors exhibited reduced Firmicutes and Bacteroidota but enrichment of Actinobacteriota, Proteobacteria, and Pseudomonas species. Anaerobic taxa such as Bacteroides, Streptococcus, and Fusobacterium were more abundant in advanced-stage HPV-positive tumors.

Conclusions- HPV infection is common in Puerto Rican PSCC and correlates with recurrence, whereas tumor grade remains the strongest determinant of survival. The microbial patterns identified suggest that HPV-positive and high-grade lesions exhibit distinct bacterial communities potentially contributing to inflammatory oncogenesis. These findings highlight the value of integrated viral, molecular, and microbial profiling to improve risk stratification and therapeutic approaches in penile cancer.

Keywords: penile squamous cell carcinoma, human papillomavirus (HPV), tumor-associated microbiome

Abstract: 20260228_021

Title: Effects of Escherichia coli Conditioned Media on Cell Viability and Cell Cycle Progression in Colorectal Cancer Cell Lines

Author: Bárbara A. Guevara Feliciano, Sheila N. López Acevedo, Byron K. Olivo Natal, Camille N. Zenón Meléndez, Madeline M. Martir Ocasio, Gabriela M. Chardon Galíndez, Elba V. Caraballo Rivera

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Background: Colorectal cancer (CRC) ranks among the most common malignancies and a leading cause of cancer mortality in the United States. In Puerto Rico, CRC is a major public health concern, with CRC-related mortality rates among the highest reported for Hispanic populations. The intestinal microbiota plays an important role in CRC, with certain pathogens activating pathways that promote cancer progression. Our preliminary data showed that CRC tumors from the Puerto Rican population exhibited elevated levels of pro-inflammatory cytokines and Escherichia coli (E. coli), a bacterium commonly associated with CRC progression. The central question of this study is whether secreted factors present in E. coli conditioned media directly impact the viability of non-metastatic (SW480) and metastatic (SW620) CRC cell lines. This research provides insight into how bacterial-derived soluble factors influence cancer cell behavior and progression.

Methods: SW480 and SW620 CRC cell lines were treated with increasing concentrations of E. coli conditioned media or purified bacterial DNA. Cell viability was assessed at 24 and 48 hours post-treatment using the Alamar Blue assay. Apoptosis, necrosis, and cell cycle distribution were analyzed at the same time points by flow cytometry following Annexin V and Propidium Iodide (PI) staining.

Results: Treatment with isolated E. coli DNA did not alter cell viability in either CRC cell line. In contrast, exposure to E. coli conditioned media induced a dose-dependent reduction in viability in both cell lines. Flow cytometry analyses demonstrated an increase in necrotic cells following treatment. Cell cycle analyses revealed an accumulation of cells in both G0/G1 and G2/M phases in response to E. coli conditioned media exposure.

Conclusion: These findings indicate that secreted factors in E. coli conditioned media, rather than isolated bacterial DNA, are primarily responsible for dose-dependent reductions in viability of SW480 and SW620 CRC cell lines. Flow cytometry results support these observations, showing increased necrosis, growth arrest, and cell cycle arrest. As these responses reflect early cellular effects, future studies will quantify gene expression and pro-inflammatory cytokine production using qPCR and Luminex to elucidate intracellular mechanisms.

Keywords: Colorectal Cancer, Escherichia coli, Bacterial Supernatant

Funding: This research was funded by the National Institute of Allergy and Infectious Diseases (NIAID) Grant #5R25AI183304-02 and supported by the UPRCCC institution.

Abstract: 20260228_024

Title: Proteomic profiling associates mucosal-immune-microbial axis to anti-PD-1 response in HPV+ oropharyngeal cancer

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Institution: [1]Department of Microbiology and Immunology, University of Puerto Rico- Medical Sciences Campus, San Juan, PR, [2]Cancer Biology Division, University of Puerto Rico, Comprehensive Cancer Center, San Juan, PR.

Background: Approximately 70% of all cases of oropharyngeal squamous cell carcinomas, a subset of head and neck squamous cell carcinomas, are caused by Human Papillomavirus (HPV). This infection induces inflammation and leads to presentation of viral neo-antigens, which confer these cancers with high immunogenicity. The increase in immune surveillance suggests that immunotherapies, like immune checkpoint inhibitors (anti-PD-1), might prove successful at treating these cancers. However, in practice, only a minority of patients (20-30%) respond to the therapy and display a full recovery. Therefore, by analyzing the proteomic landscape encompassing the immune cell responses to the anti-PD-1 therapy during oropharyngeal cancer, we will elucidate immune biomarkers that may aid in understanding the disparity in therapy response.

Methods: To achieve this, we used a preclinical murine model, in which we tongue-implanted an HPV-positive oropharyngeal cancer cell line named mEER. We monitored tumor growth and treated the mice with anti-PD-1 immunotherapy. Then, we isolated andlysed leukocytes from tumors and tumor-draining lymph nodes (tdLNs). Finally, the extracted proteins were used to perform TMT-based LC-MS/MS proteomics and protein enrichment analysis to identify biomarkers of therapy response.

Results: Our preliminary results suggest that the proteomic profile of therapy responders resembles that of therapy and tumor naïve mice, while non-responders resemble that of untreated tumor-bearing mice. Moreover, when comparing tdLNs from therapy responders versus non-responders, we found a total of 104 proteins significantly upregulated in responders and 25 significantly downregulated. Among our upregulated proteins, responders displayed increased metabolism, antigen presentation, cytotoxic activity, and anti-microbial related proteins. While non-responders displayed increased DNA-repair, inflammation, immunosuppression, and B-cell-related proteins.

Conclusions: Our immunotherapy response biomarkers suggest that the mucosal immune-microbial axis may play a role in maintaining productive anti-tumor immune activity. While pro-tumoral activity is mediated by inflammation and stress, as well as nonspecific immune responses and exhaustion. Future work will focus on identifying gene ontology and the enriched signaling and metabolic pathways that depict biomarkers for therapy responses, as well as assessing the viability of these biomarkers in patient-derived samples.

Keywords: Proteomics, Immunology, Head and Neck cancer

Funding: This study was partially funded by the Institutional National Institute of General Medical Sciences of the National Institutes of Health (NIGMS-NIH) COBRE Puerto Rico Center for Microbiome Sciences 1P20GM156713-01. This study was partially supported by the National Institute on Minority Health and Health Disparities (5U54MD007600)

Abstract: 20260228_028

Title: Microbial and Immune Signatures Associated with Colorectal Cancer in Hispanics Living in Puerto Rico

Author: Byron K. Olivo-Natal, Sheila N. López-Acevedo, Camille N. Zenón-Meléndez, Hilmaris G. Centeno-Girona, Elba V. Caraballo-Rivera

Institution: University of Puerto Rico Comprehensive Cancer Center, San Juan, PR 00921

Background: Colorectal cancer (CRC) is the leading cause of cancer-related deaths in the United States, with expected over 150,000 new cases and 55,000 deaths in 2026. In Puerto Rico (U.S territory), CRC accounts for more than 10% of new cases and deaths. Risk factors for CRC include genetic predispositions, dietary patterns, and microbiome. However, the role of microbial and immune factors in colorectal carcinogenesis among Hispanics living in Puerto Rico (PRHs) remains poorly understood. Pathogenic bacteria including Escherichia coli (E. coli), Bacteroides fragilis (B. fragilis), Fusobacterium nucleatum (F. nucleatum) and Enterococcus faecalis (E. faecalis) are known to contribute to tumorigenesis through inflammation and immune modulation. These alterations intersect with cytokine signaling, which plays a critical role in CRC development by shaping the tumor microenvironment. This study aimed to characterize microbial composition and cytokine profiles associated with CRC in PRHs.

Methods: Plasma and tissue samples were analyzed from the Puerto Rico Familial Colorectal Cancer Registry (PURIFICAR), including 15 CRC cases and 15 age- and sex-matched healthy controls. Cytokine levels were assessed using the ProcartaPlex Inflammation Panel (Luminex), while bacterial DNA was quantified by qPCR targeting uidA (E. coli), 16S rRNA (B. fragilis), fus1 (F. nucleatum), and groES (E. faecalis). Additionally, we conducted time and dose-response assays in CRC cell lines (SW480 & SW620) to assess the DNA damage produced by circulating bacterial DNA. Statistical analysis included Wilcoxon signed-rank test and ROC curve analysis with univariable and multivariable models, and three-way ANOVA.

Results: CRC patients exhibited a trend of elevated plasma levels of CD62E, CD62P, ICAM-1, IL-8, IP-10, and a significant difference of MCP-1 ($p<0.001$). In contrast, healthy controls showed higher levels of GM-CSF and IL-6 ($p<0.05$). Tumor tissues showed significantly increased levels of E. coli ($p<0.001$), with non-significant increases in F. nucleatum, E. faecalis. Among these, E. coli induced the highest DNA damage specifically in SW620 cells. A multivariable model combining MCP-1 and E. coli achieved the highest diagnostic accuracy (AUC=0.96).

Conclusion: These findings underscore the intricate interaction between microbiota, immune signaling, and CRC development in PRHs. Future studies will expand cohort size and include functional migration assays to validate these findings.

Keywords: Colorectal cancer, Microbiome dysbiosis, Cytokine profiling

Funding: This project was supported by NIAID grant award #1R25AI183304 and UPRCCC Institutional Funds.

Abstract: 20260228_029

Title: Oral Probiotic-Derived Molecules as Novel Modulators of Tumor Growth and Immunity in HPV-Associated Oropharyngeal Cancer

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Introduction: Head and neck squamous cell carcinoma (HNSCC) is the seventh leading cause of cancer-related mortality worldwide, with human papillomavirus (HPV) recognized as a principal risk factor. Currently, the survival median of patients is five years, with many side effects produced by the existing treatments, such as chemotherapy, radiotherapy, and surgery. This concern makes the search for new therapies crucial. Probiotics have emerged as promising candidates due to their ability to confer health benefits without pathogenicity. Among them, Streptococcus salivarius is a commensal bacterium mainly found in the human oral cavity and has demonstrated the capability to decrease inflammatory cytokines, activate natural killer (NK) cells, and induce apoptosis in cancer cells. This project aims to investigate the principal component by which Streptococcus salivarius K-12 regulates the tumor microenvironment and its promising therapeutic efficacy.

Methods: The HPV+ oropharyngeal cancer cell line (mEER) was injected subcutaneously into C57BL/6 mice. The mice were divided into four different groups: PBS and BHI broth as controls; heat-inactivated (HI) S. salivarius K-12, and cell-free supernatant. Treatments were injected intratumorally every four days, and tumor volume was measured twice a week. Immune phenotyping was performed using flow cytometry. To assess cytotoxicity induced in cancer cells in vitro, mEER cells were treated with bacterial supernatant and media (control), followed by an MTT assay. Lastly, the supernatant was evaluated using Gas Chromatography-Mass Spectrometry to determine the metabolic profile.

Results: The supernatant from Streptococcus salivarius K-12, but not HI bacteria or the controls, delayed tumor growth. This effect may be induced by molecules secreted by S. salivarius that impact tumor growth. The supernatant additionally increased the activation of anti-tumoral cells and decreased immunosuppressive cell populations. The supernatant also induced cytotoxicity of mEER cells in vitro. The metabolomic profile indicates higher production of glycolic and lactic acid.

Conclusions: S. salivarius K-12 supernatant delays tumor growth and modulates the tumor immune microenvironment, supporting its potential as a probiotic-based therapy. The supernatant also shows increased production of glycolic and lactic acid. Among our future plans is to evaluate the effects of other Streptococcus species on cancer cells' viability and metabolism.

Keywords: probiotic, cancer, immune cells

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Abstract: 20260228_031

Title: Changes in T cell and B cell subsets in Hispanic Patients with Cervical Dysplasia and Cervical Cancer

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Background: Cervical cancer ranks as the fourth most common cancer among women globally. It often begins with persistent human papillomavirus infections, which can progress to cervical dysplasia and, if left untreated, to invasive cervical cancer. Hispanic women face 30–40% higher rates of cervical cancer diagnosis and mortality than non-Hispanic White women. Our project aims to investigate changes in T cell and B cell subsets in Hispanic women that developed cervical dysplasia or cervical cancer, and during chemoradiation.

Methods: Our study recruits individuals in San Juan, PR, and Houston, TX, to collect blood samples and cervical cytobrushes from individuals with negative for intraepithelial lesion or malignancy (NILM), as well as patients with dysplasia and patients with cancer undergoing chemoradiation. Peripheral blood mononuclear cells and cervical samples undergo immune cell quantification and characterization by flow cytometry to analyze T and B cell populations and their activation markers. Data was stratified according to cervical disease stage and, in cancer patients, before and after 5 weeks of chemoradiation.

Results: Flow cytometry revealed changes in peripheral immune cells across cervical disease stages. Among CD4+ T cells, cancer patients exhibited reduced frequencies of acdvated memory T cells, $CD27^{+}CD38^{+}$, and increased frequencies of resting memory T cells, $CD27^{+}CD38^{-}$, compared to NILM. Among $CD8^{+}$ T cells, memory T cells ($CD27^{+}$) were significantly decreased in cancer patients compared to NILM ($p < 0.05$). Although total B cell frequencies did not change, follicular B cells frequencies were significantly reduced in cancer patient while B cells showed a decreased activation. Interestingly, chemoradiation was associated with a significant reduction in total and naïve B cells, a significant increase in activated B cells, and a downward trend in plasma cells after 5 weeks of treatment.

Conclusions: Immune shifts in B and T cell subsets suggest early dysregulation during cervical disease. During cancer, memory T cell responses are dysregulated, and chemoradiadon impacts B cell frequencies and their acdvadon. Reduced $CXCR5^{+}$ and $CD38^{+}$ B cells and altered $CD4^{+}$ T cell activation may serve as early biomarkers to guide personalized care. Chemoradiation treatment reduced the frequency of naïve and total B cells; however, it induced their activation. As future plan, these immune phenotypes will be associated with the cervicovaginal microbiome.

Keywords: Cervical cancer, dysplasia and Hispanic

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Abstract: 20260228_032

Title: In vitro evaluation of cellular metabolism and viability in oropharyngeal cancer cells in the presence of tetracycline and cefazolin.

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Background: The use of antibiotics in head and neck cancer patients, particularly in the post-operative setting, remains non-standardized and has been associated with negative alterations of the microbiome and negative implications for cancer outcomes. On the other hand, some antibiotics, such as tetracycline, may negatively influence the viability, morphology and migration of pharyngeal carcinoma cells. Furthermore, head and neck cancer is highly associated with human papillomavirus (HPV) infections, yet how antibiotics affect HPV-positive cancer cells remains unknown.

Methods: Here, our objective was to evaluate the effects of two antibiotics—tetracycline and cefazolin—on the metabolism of mEERL cells, a mouse HPV-positive oropharyngeal cancer cell line. Cell metabolism was assessed using MTT assay following 24 and 48 h exposures to five concentrations of tetracycline (270 to 16.9 μM) and ten concentrations of cefazolin (25,600 to 50 μM).

Results: As expected, tetracycline exhibited time- and concentration-dependent cytotoxic effects, reflected by MTT reduction. Cefazolin directly reduced the MTT dye even in the absence of mEERL cells, making the assay results inconclusive. Still, microscope observations revealed a possible reduction in cellular confluency.

Conclusion: In conclusion, the observed cytotoxic effects of tetracycline on HPV-positive oropharyngeal cancer cells suggests a potential role that merits further investigation as a potential consideration in patients with HPV- positive head and neck cancer who require antibiotic treatment. Ongoing apoptosis assays and planned in vivo studies will further elucidate the mechanisms of cell death and the influence of these antibiotics on the oral microbiome and immune responses.

Keywords: Cancer, antibiotics, cellular metabolism

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Abstract: 20260228_035

Title: Association of Gut Microbiome with Hypertension in Puerto Ricans

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Background: Hypertension (HTN) affects 42.2% of Puerto Rican adults, exceeding U.S. averages. Emerging evidence suggests gut microbiota may contribute to HTN through inflammatory, metabolic, and autonomic pathways; however, Caribbean Hispanic older adults remain underrepresented in microbiome studies. This study examined whether microbial diversity or specific bacterial taxa were associated with HTN in older Puerto Rican adults.

Methods: A secondary analysis was conducted on 99 adults aged 55 to 94 who were enrolled in a cross-sectional aging study. Hypertension (HTN) status was determined based on clinical history. Fecal samples were analyzed using 16S rRNA sequencing. Alpha diversity was assessed using the Shannon index, while beta diversity was evaluated with Bray-Curtis metrics. Statistical comparisons were made using the Mann-Whitney U test, ANOSIM, PERMANOVA, and PERMDISP. Additionally, associations between selected bacterial taxa and hypertension were examined through logistic regression.

Results: HTN was present in 76 participants (76.8%) and absent in 23 (23.2%). No significant associations were observed between HTN and the relative abundance of *Blautia* ($p = 0.70$), *Prevotella*, or the *Ruminococcus* torques group. Alpha diversity was significantly lower in hypertensive individuals ($p = 0.044$), while beta diversity showed no group differences (ANOSIM $p = 0.262$; PERMANOVA $p = 0.111$; PERMDISP $p = 0.808$).

Conclusions: Participants without hypertension demonstrated a richer and more diverse gut microbiota, suggesting that greater microbial diversity may offer a protective effect against elevated blood pressure. Although no specific taxa were significantly associated with hypertension status, these findings underscore the relevance of overall microbial diversity in understanding hypertension risk. Ultimately, this work highlights the critical need for larger, well-powered studies in Caribbean Hispanic populations to deepen our understanding of microbiome–cardiometabolic relationships and promote health equity.

Abstract: 20260228_046

Title: Cross-Population Analysis of High-Risk HPV in Women Born in Puerto Rico and the Dominican Republic

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Background: Human papillomavirus (HPV) is one of the most common sexually transmitted infections where high-risk HPV (HR-HPV) serotypes are strongly associated with cervical cancer. Past studies have shown that distribution of HPV genotypes varies across regions and ethnicities, but Hispanic women remain underrepresented in HPV research. The purpose of this study is to determine whether significant differences exist in cervical cytology results and genotypes between Puerto Rican-born and Dominican-born women.

Methods: Cervicovaginal swabs were collected from 81 women (39 born in the Dominican Republic and 42 born in Puerto Rico) under IRB protocol #2290033153. These samples underwent genomic DNA extraction, followed by HPV typification using short-polymerase chain reaction-fragment assay (SPF10-LiPA). Participants were matched for body mass index (BMI), age, menopausal and physiological status to reduce confounding. Statistical analyses were conducted using Fisher's exact test, with significance set at $p<0.05$.

Results: The HPV positive rate was 72.2% in the Dominican Republic cohort and 87.8% in the Puerto Ricans. Among women from the Dominican Republic, negative to intraepithelial lesions (NILM) was the most frequent cytologic finding (74.4%), followed by high grade lesions (HGSIL) (12.8%), low-grade lesions (LGSIL) (10.3%), and atypical squamous cells of undetermined significance (ASCUS) (2.6%). In Puerto Rican–born women, the distribution was NILM (43.6%), HGSIL (30.8%), and LGSIL (25.6%). The most common HR-HPV in Dominican participants were HR51 (18%), HR16 (13%), and HR33 (13%); in Puerto Ricans, HR16 (30.7%), HR51(23.1%) and HR66 (23.1%). No statistical difference was seen in HR-HPV distribution between Puerto Rican and Dominican women in this cohort ($p=0.062$).

Conclusions: These findings suggest that ethnicity may influence HPV infection patterns within Hispanic populations. Future directions include expanding the cohort with a larger sample size to further assess these results. This approach will contribute towards the development of prevention and screening strategies.

Keywords: Human Papilloma Virus (HPV), Hispanic women, cervical cancer screening

Acknowledgements: This project was supported by the UPR-Medical Sciences Campus Center for Collaborative Research in Minority Health and Health Disparities (RCMI) 2U54MD007600, the NIAID Research Education Program on Microbes, Infections and Cancer (REPMIC) R25AI183304, NIH-NIGMS Alliance Programs U54MD007587, and the COBRE Puerto Rico Center for Microbiome Sciences 1P20GM156713-01.

Abstract: 20260228_056

Title: Associations Between Body Mass Index and Vaginal Microbiome Status in Women with HPV Infection.

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Background: The cervical microbiome has been associated with high-risk Human Papillomavirus (HPV) infections, which can lead to low-grade squamous intraepithelial lesions (LGSIL) and high-grade squamous intraepithelial lesions (HGSIL). However, the influence of body mass index (BMI) on cervicovaginal microbial structure in women with HPV infections remains unknown. Host-related factors, including metabolic status, may influence microbial diversity and composition in the context of HPV infections. Understanding how BMI status relates to the cervicovaginal microbiome environment can provide insight into host-microbe interactions and cervical diseases.

Methods: Cervical swabs from 398 non-pregnant, non-menopausal, and menopausal women were collected (Streamlyne #2290033153, IRB #1050114) for genomic DNA extractions. The extracted DNA was used for HPV genotyping (LiPA25) and for bacterial community profiling with 16S rRNA sequencing. Participants were stratified by BMI category and cervical lesion status, including negative intraepithelial lesion or malignancy (NILM), LGSIL, and HGSIL. Quality control of the sequenced data was performed using QIIME2 and QIITA, with 250-bp trimming and rarefaction to 1,030 reads. Taxonomic assignment was done using the extended Greengenes2 database. Bacterial assessment accompanied with corresponding statistical analyses were performed downstream with QIIME2.

Results: Significant differences in bacterial composition and profiling were observed across BMI categories. Beta-diversity analyses (Bray-Curtis) demonstrated that patients with no intraepithelial lesions and positive HPV status showed distinct microbial structures when comparing BMI groups: normal weight versus obese (PERMANOVA, $p=0.045$) and overweight versus obese ($p=0.014$). Additionally, patients with high-grade lesions showed significant differences between the overweight and obese groups ($p=0.028$). Alpha diversity metrics showed lower microbial diversity in individuals with NILM and HPV infection, when comparing the overweight and obese patients (Kruskal-Wallis, $p=0.019$). Taxonomic profiling further revealed significant shifts in relative abundance at both phylum and species levels across BMI status categories.

Conclusion: These findings suggest that body mass index-related host factors may shape the cervicovaginal microbiome environment during HPV infection and could play a role in cervical disease progression. Further assessment is warranted to fully understand BMI-related host-microbe interactions.

Keywords: Cervical Microbiome, BMI, HPV

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Abstract: 20260228_057

Title: Gut Dysbiosis Associated with Polycystic Ovary Syndrome and Hirsutism in Hispanic Patients

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Abstract: Polycystic Ovary Syndrome (PCOS) is a widespread endocrine condition impacting women of reproductive age. It is identified by features including irregular menstrual cycles, elevated androgen levels and polycystic ovaries. Women with PCOS commonly present insulin resistance independent of adiposity and have been linked to risk of diabetes mellitus, cardiovascular disease, and mood disorders. The gut microbiota, the collection of microorganisms inhabiting the human gastrointestinal tract, plays a key role in human health and has been linked to several diseases.

Methods: We aimed to characterize the gut microbiota in a sample of Hispanic women living in Puerto Rico (n=50). This will be a cross-sectional study.The study population will include women aged 21–45 years old. A stool sample was collected for genomic DNA extractions followed by amplification and sequencing of 16S rRNA genes (V4 region) with Illumina MiSEQ. Data analyses were performed with standard pipelines with variables sample group (PCOS vs Controls), alopecia assessment, O-GTT, FAI, acne assessment, HOMA-IR and Hirsutism status. Questionnaire about lifestyle and dietary patterns (Spanish-version)

Results: Despite there were no changes in alpha or beta diversity among the microbiota of these groups, composition was significantly different. Women with PCOS had significantly lower levels of Enterococcus species as well as Hungatella, taxa that are part of a physiologically normal gut flora. Enterococcus species contribute to the balance of the microbial community and play roles in the metabolism and immune function and are very resilient. Hungatella species are a known source of catabolic enzymes that degrade glycosaminoglycans which are important in tissue repair. These dominant taxa in controls were substituted by other taxa in PCOS. Women with prominent hirsutism had significantly lower levels of Faecalibacterium while those with insulin resistance had increased levels of Clostridium. We found that higher levels of Clostridium, and lower levels of protective anti-inflammatory taxa such as Faecalibacterium or Enterococci, which are important for gut health and metabolic regulation, are linked to this metabolic disturbance.

Conclusion: Even though this is a preliminary report, it opens potential therapeutic strategies, such as the use of probiotics, and dietary modifications to modulate the gut microbiome and improve PCOS outcomes.

Abstract: 20260228_060

Title: Influence of Menopausal Status on Vaginal Microbiota and Cervical Lesion Severity

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Background: The vaginal microbiota is a dynamic ecosystem that plays a critical role in women's cervical health and is strongly influenced by hormonal, environmental, and lifestyle factors. Changes in microbial composition may increase susceptibility to human papillomavirus (HPV) infection and contribute to the development of cervical desiease. This study examined the relationship between menopausal status, cervical cytology, and vaginal microbiota diversity and composition among women in Puerto Rico.

Methods: In this cross-sectional study, vaginal samples were collected from 110 women (51 menopausal, 59 non-menopausal; IRB# 2290033153A014). Participants were classified by menopausal status. Cervical cytology and HPV testing categorized samples as negative for intraepithelial lesion or malignancy (NILM; HPV–/HPV+), low-grade squamous intraepithelial lesions (LGSIL), or high-grade squamous intraepithelial lesions (HGSIL). Vaginal microbial composition and diversity were characterized using 16S rRNA gene sequencing. Correlation analyses were conducted to identify bacterial taxa associated with menopausal status and cervical lesion severity.

Results: Menopause was associated with increased alpha diversity and a compositional shift from Lactobacillus-dominated to mixed anaerobic communities. Across cervical phenotypes, Lactobacillus crispatus decreased while Lactobacillus iners, Gardnerella vaginalis, and Atopobium vaginae increased with lesion severity. Correlation analysis confirmed negative associations of Lactobacillus crispatus and positive correlations of Gardnerella vaginalis, Prevotella bivia, and Atopobium vaginae with menopausal and HGSIL.

Conclusion: Menopause alters the vaginal microbiome, diminishing protective Lactobacillus species while promoting anaerobic taxa associated with HPV persistence and cervical dysplasia. These findings highlight the interaction between hormonal status and cervical pathology in shaping the vaginal microbial ecosystem and influencing disease risk.

Keywords: Menopause; Vaginal microbiome; Cervical dysplasia

Funding: This study was supported by the Center for Collaborative Research in Minority Health and Health Disparities (RCMI; Grant 2U54MD007600), NIH/NIGMS Alliance program (Grant U54MD007587), and PR-INBRE (Grant 5P20GM103475-17).

Abstract: 20260228_063

Title: Penile Squamous Cell Carcinoma in Puerto Rico: Integration of HPV, p16, survival, and microbiome data

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Background/Objectives- Penile squamous cell carcinoma (PSCC) is a rare but aggressive malignancy with substantia lmorbidity and mortality. Puerto Rico exhibits one of the highest PSCC incidence and mortality rates worldwide. Human papillomavirus (HPV) infection and p16INK4a expression are potential prognostic biomarkers, but their roles in survival remain unclear. In addition, the tumor-associated microbiome may influence HPV-driven oncogenesis. This study aimed to investigate the relationship between HPV prevalence, p16 expression, tumor microbiome composition, and clinical outcomes to identify prognostic factors in PSCC.

Methods- A retrospective cohort of 100 PSCC patients diagnosed between 2009 and 2023 was analyzed. HPV genotyping was performed using the InnoLipa and LBP DNA ELISA HPV-SPF10/RHA kits. p16 immunohistochemistry and clinicopathologic variables (tumor grade, stage, recurrence, survival) were recorded. Survival analyses used Kaplan-Meier and Cox regression. A subcohort of 54 patients tumors underwent 16S rRNA sequencing (Illumina MiSeq). QIIME2 and R were used for alpha/beta diversity and taxonomic analyses to assess associations with HPV status and histopathology.

Results- HPV DNA was detected in 56% of tumors, with HPV-16 being most frequent (58.9%). High-risk genotypes were present in 80.4% of HPV-positive cases, and p16 expression was observed in 27.8%. Recurrence occurred exclusively among HPV-positive patients ($p = 0.002$). Although HPV-positive tumors showed a nonsignificant trend toward longer mean survival (6.22 vs 4.55 years, $p = 0.095$), tumor grade was significantly associated with prognosis ($p = 0.009$). In the 54-patient microbiome subcohort, HPV-positive and high-grade tumors exhibited reduced Firmicutes and Bacteroidota but enrichment of Actinobacteriota, Proteobacteria, and Pseudomonas species. Anaerobic taxa such as Bacteroides, Streptococcus, and Fusobacterium were more abundant in advanced-stage HPV-positive tumors.

Conclusions- HPV infection is common in Puerto Rican PSCC and correlates with recurrence, whereas tumor grade remains the strongest determinant of survival. The microbial patterns identified suggest that HPV-positive and high-grade lesions exhibit distinct bacterial communities potentially contributing to inflammatory oncogenesis. These findings highlight the value of integrated viral, molecular, and microbial profiling to improve risk stratification and therapeutic approaches in penile cancer.

Keywords: penile squamous cell carcinoma, human papillomavirus (HPV), tumor-associated microbiome

Abstract: 20260228_064

Title: The Effects of Antibiotics on Neurobiology of Avoidance Behavior and Serotonin Availability

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Background: Use of antibiotics can harm the gut microbiota and cause an imbalance in the Gut Brain-Axis (Glover et. al, 2022). Studies have shown that antibiotic consumption can increase anxiety-like behaviors (Wang et. al, 2021). However, the influence of antibiotics on other defensive behaviors, like avoidance, is largely unexplored. Also, gut microbiota can modulate neurotransmitter levels, one in particular is serotonin which is involved in mood and anxiety regulation (Karu et al., 2016). In addition, 90% of serotonin is produced in the gastrointestinal tract (Cleveland Clinic). By integrating microbiome research, this study in rodents aims to clarify the associations between antibiotic exposure and emotionally-relevant behaviors within the gut microbiome-brain axis.

Methods: The objective of the study is to determine if antibiotic exposure increases anxiety-like behaviors which could exacerbate other defensive behaviors, like avoidance. Avoidance can be complicated in the presence of appetitive and aversive stimuli. Choice behaviors between appetitive and aversive stimuli can be modeled in rodents using platform-mediated avoidance. Here, rodents learn to avoid a foot shock by stepping onto a safe platform during presentation of a conditioned auditory stimulus (e.g. tone). Stepping on the platform protects the rodent from the shock, but does not eliminate the auditory stimulus. Of note, when the animal steps onto the avoidance platform, it cannot access a sugar-pellet reward. Thus, platform-mediated avoidance creates a conflict that requires rodents to make a choice between avoidance (no shock) and reward (receiving sugar pellets). In the current study, we hypothesized that antibiotic exposure would result in excess avoidance as observed by more time on the platform. Once training is done, rodents will consume a daily dose of an antibiotic cocktail for 3 weeks. Lastly, they will be tested for avoidance extinction and euthanized. Brains will be extracted for immunohistochemistry, particularly regions involved in avoidance behavior like ventral striatum and basal lateral amygdala will be analyzed for cellular activity. Furthermore, analysis of biomarkers in the blood and gut are being incorporated to gain further insight into the mechanisms by which antibiotics influence the gut-microbiome-brain axis.

Results: Preliminary data revealed an increase of time spent on platform for rats that consumed antibiotics ($p=0.0412$). Also, brain subregions involved in avoidance expression like ventral striatum and basal lateral amygdala showed an increase of cellular activity in rats that consumed antibiotics. Biomarker assessments in blood and metabolomic analysis in the gut are in progress.

Conclusion: Current results suggest antibiotic consumption increased avoidance behavior. This could be explained by the increase of cellular activity in ventral striatum and basal lateral amygdala. Based on these preliminary results, future directions include assessing for changes in neurotransmitters, such as serotonin, along the gut-microbiome-brain axis.

Keywords: Antibiotics, Neurobiology of Avoidance, Gut-Brain-Axis

Funding: U54-MD007600 and RCMI Pilot

Abstract: 20260228_080

Title: Modulation of Macrophage–Barrier Interactions by Edelfosine Under Seizure-Like Conditions

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Epileptic seizures disrupt the molecular integrity of the blood–brain barrier (BBB), increasing permeability and facilitating infiltration of peripheral immune cells such as macrophages. This immune cell recruitment increases neuroinflammation through cytokine release and glial activation, enhancing neuronal hyperexcitability and correlating with seizure severity. Emerging evidence further links epilepsy to disruption of the gut–vascular barrier (“leaky gut”) and gut dysbiosis, where intestinal epithelial failure permits translocation of microbial products (e.g., LPS) that drive inflammatory monocyte recruitment and differentiation into pro-inflammatory macrophages. Together, these central and peripheral inflammatory processes contribute to disease progression and underscore the need for novel anti-inflammatory therapies, particularly given that approximately 30% of patients develop resistance to current antiepileptic drugs.

Here, we evaluate Edelfosine (Ef), a phospholipase C-β (PLC-β) inhibitor with established anti-inflammatory effects in immune cells, as a potential modulator of macrophage–barrier interactions. Using an in vitro BBB–macrophage adhesion model, murine brain endothelial cells (bEND.3) were exposed to pilocarpine to mimic seizure-like conditions, followed by the addition of fluorescently labeled macrophages (RAW 264.7) in the presence or absence of Ef. Macrophage adhesion was quantified using confocal microscopy and image analysis, with dexamethasone serving as an anti-inflammatory control.

Preliminary results demonstrate that pilocarpine significantly increases macrophage adhesion to BBB endothelial cells, while Ef reduces this adhesion to levels comparable to dexamethasone. These findings suggest that Ef attenuates neuroinflammatory responses under seizure-like conditions by limiting immune cell recruitment to BBB cells. Together, this work establishes an in vitro platform for studying barrier–immune interactions in epilepsy and supports the therapeutic potential of edelfosine as a novel anti-inflammatory agent targeting both BBB dysfunction and systemic inflammatory contributions to seizure pathology. Future studies will extend this approach to intestinal epithelial models to assess Ef’s ability to modulate gut–immune interactions under epilepsy-like conditions.

Keywords: Blood-brain barrier, epilepsy, inflammation

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Abstract: 20260228_082

Title: Lipidomic profiling of prostate tumors reveals candidate microbes associated with risk of disease progression

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Background: Although prostatic inflammation has long been linked to the development of prostate cancer, the definitive contribution of microbial infection to this process has remained unclear. However, the advent of deep sequencing and machine learning tools is rapidly enabling the systematic characterization of microorganisms associated with cancer. Growing evidence implicates biochemical and metabolic crosstalk between vulnerable host tissues and microbial dysbiosis as a predisposing factor for cancer. The prostate, with its relative close proximity to the rectum, represents a unique context to study the role of the microbiome in cancer development and disease progression. This study aims to characterize the lipidomic profiles of prostate tumors according to risk of disease progression, and to explore microbes implicated in the production of key outcome-driving lipid profiles.

Methods: Consenting men aged 40-80 diagnosed with prostate cancer and undergoing robot-assisted radical prostatectomy were included in this study. Global untargeted lipidomics was performed from n=80 prostate tumors using a Thermo Orbitrap Fusion Tribrid Mass Sepctrometer under ESI negative ionization mode at a resolution of 240,000. Risk stratification at primary intervention was performed using the post-surgical cancer of the prostate risk assessment score (CAPRA-S). Downstream data analyses were performed using LipidMaps, LipidSig, MicrobiomeAnalyst, Graphpad Prism, and JASP.

Results: The total number of lipids detected among all n=80 tumor samples was 717. Of these, 7 were associated with bacteria; 15 were associated with fungi. Most bacteria-associated lipids were differentially elevated in low-risk tumors, with *Escherichia coli, Mycobacterium tuberculosis*, and *Alicyclobacillus cycloheptanicus* emerging as the affiliated microbes. In contrast, all fungi-associated lipids were differentially elevated in high-risk tumors; notably, only *Saccharomyces cerevisiae* was implicated in production of these lipids.

Conclusion: These findings underscore the importance of molecular studies to interrogate the metabolic crosstalk between tumors and surrounding microbiome landscapes to inform potential prognostic and predictive tools for cancer. Future studies will incorporate rectal microbiome and metabolomic profiles to evaluate spatial interactions between tissues of different organ systems.

Keywords: Prostate cancer, lipidomics, CAPRA-S

Funding: This work was sponsored by the National Institute of Allergy and Infectious Diseases (NIAID)-funded REPMIC training program (grant #5R25AI183304-02) (GPT) and the National Institute of General Medical Sciences (NIGMS) Puerto Rico IDeA Network for Biomedical Research Excellence (PR-INBRE) program (grant #P20GM103475 and U54MD007600).

Abstract: 20260228_085

Title: HPV Persistence and Progression Dynamics among Hispanic Women Living in Puerto Rico: A Longitudinal Study

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Background: Persistent infection with carcinogenic human papillomavirus (HPV) types is the primary etiologic factor for cervical cancer. Although most HPV infections are transient and resolve spontaneously, the mechanisms driving viral persistence and progression, particularly among Hispanic women, remain poorly understood. This study aimed to evaluate longitudinal changes in HPV infection status and assess the impact of persistent high-risk HPV (hr-HPV) infections among women living in Puerto Rico.

Methods: A cohort of 71 women aged 21-70 was recruited from gynecology clinics in San Juan (IRB #2290033153). Participants underwent an initial cervical swab collection, with follow-up visits scheduled within one year for those with Negative Intraepithelial Lesions (NILM) and within six months for those with High-Grade Squamous Intraepithelial Lesions (HGSIL). HPV genotyping was performed using the SPF10 assay and LiPA25, targeting 25 clinically relevant HPV genotypes. Changes in HPV type, risk category, and cervical lesion status were assessed across two visits.

Results: Of the women initially enrolled, 10.53% remained HPV-negative throughout follow-up, while 47.37% continued to test positive for HPV. Among participants who were HPV-positive at baseline, 36.84% cleared the infection by the second visit. Transitions between high-hisk (hr-HPV) and low-risk HPV genotypes, as well as shifts among different high-risk types, accounted for 12.82% of the observed changes. Despite the persistence of HPV infections, particularly high-risk types, 22.81% of women experienced regression from hr-HPV infection to an HPV-negative status overtime.

Conclusion: These findings highlight the dynamic behavior of HPV infections, with both persistence and clearance observed within a relatively short timeframe. Understanding the factors influencing these transitions is critical for improving patient monitoring, risk assessment, and prevention strategies in Hispanic populations.

Keywords: High-risk HPV, HPV persistence, Cervical lesion

Funding: This project was funded by the Center for Collaborative Research in Minority Health and Health Disparities (RCMI) 2U54MD007600, NIH-NIGMS programs Alliance U54MD007587 and PR-INBRE 5P20GM103475-17

Abstract: 20260228_087

Title: Association of Cervical Tumor Microbiome Profile with HPV Clade in Cervical Cancer

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Background: Cervical cancer ranks as the fourth most common malignancy among women worldwide, causing over 660,000 new cases and 340,000 deaths in 2022, with human papillomavirus (HPV) as the primary etiological agent. Among the over 200 HPV genotypes, 14 are classified as high-risk owing to their association with cancer, with most of these high-risk genotypes encompassed within HPV clades A7 (18, 39, 45, 59, 68, 70, 85, and 97) and A9 (16, 31, 33, 35, 52, 58, and 67). The structure of the cervical microbiome undergoes dynamic changes during the development of cervical cancer, and its composition plays a crucial role in the response to treatment. However, whether the cervical microbiome profile differs by HPV clade is unknown. This study aims to determine whether there is a correlation between HPV clade and the cervical microbiome profile of cervical cancer patients.

Methods: Tumor swabs were collected from 77 newly diagnosed cervical cancer patients and subjected to 16S V4 rRNA gene sequencing for microbiome profiling. Patients were categorized as HPV clade A7- or A9-positive using VirMAP. Taxonomic species classification was performed using a previously developed custom Bayesian classifier trained on a cervicovaginal-specific database. Alpha and beta diversity were assessed using the microeco R package. Microbiome composition and diversity were evaluated across HPV clade groups. Alpha and beta diversity were compared between HPV clade groups using the Wilcoxon test and PerMANOVA in R,respectively. LEfSe was used to evaluate differentially abundant taxa between the two groups.

Results: In the study cohort, 31% of tumors (N = 24) were classified as HPV clade A7-positive and 69% (N = 53) as A9-positive. At the genus level, the cervical microbiome is dominated by Prevotella, Lactobacillus, and Bacteroides. Alpha diversity comparisons between the two groups demonstrated no significant differences in richness (observed feature, p = 0.06; Fisher's alpha, p= 0.13), but A9-positive patients had significantly higher community evenness (Simpson, p = 0.02; Pielou, p = 0.02) and overall community richness and evenness (Shannon Diversity Index, p =0.02). Beta diversity was significantly higher for HPV clade A7-positive compared to A9-positive (PerMANOVA; p = 0.009); however, LEfSe failed to identify any distinct taxa.

Conclusion: Overall, this study reveals no significant differences in the cervical microbiome profile between HPV clade A7- and A9-positive cervical cancer patients; however, further research is necessary to explore taxonomic differences related to HPV-associated environments.

Keywords: cervical cancer, human papillomavirus, cervical microbiome

Funding: This study is supported by the MDACC FY24 HPV Moonshot Priority Project – Microbiome and National Institutes of Health (NIH) UPR/MDACC: Partnership for Excellence in Cancer Research under Award Number 2U54CA096297-17

Abstract: 20260228_089

Title: Evaluating the Therapeutic Potential of Short Chain Fatty Acids on the Cell Viability of Triple-negative Inflammatory Breast Cancer

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Background: Inflammatory breast cancer (IBC) is the most aggressive form of breast cancer, accounting for 2-4% of cases but contributing to approximately 10% of annual breast cancer mortality in the USA. Studies have shown that the molecular profile of IBC differs significantly from other subtypes, however, these changes do not fully account for its aggressive and rapid phenotype. The microbiome, consisting of a diverse community of microorganisms living in the human body, has emerged as an influential player in cancer development and progression of different cancers, including breast cancer. There is evidence suggesting that microbial metabolites, such as short-chain fatty acids (SCFA), contribute to immune response, tumor growth, and the efficacy of chemotherapeutic drugs by decreasing cell proliferation and increasing apoptosis. However, while the therapeutic potential of SCFA in treating different cancers is established, their use in IBC treatment has not been assessed.

Methods: In this study, we treated SUM149PT cells with multiple concentrations of SCFA, butyrate, acetate, and propionate, and evaluated them in the context of cell proliferation, apoptosis, and 2D cell migration. SUM149PT (Triple-negative IBC) cells were treated with different concentrations of sodium acetate, butyrate, and propionate for 24h. Proliferating and apoptotic cells were detected by fluorescence microscopy of KI67-FITC and Annexin V-Cy3 stained cells respectively. Cell motility was evaluated using a wound healing assay that compared the difference in the area of wound closure after 24 hours between cells treated with varying concentrations of acetate, butyrate, or propionate, and untreated cells.

Results: We saw a significant decrease in cell proliferation but no increase in cell apoptosis in SUM149PT cells treated with propionate after 24h. Additionally, while we didn't see a significant decrease in cell proliferation we did see a trending increase in apoptosis in cells treated with butyrate after 24h. Furthermore, for all three SCFA, we saw a significant decrease in cell migration at higher concentrations after 24h, however, we observed an increase in cell death in cells treated with higher concentrations of butyrate.

Conclusion, SCFA can decrease cell proliferation and cell migration while not significantly increasing apoptosis in SUM149PT cells after 24h.

Keywords: cancer, microbiome, metabolites

Funding: This project was supported by the National Cancer Institute: NIH-RISE grant (5R25GM061151-22), CAPAC Program (R25 CA240120), and an NIH-R21 (1R21CA253609-1).

Microbiome Project ideas

Abstract: 20260228_001

Title: The Vieques Septic Systems Project Second Phase

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In September 2019, the Vieques Conservation and Historical Trust (VCHT) received grant funding from U.S. EPA to monitoring the status after improving of old decaying septic systems in five densely populated waterfront neighbourhoods on north coast of Vieques, P.R. If these septic systems are discharging wastewater into the environment, this could become breeding grounds for mosquitoes and vectors of diseases such as dengue and create health problems. The research objectives were to repair of septic tanks or pits have been as ideal places for Aedes aegypti mosquitoes to lay their eggs and educate the communities about what dengue is, recognize the symptoms and when to visit the doctor. In addition, we need to increase public awareness of arboviral diseases like dengue, chikungunya and zika and promote preventive measures to avoid mosquito bites Aedes aegypti. Maps were created of the communities Tortuguero, Lucila Franco, Monte Santo Playa, Morropó and Bravos de Boston to know the septic tank's location. Field inspections to UIS were realized every three (3) months because can be a breeding ground for mosquitoes in any of the following circumstances: when it is open or not properly sealed; when the walls are broken; it has cracks or spaces between the cement blocks; and/or, when the vent is not covered by wire mesh. This represents an additional challenge for the control of vectors that transmit arboviral diseases. In addition, we work together with The Arboviral Disease Report (https://www.salud.pr.gov/CMS/365).This report is produced weekly by the Disease Surveillance System Arbovirals of the Health Department of Puerto Rico (HDPR) through the Division of Epidemiology and Research. It is produced after validating and analyzing the epidemiological information related to the samples received for analysis. The field study was carried out from April to June 2020 to June 2025. The goals of the project were establishing a mosquito and vector control program of Municipality of Vieques to inform them of the risks of vector-borne disease and help them better protect themselves. As public health recommendations we teach to residents how check that wells are free of cracks and that they are sealed or hermetically covered, ventilation tubes should be covered with mesh or wire mesh to prevent mosquitoes were entering. In the case of abandoned UIS or those that are not in use, the must be filled with sand or gravel. Will continue the epidemiological surveillance effort to prevent arboviral diseases.

Keywords: septic systems, public health, mosquito and vector control program

Abstract: 20260228_007

Title: From High Microbial Diversity to Functional Soil Health: An Early-Stage Regenerative Soil Experiment in Tropical Avocado Orchards

Author: Josefina Arce-Quiñones[1]*,Betzaida Ortiz-Carrión[2],

Institution: University of Puerto Rico, Rio Piedras Campus, Agroempresas Atabey, Santa Isabel, PR

Regenerative agriculture often assumes that increasing soil microbial diversity will inherently lead to improved soil health, resilience, and disease suppression. However, early metagenomic analyses conducted at Finca Atabey (Santa Isabel, Puerto Rico) challenge this assumption. BeCrop functional microbiome profiles from two avocado orchard soils with contrasting histories (San Antón and Jacagua) revealed a clear decoupling between microbial diversity and functional soil health: one site exhibited very high microbial biodiversity but low resilience, low biocontrol potential, and elevated risk of opportunistic pathogens, while the second showed lower diversity but greater functional stability.

This contribution presents an early-stage, field-based experimental framework designed to explore how soils can transition from high microbial diversity toward organized, resilient, and functionally regenerative microbiomes under tropical perennial cropping systems. The proposed design integrates (i) metagenomic functional profiling, (ii) low-cost field indicators of biological activity and soil physical condition (soil respiration, infiltration, aggregate stability), and (iii) a targeted set of chemical measurements selected for mechanistic relevance rather than completeness. Chemical variables include pH, electrical conductivity, organic carbon, phosphorus availability, and cation balance (Ca, Mg, K, Na, CEC), chosen to evaluate how soil chemical environments constrain or enable microbial function, plant–microbe signaling, and system resilience.

Rather than reporting completed outcomes, this poster outlines the conceptual framework, experimental design, and predicted trajectories over 6–12 months under regenerative management (permanent ground cover, carbon inputs, reduced disturbance). The goal is to foster interdisciplinary dialogue and attract collaboration with microbiologists interested in linking microbial community function, soil chemistry, and physical structure in real agricultural systems, and in co-developing accessible, field-relevant approaches for monitoring soil regeneration.

Abstract: 20260228_016

Title: The role of the skin mucus microbiome in shaping development of sensory systems in *Astyanax mexicanus*

Author: Alana López-Cruz[1,2,3], Axel Y. Rodríguez-Cortés[1,2], Claudia B. Carrión-Maldonado[1,2], Cristopher L. Montes-Cuevas[1,2,3], Jean M. Mendoza-Anduce[1,2,3], Roberto E. Rodriguez Morales[1,2,3], PhD

Institution: University of Puerto Rico, Medical Sciences Campus[1], Molecular Research Center[2], University of Puerto Rico, Río Piedras Campus[3].

The skin constitutes the primary physical barrier between vertebrates and their external environment. In fish, the skin harbors a diverse and metabolically active mucus-associated microbiota that contributes to immune regulation, tissue homeostasis, and developmental signaling. The skin mucus microbial community plays crucial roles for fish holobionts, impacting the cellular function at tissue integrity of superficial sensory systems. An example of these in fish is the mechanosensory lateral line, a system composed of composed of superficially located neuromasts that contain central hair cells that are important for water current detection, as well as prey and predator interactions. These neuromasts are numerous and undergo tightly regulated developmental processes involving cell migration, differentiation, patterning, and later on, regeneration. Because of its superficial nature, it is reasonable to expect that the skin microbiome may impact development, function and integrity of neuromasts in the lateral line. We propose to test this. However, the relationship between skin-associated microbial communities and lateral line development and function remains largely unexplored. Here, we propose to use the Mexican tetra, *Astyanax mexicanus*, as a model system to explore how environmentally driven variation in skin mucus microbiota may contribute to the developmental and evolutionary diversification of mechanosensory systems. Taking advantage of the availability of populations of this species adapted to different ecosystem throughout thousands of years (rivers versus caves), we will test whether these environmental conditions induce changes in the skin microbiome, and whether these impact natural expansions of cavefish lateral lines that have been previously documented. This work will be a steppingstone in a large unexplored field elucidating the complex interplay between superficial microbial communities and sensory systems.

Funding: (NIGMS-NIH) P20 GM156713, RCMI U54 grant MD007600, 5R16EY037336-02

Keywords: development, sensory systems, skin microbiome

Abstract: 20260228_022

Title: The impact of the gut microbiome on sleep behavior in Astyanax mexicanus

Author: Oswaldo L. Echevarría-Bonilla[1,2,3], Roberto E. Rodríguez-Morales[1,2,3,] PhD

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Sleep is a fundamental physiological process essential in metabolic homeostasis, immune regulation, and neurocognitive function. Although sleep duration and timing vary across species, sleep function seems to be highly conserved throughout the animal kingdom. Despite its essential role, the prevalence of sleep disorders is increasing in modern society. While significant advances have been made in understanding the neural mechanisms that regulate sleep-wake cycles, growing evidence highlights the contribution of peripheral organs, particularly the digestive system, in modulating brain function and behavior via the gut-brain axis. The gut brain axis facilitates bidirectional communication between the gastrointestinal tract and the central nervous system, with recent evidence supporting gut microbiota dysbiosis' effects on sleep and circadian regulation. However, establishing causal relationships between microbiota diversity and specific host phenotypes remain a major challenge. Thus, identifying the evolutionary and ecological factors between and within species is crucial for understanding sleep function in a broader scale. Here, we propose to use the Mexican tetra, Astyanax mexicanus, as a model system for investigating how environmentally driven microbial fluctuations can impact sleep function. This is an ideal model to ask this question as it is composed of diurnal surface-dwelling populations and blind cavefish that reduced sleep and circadian rhythmicity. Using A. mexicanus, we can disentangle the relationships between environmental pressures, adaptation of microbiota between habitats and populations, and sleep variation. We will assess whether environmentally associated differences in gut microbiota composition are present across populations and whether these differences are associated to sleep function. This work aims to elucidate how gut microbial diversity may contribute to sleep regulation, trait adaptation, and behavioral evolution, and will ultimately shed light on the mechanisms underlying sleep variation in the context of microbiota change.

Keywords: sleep, trait adaptation, gut microbiome

Funding: (NIGMS-NIH) P20 GM156713, RCMI U54 grant MD007600, 5R16EY037336-02

Abstract: 20260228_079

Title: The impact of darkness on foraging and gut microbiota of surface fish of the Mexican tetra surface fish, Astyanax mexicanus

Author: Antonio José Morales Cintrón[1,2,3], Homar A. Cardona-Sierra[1,2,3,] Adrián J. Rivera-Rodríguez[1,2,3], Dhalma I. Bayrón-Ho[2,3], Valeria De La Rosa-Reyes[1,3], Roberto E. Rodríguez-Morales[2,3]

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Background: Animals rely on sensory and neural systems to find food and survive, and these are influenced by environmental changes, including habitat-induced variation in the microbiome. These changes may impact foraging strategies across the evolution of a number of species, including fish populations of the Mexican tetra, Astyanax mexicanus. This species consists of two morphotypes: the surface dwelling and multiple cave dwelling populations that evolved independently in dark environments, developing a loss of vision and compensating mechanosensory systems that impact prey capture strategies. While sensory systems have been largely implicated in adaptation of foraging, less is known about how gut microbiota diversity affects these types of behaviors. In surface morphs foraging geometry, defined by their angle and distance, differs from cave adapted morphs since they depend mostly on vision. However when in darkness, surface fishes' foraging measurements shift, relying more on their lateral line.

Methods: To determine if surface dwelling fish adopt cave dwelling feeding behavior, in which the fish angles itself so that its posterior is pointed upwards, we raised a population of surface fish in complete darkness and run through an 18 hour acclimatation,and 40 minute feeding assay in which the fish is later analyzed and angularly measured through an image processor named FIJI to determine if the behavior exhibited was in fact adopted manner of feeding.

Results: Preliminary data shows that the surface fish are adopting cave dwelling feeding behaviors. The first 10 of the 12 assays show fish positioning themselves in angles of 45°-90° which are only seen on the cave morphotypes.

Conclusion: Our findings suggest that behavioral differences that were thought as evolutionary adaptation may be driven by environmental change and not strictly on fixed genetic traits. This means that cave fish didn't evolve unique feeding strategies but exploit latent neural abilities that could be unmasked by environmental perturbations, including gut microbiota manipulations. Using gnotobiotic approaches, future work could shed light on whether cave-like foraging could lead to differences in microbiota diversity and composition, or vice versa.

Keywords: Astyanax mexicanus, Foraging behavior, Gut microbiota

Funding: COBRE Puerto Rico Center for Microbiome Sciences (NIGMS-NIH) P20 GM156713

Abstract: 20260228_059

Title: Activation of the NLRP3 Inflammasome Along the Gut-Brain Axis Following Traumatic Brain Injury

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Background: After a traumatic brain injury (TBI), one of the most important events is the activation of the NLRP3 inflammasome, a signaling pathway that promotes neuroinflammation in response to stress or injury. This multiprotein complex activates pro-inflammatory cytokines such as IL-1β and triggers cell death via pyroptosis, increasing the neuronal loss after an insult. Subsequently, this release of pro-inflammatory cytokines affects the gut-brain barrier increasing intestinal permeability. These alterations causes toxic metabolites to seep into the blood amplifying inflammation, both in systemic and neurological aspects, due to sustained activation of the NLRP3 inflammasome.

Methods: We used a weight-drop method, consisting of three separate impacts administered in one week, as a model of repeat concussive TBI in adult female rats. Following behavioral assessments, we will measure for inflammatory biomarkers in serum, cerebral cortex, and ileum tissues collected at 49 days post-injury to evaluate the chronic phase. Protein levels of key inflammasome-related markers, including cleaved caspase-1, IL-1β, IL-18, and TNF-α, will be quantified via ELISA. We will also use metabolomics to assess changes in the gut and brain.

Expected Results: We hypothesize that at 49 days post-injury, TBI will result in sustained elevations of cleaved caspase-1, IL-1β, IL-18, and TNF-α in the brain, serum, and ileum compared to sham controls. We will also use techniques such as immunofluorescent to measure neuronal loss in the brain tissue.

Conclusion: This study aims to characterize the chronic activation of NLRP3 inflammasome along the gut-brain axis following TBI. By demonstrating a persistent pro-inflammatory cytokines in the gut and brain, these findings will support the hypothesis that a continuous self-sustaining inflammatory loop contributes to long-term TBI pathology. This work will establish a basis for future studies characterizing the relationship between chronic gut dysbiosis and sustained NLRP3 activation.

Keywords: rodent model, concussion, inflammation

Funding: P20 GM103642 COBRE Pilot Award, R21 NS119991, Title V Pilot Project

Abstract: 20260228_075

Title: Exploring Edelfosine's Therapeutic Potential in Gut Dysbiosis following an Epileptic Insult

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Background- Epilepsy is a neurological disorder characterized by recurrent seizures driven by neuronal hyperexcitability and neuroinflammation. Emerging evidence indicates that gut dysbiosis contributes to progression of epilepsy and is associated with drug-resistant phenotypes. Current antiepileptic therapies are limited by adverse effects, reduced quality of life, and pharmacoresistance in approximately 30% of patients. To identify novel therapeutic strategies, we are investigating Edelfosine (Ef), a phospholipase C-β (PLC-β) inhibitor, as a potential anticonvulsant while concurrently examining its impact on gut microbiome integrity in a mouse model of epilepsy. Previous ex vivo studies in hippocampal tissue demonstrated that Ef confers neuroprotection against pilocarpine-induced neuronal hyperstimulation. Complementary in vitro findings showed that Ef reduces the transcription of key pro-inflammatory mediators, including TNFα, IL-6, and NFκB1. We hypothesize that Ef-loaded nanoparticles (NPs) will attenuate seizure-like behavior and preserve gut microbiome resilience following an epileptic insult.

Methods- A pilocarpine-induced epilepsy model was used in CD1 mice to evaluate seizure severity and microbiome alterations. Mice received a single pilocarpine injection (240 mg/kg), followed by treatment with Ef-loaded NPs (10 mg/kg) to overcome limited blood–brain barrier permeability. Seizure severity was quantified using the Racine scale during 2-hour daily observation sessions for up to eight days. Fecal samples were collected longitudinally, and gut tissue was harvested on day eight for microbiome profiling using 16S rRNA sequencing.

Results and Conclusions- Pilocarpine administration induced robust seizure-like behaviors, most prominently during the first three days, with persistent effects detectable up to eight days. Ongoing studies with Ef-loaded NPs will determine their efficacy in reducing seizure severity and modulating gut microbiome composition. Successful DNA extraction from fecal and intestinal samples supports downstream sequencing analyses. Collectively, these findings establish a reliable epilepsy model and support the continued evaluation of Edelfosine as a repurposed, neuroprotective, and anti-inflammatory therapy with potential to restore gut homeostasis

Keywords: Gut, Epilepsy, Edelfosine, Dysbiosis, Microbiome

Funding: The Alliance Pilot Project (U54GM133807), COBRE Center for Neuroplasticity (P30GM149367).

Abstract: 20260228_076

Title: Radia/on-Induced Gut Microbiome Altera/ons in Adult Zebrafish: Implica/ons for Endovascular Risk Factors

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Section: innovative ideas, emerging hypotheses, or early-stage proposals in microbiome research. Conceptual and exploratory submissions

The optimal function of the central nervous system depends on multiple important factors, including the balanced composition of the gastrointestinal microbiota. Increasing evidence suggests that radiation-induced microbiome alterations may influence post-treatment inflammatory regulation and patient recovery, highlighting the role of the gut microbiome in treatment outcomes. These findings are pertinent to neurovascular practice, as radiation-based therapies are established treatment options for vascular lesions associated with significant risk if not appropriately treated. Although radiation-associated microbiome changes have been observed in human samples, these studies remain largely associative and do not allow controlled experimentation. To address this gap, we propose a clinical–translational adult zebrafish model to experimentally characterize shifts in gut microbiome composition, particularly affecting core bacterial communities with anti-inflammatory or barrier-supportive functions that may serve as measurable biological indicators of radiation exposure and vascular risk like radionecrosis when neurovascular damage becomes progressive and irreversible. We hypothesize that radiation-induced alterations in gut microbiome composition, can be systematically characterized in adult zebrafish model and may represent a measurable biological indicator associated with radiation exposure and vascular risk factor for radionecrosis. To test this hypotheis, gut microbiome composition will first be characterized under baseline conditions in a adult clinical–translational zebrafish model (Tg(kdrl:mCherry)^y206; Tg(mrc1a:eGFP)^y251) using 16S rRNA gene amplicon sequencing. Following baseline profiling, adult zebrafish will undergo controlled radiation exposure, after which microbiome composition will be reassessed to identify radiation-associated shifts. Then complementary approaches such as shotgun metagenomics are proposed to enable functional pathways and relevant metabolite profiles. Water and diet sequencing will be performed, and intestinal claudin-b expression will be quiantify. This work is directly relevant to microbiome research because it addresses how radiation, an essential and widely used medical intervention, perturbs gut microbiome homeostasis under controlled experimental conditions, with a specific focus on a beneficial taxon linked to epithelial and endothelial integrity. By moving beyond associative human data, this study establishes an experimentally tractable translational model to characterize dose and time-dependent microbiome alterations and to identify microbial signatures that may serve as measurable biological indicators of radiation exposure and vascular risk factors that could be incorporated into pre-treatment patient evaluation.

Keywords: Radia/on microbiome; Adult zebrafish; Endovascular risk factors, Therapy-induced microbiome dysbiosis

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