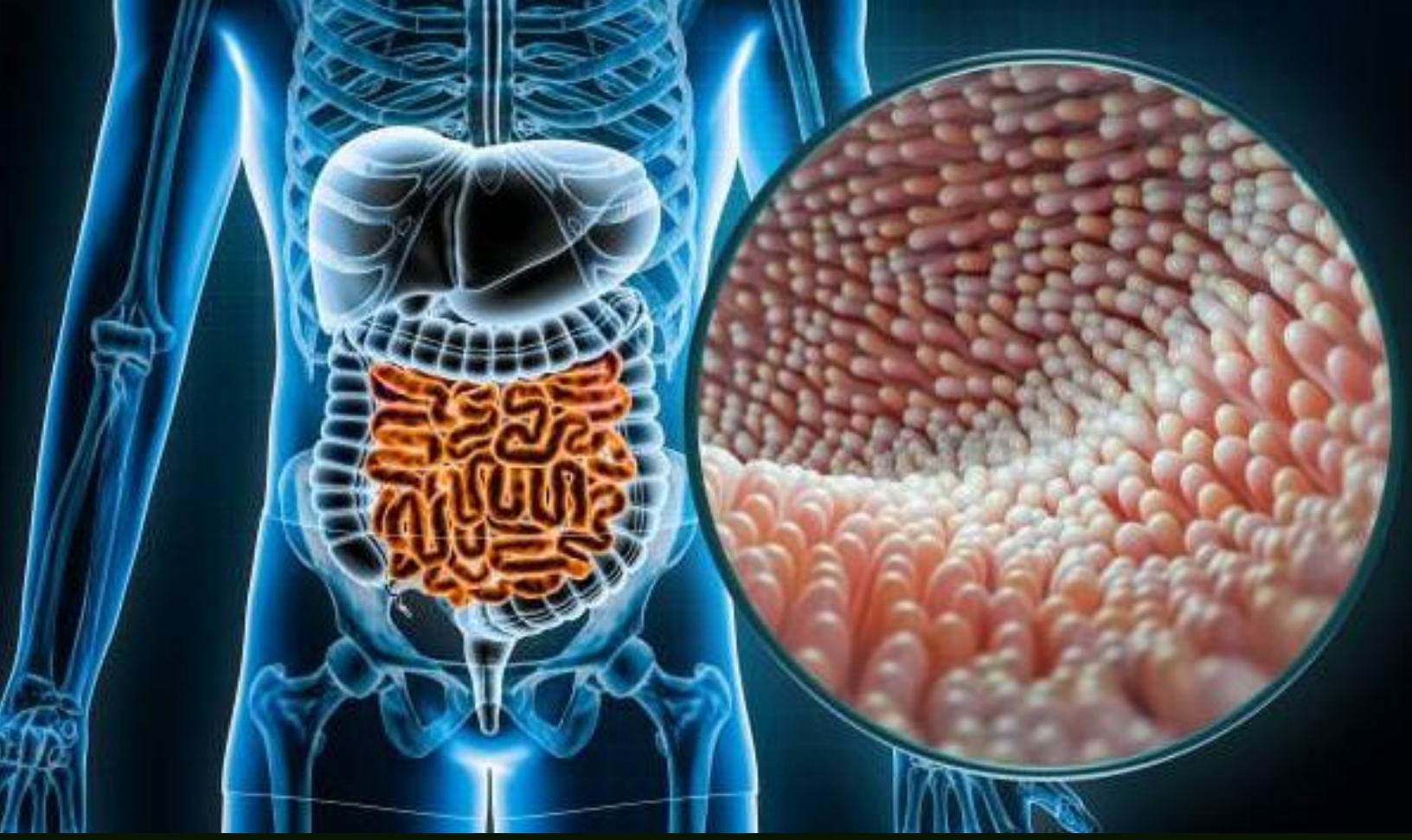

Global Microbiome Congress

May 12th, 2025

www.microbiomecongress.org

PROCEEDING BOOK

sciinov
Excelling in Excellence

Introduction

The Global Microbiome Congress 2025, organized by the Sciinov Group, was successfully held on May 12th, 2025. This global event brought together leading scientists, clinicians, researchers, and thought leaders to explore the intricate relationships between the human microbiome and health, disease, lifestyle, and environmental factors. Discussions focused on how microbiome science is advancing our understanding of human biology, shaping innovative therapeutic strategies, and redefining personalized medicine across various disciplines.

The event provided a platform for both established and emerging voices, with participants from diverse scientific and clinical backgrounds contributing to dynamic discussions about the rapidly evolving understanding of the human microbiome. The Sciinov Group was proud to host this inspiring and impactful congress, which not only highlighted critical advances in microbiome science but also offered hope and actionable insights for improving health outcomes and driving innovation in precision medicine.

Oral Presentations

Tumor-resident Prevotella intermedia reshapes the epigenetic reprogramming of nasopharyngeal carcinoma

Na Liu

Sun Yat-sen University Cancer Center, China

Abstract:

Although cancer is considered as a genetic disease, epigenetic dysregulation are intensively implicated in human cancers, especially nasopharyngeal carcinoma (NPC). As a newly active component, tumor-resident microbiota is present in various types of cancer, however its impact on cancer epigenetic program remains obscure. Here, through an integration of microbiome profiling, methylation sequencing, transcriptomics, clinical analysis, bacterial culture, and in vitro and in vivo experiments, we identified a representative strain Prevotella intermedia, which profoundly reshapes host metabolic signals and epigenetic changes to promote NPC metastasis. DnaK, as a secretory protein of P. intermedia, forms a complex with host glucose regulatory protein 78 (GRP78) to activate the protein kinase R-like endoplasmic reticulum kinase (PERK) /activating transcription factor 4 (ATF4) axis. ATF4 transcriptionally activates the key metabolic enzymes involved in serine, glycine, and one-carbon (SGOC) metabolism, leading to an increased generation of S-adenosylmethionine (SAM). Furthermore, we demonstrate a positive feedback loop in which SAM accumulation elevates H3K4Me3 levels and regulates chromatin accessibility to potentiate the ATF4 function, ultimately synergistically facilitating DNA hypermethylation. Our study reveals a novel epigenetic reprogramming mechanism of host cells modulated by the intratumoral microbiota and provides novel perspectives for future cancer therapy.

Biography:

Dr. Na Liu obtained her M.D. of Oncology at University of South China in 2007 and Ph.D. of Oncology at Sun Yat-sen University in 2013. She is currently a Prociple investigator (PI) in State Key Laboratory of Oncology in South China, Sun Yat-sen University Cancer Center. She has published more than 50 papers in reputed journals

The Influence of Birth Type on Neonatal Gut Microbiota Diversity

Dudas Marcela-Aura

Babes-Bolyai University Cluj-Napoca, Romania

Abstract:

C section birth alters the natural course of intestinal colonization, leading to notable differences in the diversity and abundance of microbial species compared to natural birth. This study aimed to investigate the impact of delivery mode on gut microbial composition during the first three days of life. Fecal samples were collected three days after birth from 49 healthy newborns 34 born vaginally and C section at the neonatology department of the county emergency hospital of tg murex gut micro biota analysis was conducted by sequencing the r-rna gene using the Illumine miseq platform. The study s findings highlight significant differences in the neonatal gut microbiome based on the mode of delivery. Compared to vaginally delivered neonates those born via C section exhibited a markedly lower Shannon index p 0 point 0165, indicating reduced microbial diversity. Additionally, a less balanced microbial community was evidenced by a lower Simpson index p 0 point 0439 in C section-delivered neonates, suggesting a less balanced and stable early gut colonization pattern. Neonates born via C section exhibited a reduced abundance of Bacteroides Lactobacillus, Bifidobacterium and Escherichia coli compared to those born vaginally who showed richer microbial diversity and higher levels of beneficial taxa.These results support the hypothesis that cesarean delivery influences the composition of the gut microbiota, which may have implications for immune development and metabolic health. Further studies are needed to evaluate long-term effects and potential interventions for restoring microbial balance

Biography:

Pronutrition Association, Targu Mures, Romania, founded in 2013, is dedicated to promoting a healthy lifestyle through balanced nutrition and scientific research. Led by experts in clinical nutrition and molecular biology, the organization has implemented multiple community health programs. The association collaborates with academic and medical institutions to advance knowledge in microbiome studies and nutrigenomics. This study is part of a prevention project, An optimal start in life for your child, which involves a multidisciplinary team made up of neonatologists, pediatricians, nutritionists-dietitians and biologists.

Project funded by SNGN ROMGAZ SA

The Impact of Early Microbiota on Infant Health

Camelia Râtea
Babes-Bolyai University Cluj-Napoca, Romania

Abstract:
Alpha-1 Antitrypsin and Eosinophilia Protein X are important biomarkers for assessing gastrointestinal inflammation and immune response in newborns. Their levels can provide insight into potential digestive and immune system imbalances early in life. This study investigates the role of gut micro biota in preventing chronic diseases and immune-related conditions. Fecal samples were collected on the third day after birth from 49 healthy newborns in the Neonatology Department of the County Emergency Hospital of Tg. Murex. Of these 34 were delivered naturally and 15 by C section. Stool samples from all newborns were analyzed to assess Alpha-1 Antitrypsin and Eosinophilia Protein X levels using the ELISA method. The analysis was conducted by Ganzimmune Laboratory, Germany. In the study group 52.7% of newborns exhibited elevated Alpha-1 Antitrypsin levels with higher values observed in boys compared to girls. Additionally, 57.0% of newborns had elevated Eosinophilia Protein X levels surpassing the reference threshold. Newborns delivered via C section showed a higher prevalence of elevated Alpha-1 Antitrypsin suggesting increased intestinal permeability and a greater risk of inflammation. Eosinophilia Protein X levels were comparable between both delivery groups indicating similar immune responses. These findings highlight the influence of birth mode on gut biomarkers and reinforce the importance of early micro biota testing for long-term health monitoring. Understanding these early changes could help guide preventive strategies and interventions to support gut health in newborns. Further research is needed to explore the impact of early micro biota alterations on immune system development and their potential role in disease prevention.

Biography:
Pronutrition Association, Targu Mures, Romania, founded in 2013, is dedicated to promoting a healthy lifestyle through balanced nutrition and scientific research. Led by experts in clinical nutrition and molecular biology, the organization has implemented multiple community health programs. The association collaborates with academic and medical institutions to advance knowledge in microbiome studies and nutrigenomics. This study is part of a prevention project, "An optimal start in life for your child", which involves a multidisciplinary team made up of neonatologists, pediatricians, nutritionists-dietitians, biologists. Project funded by SNGNROMGAZSA MEDIAS.

Precision Bioinformatics in Action: Driving Discoveries from Space Science to Human Health

Emmanuel Gonzalez
McGill University, Canada

Abstract:
Microbial ecosystems are among the most resilient and adaptable on Earth, but what happens when they face extreme conditions like microgravity or chronic illness? Using advanced high-resolution bioinformatics, this work uncovers how microbial communities adapt and respond to some of the most challenging environments: space and the human body.In space exploration, the analysis of micro biota from the Mars500 mission, a 520-day confinement experiment, revealed significant microbial shifts that could inform the design of future long-term missions. Studies of microbial communities on the surfaces of the International Space Station showed unexpected diversity, offering critical insights into microbial survival in microgravity and its potential risks for astronaut health.In human health, these methods have illuminated how the gut micro biome impacts chronic pain conditions, where changes in bile acid metabolizing taxa may influence symptom severity, and colorectal cancer, where specific species play a role in healing post-surgery.This presentation will explore how high-resolution micro biome analysis is not only advancing our understanding of microbial ecosystems in extreme conditions but also paving the way for innovations in medicine and space biology, bridging the gap between cutting-edge research and real-world application.

Biography:
Emmanuel Gonzalez, PhD, is a bioinformatician and researcher at the Canadian Centre for Computational Genomics at McGill University, specializing in bioinformatics methods applied to multiomics. Following the publication of one of his high-resolution bioinformatics pipelines, he was invited to join NASA's GeneLab International Groups, leading to a fruitful collaboration. His contributions include studies on microbial life aboard the ISS, the effects of long-term isolation during the Mars 500 mission, and research on host-microbe interactions in spaceflight. His work was recently featured in Nature Portfolio as part of the SOMA (Space Omics and Medical Atlas) initiative, which represents the largest-ever collection of aerospace medicine and space biology data.
In addition to his work in space science, Emmanuel's expertise extends to human health research, where his contributions have advanced the understanding and treatment of conditions such as chronic pain, fibromyalgia, and colorectal cancer. His bioinformatics tools have driven significant progress in clinical trials and the identification of microbial markers, positioning him as a key player in both space and health-related bioinformatics.

Microbiome swift in membership and function in function of digestive resection in ostomates

Jacques Izard
University of Nebraska Medical Center, United States

Abstract:
The gut micro biome plays a crucial role in maintaining our overall health, and disruption to its composition can lead to a range of health problems. Ostomy creation is a life-saving surgery altering the length of the digestive tract. It is used to treat severe gastrointestinal and medical conditions, including Crohns disease, ulcerative colitis, and colorectal cancer. The understanding of the impact of the differential presence/absence of a colon, as well as the impact of a partial colon on the micro biome and its functional representation, is still nascent. Our approach focused on comparing microbial and expected function representation in the context of digestive resection and control groups. The population was composed of adults enrolled in a remote nationwide cross-sectional stool-sample collection. The comparison of the ileostomy group and the other two groups allowed us to explore the microbial differences between the small intestine and the colon. The ileostomy micro biome had a distinct alpha and beta diversity compared to the other two groups. These differences in membership extend to the functional representation of pathways. These findings suggest that the complex interplay between the host and intestinal micro biota extends to postbiotics, and may influence the quality of life in ostomies

Biography:
Jacques Izard, Ph.D., has been involved for the last 20 years in the human microbiome research field. As the health status of the population is getting more complex, the Izard's laboratory leverages a multi-disciplinary approach to obtain a greater understanding of our microbiome function to empower everyone to nurture a supportive microbiome

Comparative analysis of gut microbiota in long-tailed macaques: Habitat and genetic influences on microbial profiles

Raza Muhammad
Chulalongkorn University, Thailand

Abstract:
The environment, diet, and host genetics play a pivotal role in shaping hosts' gut micro biota composition and health. This study investigates the comparative analysis of gut micro biota between four populations of long-tailed macaques (Macaca fascicular is) including two phylogenetic ally distinct subspecies (M. f. fascicularis and M. f. aurea) inhabiting two habitat types (mangrove forest and island). Employing the full-length16S rRNA gene sequencing on a Nan pore platform, the study investigated the bacterial species richness and evenness between the two subspecies at two habitat types. Two M. f. fascicular is populations that were exposed to anthropogenic food sources exhibited higher bacterial diversity in their gut micro biota compared to their M. f. aurea counterparts living in respective habitats. While Firm cutes and Bacteroidetes emerged as the predominant bacterial phyla within the gut micro biota of both subspecies, however, their relative abundances displayed significant differences. M. f. aurea displayed notably higher relative levels of these phyla compared to M. f. fascicular is. Furthermore, the differential species abundance analysis by LEfSe revealed variations in the gut micro biota between M. f. fascicular is and M. f. aurea, indicating dietary differences corresponding to their respective habitats. In conclusion, this study underscores the intricate relationship between environment, diet, host genetics, and gut micro biota in non-human primates. The study contributes to a broader understanding of how host-environment interactions modulate gut micro biota, emphasizing the role of dietary habits in shaping these microbial communities.

Biography:
Raza Muhammad has completed a PhD in Zoology from Chulalongkorn University, Thailand, at the age of 29. His doctoral research explored the gut microbiome of long-tailed macaques, investigating its interaction with environmental and dietary factors. This innovative work led to publications in reputed international journals. In addition to research, he contributed to academia as a visiting lecturer at Xinxiang Medical University, China, where he shared his expertise in biology and bioinformatics.

Auto-Brewery Syndrome: An Underdiagnosed Condition

Barbara Cordell
Auto-Brewery Syndrome Info & Research, United States

Abstract:
Auto-brewery syndrome (ABS) is a rare infection caused by yeast or bacteria that produces endogenous alcohol and wreaks havoc on people's lives and health. The location of the infection is most often in the GI tract but has also been found in the bladder and oropharyngeal cavity. Patients are accused of lying and are often turned away by primary providers and specialists. Conventional medical treatments sometimes help, but many sufferers continue to have "flares" where they are intoxicated without ingesting alcohol. Often extraordinarily high blood alcohol levels are detected while the patient continues to function, albeit not optimally. Fecal micro biota transplants have been used in three extreme cases to date. A holistic functional approach to treatment that includes nutritional and psychosocial counseling is warranted in nearly all cases of ABS.

Biography:
Barbara Cordell earned her doctoral degree in Health Counseling at the University of Utah. She worked as Dean of Health Sciences at a local college and a Holistic Nursing private Consultant for over twenty years. She now spends her time advocating for patients with auto brewery syndrome (ABS) and their caregivers. She has numerous publications on ABS.

Systemics Effect of the Aging Microbiome on Metabolism and Health

Arianna Lamanna
*Luxembourg Centre for Systems Biomedicine, L*uxembourg

Abstract:
The gut microbiome is made of around 4 trillion microorganisms, predominantly bacteria, which play an important role in the nutrient digestion as well as in the general immune response. The dysbiosis and alterations of the gut microbiome can lead to an overreaction of the immune system and so to inflammation and autoimmune disease like the inflammatory bowel disease.
In the following project, the effects of high fat diet and exercise on different strains of BXD mice, with diverse susceptibilities to metabolic diseases, are analyzed during their lifespan.
Associations between certain bacteria and metabolic diseases have been identified by analyzing the meta-genome and meta-transcriptome in parallel with the transcriptome of the host's cecum. This has been achieved by performing classical bioinformatic analysis, but also by implementing different machine learning algorithms, permitting multi-omics integration.
The genera Lactococcus, Bacteroides, Lachnospiraceae_unclassified and the unannotated genus GGB28904 are more abundant in mice fed with a high fat diet, whereas the genera Prevotella, Duncaniella and Heminiphilus are more abundant in those fed with a chow diet, considered as healthy. A decrease in the abundance of the genera Lachnospiraceae_unclassified and GGB28904 has also been observed in mice with access to voluntary exercise.
These findings will guide us in designing mechanistic experiments to understand how health can be improved by altering the microbiome composition, which may become an indispensable pillar to precision medicine through gut microbiome engineering

Biography:
Arianna Lamanna is a PhD student at Luxembourg Centre for Systems Biomedicine, an interdisciplinary centre of the University of Luxembourg, in the research group Gene-Expression and Metabolism led by Associate ProfessorEvan Williams. She has completed a bachelor's degree in physics at the University of Luxembourg and a master's degree in systems biology at Maastricht University.

Microbiota-gut-brain axis in the progression of cognitive disorders associated with Alzheimer's disease

Mirko Paparella
Institute for Bioengineering of Catalonia (IBEC), Spain

Abstract:
Alzheimer's disease (AD) is one of the major global health challenges, with no effective treatments. Epidemiological studies indicate that AD has a long prodromal phase starting 15–20 years before clinical symptoms appear. Alterations in gut microbiota composition have been observed in AD patients, and these changes may influence neuroinflammation and contribute to early disease progression. This study proposes an integrated approach using humanized murine models (APP/PS1 transgenic mice) and Drosophila melanogaster screening to better understand the role of microbiota in AD and develop targeted interventions. From a larger longitudinal study, 90 representative samples were selected, including healthy controls, AD patients, and individuals with mild cognitive impairment (MCI), of whom half developed AD over the three-year observation period (MCI-AD). Using shotgun metagenomic sequencing, we characterized the gut microbiota composition. In parallel, metabolomics analysis allowed us to evaluate key metabolites involved in gut-brain communication, such as short-chain fatty acids, bile acids, trimethylamine , tryptophan metabolites, lipids and one carbon metabolism, previously associated with cognitive decline and AD progression. The impact of different bacterial strains on disease progression was assessed in flies through multiple cognitive tests and histological analyses. In mice, fecal microbiota transplantation was performed using samples from healthy donors and individuals with MCI-AD to investigate the role of gut microbiota in cognitive decline. Additionally, the combined effect of microbiota modulation and probiotic supplementation was evaluated. To explore potential mechanisms, epigenetic analyses of the hippocampus were conducted to assess microbiota-driven changes in gene regulation associated with neurodegeneration.

Biography:
Mirko Paparella completed his Master's Degree in Biology Science and Human Nutrition from Università Campus Bio-Medico di Roma in 2023. He is currently a researcher at the Genomics Unit of IBEC (Institute for Bioengineering of Catalonia) in collaboration with the Center for Omic Sciences at EURECAT. His research focuses on genomics, epigenetics, and the gut-microbiotabrain axis, particularly in Alzheimer's disease and antibiotic resistance..

HDAC3 integrates TGF-Beta and microbial cues to program tuft cell biogenesis and diurnal rhythms in mucosal immune surveillance

Jianglin Zhang
Carnegie Mellon University, United States

Abstract:
The intestinal mucosal surface is directly exposed to daily fluctuations in food and microbes driven by 24-hour light and feeding cycles. Intestinal epithelial tuft cells are key sentinels that surveil the gut luminal environment, but how these cells are diurnally programmed remains unknown. Here, we show that histone deacetylase 3 (HDAC3) controls tuft cell specification and the diurnal rhythm of its biogenesis, which is regulated by the gut microbiota and feeding schedule. Disruption of epithelial HDAC3 decreases tuft cell numbers, impairing anti-helminth immunity and norovirus infection. Mechanistically, HDAC3 functions noncanonically to activate transforming growth factor–β (TGF-β) signaling, which promotes rhythmic expression of Pou2f3, a lineagedefining transcription factor of tuft cells. Our findings reveal an environmental-epigenetic link that controls the diurnal differentiation of tuft cells and promotes rhythmic mucosal surveillance and immune responses in anticipation of exogenous challenges.

Biography:
Dr. Jianglin Zhang obtained his PhD at Zhejiang University in 2019 at Hangzhou, China, followed by postdoctoral studies at the University of Sourthern Carlifornia and the Carnegie Mellon University. He is currently an faculty in the Department of Biological Sciences at the Carnegie Mellon University. Dr. Jianglin Zhang has published 14 research papers in prestigious journals including Science Immunology His research focuses on the interplay between gut microbiota, epigenetic regulation, and circadian rhythm in the intestine, with particular emphasis on their roles in controlling pathogen infections and metabolic diseases.

Canine Gut Benchmark: A 106 GB Cross-Platform Dataset Exposing Extraction, Primer, and Sequencing Biases in Metagenomics

Balázs Kakuk
University of Szeged, Hungary

Abstract:
Reproducible metagenomic insights depend on harmonised laboratory workflows, yet cross-platform benchmarks that span the entire wet-lab pipeline are still limited. We created an open, 106 GB multi-omic resource that quantifies how DNA extraction, primer design and sequencing technology interact to shape gut-microbiome profiles. Using the dog gut —an established proxy for the human microbiome—we:
Deep-benchmarked a reference stool sample with five extraction kits, eight library chemistries and four sequencing platforms (short- and long-read WGS, full-length 16S).
Profiled 40 longitudinal canine samples processed in parallel with two widely used extraction kits to capture population-scale effects.
Compared three full-length 16S primer sets (standard ONT, degenerate ONT, PacBio) across synthetic mocks, human stool and canine stool to expose primer-driven taxonomic distortions.
Cross-species analysis of the primer-comparison revealed that in some cases (e.g., Bifidobacterium, Ruminococcus), the human fecal reference mock community's relative abundance aligned more closely with the canine than the human sample, reaffirming reports that the canine gut microbiome more closely mirrors the human counterpart than those of traditional rodent models. Extraction chemistry explains the largest share of compositional variance; degenerate primers rescue under-represented clades such as Bifidobacterium; and long-read WGS helps disentangle platform-specific biases that confound short-read studies.
All raw reads, metadata and R scripts are publicly released, offering a plug-and-play benchmark for validating human metagenomic pipelines, optimising cross-study comparisons and designing translational dog–human projects. By delivering a rigorously controlled, species-bridging testbed, we provide actionable guidance for standardising gut-microbiome workflows that will accelerate reproducible discoveries in human health research.

XA-511: A Live Biotherapeutic Product That Enhances The Efficacies Of ICI Therapies Through Reprogramming Of The Tumor Microenvironment

Christophe Bonny
Xbiome, China

Abstract:
The XA-511 lines of wt and genetically modified bacteria are the first therapies aimed at selectively modifying the tumor microenvironment (TME) for improving the efficacies of ICI treatments. XA-511 wt were found to be specifically associated within the tumors of long-term survivors of pancreatic cancers (Frontiers in Immunology, 2022, 785422).
The TME represents a significant barrier to the efficacies of ICIs as its mostly immunosuppressive components limit T-cell activation and induces T-cell dysfunction. XA-511 have shown high capacity to reprogram important aspects of the immunosuppressive TME by consuming lactate, normalizing pH, locally releasing high concentrations of relevant SCFAs, and metabolizing adenosine to inosine. Following iv administration, XA-511 colonize and expand within the hypoxic tumor niches, from where they generate massive T-cells infiltration, reduce tumor masses and prevent metastatic events. Concomitantly, these strict anaerobes are unable to survive in healthy, normoxic organs; they also produce under-acylated LPS variants which act as antagonists of the TLR4s. Altogether, these properties allow for maximal intra-tumor efficacy, while avoiding the generation of a "cytokine storm" or scepsis. XA-511 administration thus appears to be presenting a very favorable safety and tolerability profile.

As a re-programmer of the TME, the XA-511 bacteria should be considered in combination treatment together with CPI and other immune-based therapeutical modalities including CAR-T and vaccines.

Accepted Abstracts

Utilizing AI Derived Bioinformatic Methods which Identify Strain-Level Differences in Consumer Microbiomes

Oliver Worsley
Sequential, United Kingdom

• Discussing the use of AI identifying new targets for qPCR probe sets
• Exploring the resilience of the skin microbiome down to an intra-species level
• Interpreting the impacts of active ingredients, preservatives, and pH changing
ingredients on the diversity of consumer microbial communities.
In this presentation, we will explore three interconnected topics in microbiome research and technology. First, we'll discuss how artificial intelligence (AI) can be leveraged to identify new targets for quantitative PCR (qPCR) probe sets, potentially improving the accuracy and efficiency of microbial detection. Next, we'll delve into the resilience of the skin microbiome, examining how stability and adaptability are maintained at an intra-species level. Finally, we'll interpret the effects of active ingredients, preservatives, and pH-altering components onthe diversity of microbial communities in consumer products. This research aims to advance our understanding of microbiome dynamics and enhance the design of targeted microbial interventions.

Biography:
Prior to co-founding Sequential, Oliver completed his PhD in molecular genetics as an A*STAR scholar at the Genome Institute of Singapore, and has won multiple awards including the P&G Young Entrepreneurship Scheme; the top prize at the L'Oréal Innovation Runway, and is a scholar at the Royal Academy of Engineering. Oliver has published >150 articles for the Fierce Health publication, under John Carroll. He completed his BSc with honours in pharmacology at Edinburgh University, including six months at Leiden University Medical Centre through the Erasmus Programme. Sequential is a pioneer in the skin microbiome world. Having initially launched the world's first at-home, consumer skin microbiome test in 2019, and with over 4 years of R&D into the human microbiome have developed out their R&D testing and formulation platform. They are backed by the global leaders such as Innovate UK, Enterprise SG, A*STAR, Genome Institute of Singapore, SOSV, Metaplanet, Scrum Ventures, Corundum Systems Biology, and operate three independent labs in London, Singapore and NYC.

Cutaneous bacterial endocrinology: The dialog between neurohormones and the cutaneous microbiota at the center of skin homeostasis.

Marc G.J. FEUILLOLEY
University of Rouen Normandy, France

Abstract:
The cutaneous microbiota is the second of the human body by its size and diversity. It is also the first barrier between the environment and our skin, protecting against pathogens, pollutants and UVs but also modulating skin regeneration, training local immunity and regulating inflammation. It appears nowadays that these roles are linked to a continuous dialog between the microbiota and skin through hormones, neurotransmitters and bacterial analogs of eukaryotic communication factors. Indeed, cutaneous bacteria among the more abundant, such as Staphylococcus epidermidis and Staphylococcus epidermidis synthesize γ-aminobutyric acid (GABA) while Cutibacterium (former Propionibacterium) acnes is known for producing high amounts of histamine that can diffuse into the skin. Corynebacteria release glutamate while many skin bacteria encode for a ClpB orthog, an α-MSH mimic protein. Until now, the role of those factors has been poorly studied. Conversely, we have shown that skin bacteria can sense neurohormones and neurotransmitters released locally in skin, such as Substance P, Calcitonin Gene Related Peptide, natriuretic peptides (ANP, CNP) and catecholamines (adrenalin, noradrenaline). Even steroid hormones can act on bacteria as demonstrated with estradiol on Lactobacillus crispatus in the vaginal environment. This capacity of bacteria to detect host hormones is linked to the expression of multifunctional proteins and "moonlighting proteins", such as EfTu, DnaK, AmiC, KdpD or SPFH acting both as surface signal transducers, chaperones and translational factors allowing bacterial adaptation. A role of skin neurohormones in phages expression is even suspected. Cutaneous bacterial endocrinology is a recently emerged research field with immense perspectives.

Biography:
Marc Feuilloley is Professor at the University of Rouen Normandy. He was Director of the Laboratory of Microbiology Signals and Microenvironment (LMSM EA4312) for 12 years and is now head of the team "Communication in the Human Microbiota" of UR4312 CBSA and Director the Expertise Center Cosmetomics@URN. Board member of Rouen University and industrial networks such as Cosmetic Valley and PôlePharma, he is the author of 256 articles in international peered journals, 7 books or journal special issues and 228 invited and oral communications. (H-index: 50)

Targeted Microbiome Strain Analysis using SIMBA Capsule Showed Fecal Samples may not Accurately Represent the Relative Abundance of key Strains in the Small Intestine for Gut-Brain Axis

Joseph Wang
University of Calgary, Canada

Abstract:
Introduction
The metabolic activities of the gastrointestinal (GI) microbiota have a wide-range effects on influencing neurotransmitter synthesis, immune function, and inflammation [1-2]. Tryrosine-decarboxylating (TDC) bacteria are of particular interest, as they produce the neurotransmitter dopamine from the breakdown of L-Dopa and play a significant limiting factor in the efficacy of Parkinson's Disease treatment [3]. Traditionally, fecal sampling has been the primary approach for studying microbial metabolism in the GI, however it fails to capture the activity of the small intestine (SI) where the majority of the L-Dopa absorption occurs [4]. The gold standard endoscopy aspirate may similarly not be representative of the … The Small Intestinal MicroBiome Aspiration (SIMBA) Capsule has been developed and clinically validated to sample and preserve the SI microbiota collected from humans [5-6]. This preliminary study aims to demonstrate that SIMBA can detect and characterize TDC species in a larger population cohort.
Method
In total, 87 individual SI luminal samples collected using the SIMBA capsule along with a matching fecal sample were selected, which also included a subset of 13 individuals from a previously published clinical cohort study [6] with additional matching endoscopic aspirate and saliva samples. All samples were subject to paired-end shotgun metagenomics sequencing to an average sequencing depth of ~11GB. Following downstream human host-read read removal and read quality filtering, high-quality reads were taxonomically profiled using Kraken2 [7] and species relative abundance was re-estimated with Bracken [8]. To examine the detectability of TDC species across the GI tract, sample taxonomic profiles were analyzed for the presence of three previously characterized TDC species, Enterococcus faecalis, Enterococcus faecium, and Levilactobacillus brevis (formerly Lactobacillus brevis) [3].

Biography:
Dr. Gang Wang earned his B.Eng in Bioengineering from the National University of Singapore in 2010 and completed his Ph.D. in Biomedical Engineering at the University of Calgary in 2017. He is the co-founder and Chief Technology Officer (CTO) of Nimble Science, a health technology company commercializing the SIMBA GI Platform, an advanced capsule sampling technology that collects endoscopic quality intestinal liquid biopsies directly from the small intestine. He has published 20 papers of in reputed journals in the fields of biomedical engineering, medical devices and medical imaging.

Integrative multi-omic analysis reveals oral microbiome-metabolome signatures of obesity

Aashish Jha
New York University Abu Dhabi, United Arab Emirate

Abstract:
Obesity is a major global health challenge and a leading risk factor for cardiometabolic disorders. The global surge in obesity, driven by industrialization and the widespread consumption of lowfiber, ultra-processed food, highlight an urgent need for deeper biological insights. While the gut microbiome has been studied in the context of obesity, the contribution of the oral microbiome– the second largest microbial ecosystem in the human body– remains largely underexplored. Here we report findings from a deeply-phenotyped prospective-cohort of 628 Emirati adults, leveraging amplicon sequencing of mouthwash samples and multi-omics profiling and functional and metabolic activity analysis of 97 obese individuals and 95 matched controls, making this the most comprehensive multi-omics analysis of the oral microbiome. We identified significant differences in oral microbial diversity, composition, functional pathways, and metabolic profiles between obese and non-obese groups. Integrated multi-omics analysis of the 192 matched metagenomes and metabolome samples uncovered significant metabolic reprogramming and altered energy regulation in obesity. Specifically, the oral microbiome of obese participants were enriched for the proinflammatory Streptococcus parasanguinis and Actinomyces oris, and the lactate-producing Oribacterium sinus. Many microbial pathways involved in dietary carbohydrate metabolism, histidine degradation, as well as the production of obesogenic biomolecules were also enriched in obese participants; however, B-vitamin and heme production pathways were depleted. Consequently, metabolites resulting from these pathways such as lactate, histidine derivatives, choline, uridine, and uracil were elevated in obesity. These consistent microbiome-metabolite shifts were strongly associated with prominent obesity-associated cardiometabolic markers, including serum triglycerides and alkaline phosphatases. These findings provide the most comprehensive insights into how disrupted microbial-metabolic cross-talk in the oral cavity may contribute to obesity and related cardiometabolic disease risk, underscoring the potential of targeting of oral microbiome-host interactions as a novel avenue for obesity prevention and intervention.

Comparative Analysis of Gut Microbial Diversity in Early Decomposition Stages of Human Cadavers in Thai Population

Ameer Muhammad Khan
Chulalongkorn University, Thailand

Abstract:
The human microbiome plays a crucial role in maintaining health and normal functioning during life, yet its fate after death remains poorly understood. Microbial communities are integral to the decomposition process, with their post-mortem succession offering potential forensic applications, such as estimating the post-mortem interval (PMI). While research in temperate climates has advanced our understanding of microbial activity during decomposition, studies in tropical regions, such as Thailand, are limited. Tropical climates, characterized by higher temperatures and humidity, likely influence microbial activity and succession differently compared to temperate zones.
This study investigates microbial diversity in human cadavers during the fresh and late fresh decomposition stages within the first 1–12 hours post-mortem in Thailand's tropical environment. By focusing on the cecum, this research aims to elucidate microorganisms' biochemical and metabolic processes in this critical early PMI period. The findings will provide essential data on microbial dynamics in tropical climates, addressing significant gaps in forensic science. This study can potentially improve forensic methodologies, offering more reliable PMI estimation models tailored to tropical regions and enhancing forensic investigations in Thailand and similar environments.

Biography:
My name is Ameer Muhammad Khan. I hold a Bachelor's degree in Biotechnology from Pakistan. During my undergraduate studies, I published a first-author research paper and a review article. Currently, I am pursuing a Master's degree in Forensic Sciences at Chulalongkorn University, Thailand. .

Comparative Analysis of Gut Microbiota in Post-Mortem Chronic Alcoholics versus Minimal to No Alcohol Users in the Thai Population

Laiba Pervez
Chulalongkorn University, Thailand

Abstract:
This study aims to investigate and compare the microbial composition of post-mortem cecum and feces samples in chronic alcohol users and non-alcoholic control groups. The objective is to identify alterations in gut microbiota linked to long-term alcohol consumption and to explore how microbial taxa differ between the cecum and feces across both groups.
Post-mortem samples from chronic alcoholic individuals and non-alcoholic controls will be collected. DNA will be extracted from the cecum and feces samples, followed by amplification of the bacterial V3-V4 region of 16S rRNA gene using universal primers through PCR. The amplified products will be sequenced using the Illumina MiSeq platform. Sequencing data will be analyzed using QIIME 2 to evaluate microbial composition and relative abundance changes between gut regions and between the two groups.
It is anticipated that microbial diversity will differ between chronic alcohol users and controls. These microbial shifts may reveal alcohol-induced dysbiosis, providing valuable information on the microbial changes linked to long-term alcohol consumption.
By identifying specific microbial alterations in the gut microbiome of chronic alcohol users, this research aims to contribute to the understanding of alcohol-induced gut dysbiosis. The results of this study could have significant implications in clinical diagnostics and forensic science, helping to trace microbial changes in alcohol-related post-mortem cases

Biography:

ZMy name is Laiba Pervez. I hold a Bachelor's degree in Biotechnology from Pakistan. During my undergraduate studies, I published a research paper and a review article. Currently, I am pursuing a Master's degree in Forensic Sciences at Chulalongkorn University, Thailand.

Abstract is accepted and will be included in the conference proceedings

Mario Villamiel
Terranima, Italy

Abstract:
Although seemingly independent, the soil and the gut microbiomes have astonishing similarities in regard to their structure, function, and importance for the health at the ecosystem level.
In plants, the rhizosphere acts as an external digestive system, where roots exudates feed and attract microbial communities that bring nutrients, vitamins, hormones, and even water using mycorrhizal fungi, in exchange. This relationship is beneficial to both plants and soil microbiota and is important for the health and resilience of the ecosystem.
Similarly, the gut microbiome plays a crucial role in human health. Apart from the digestion process itself, it is intimately connected to our immune system, physical and emotional well-being, and even our behavior. Latest studies on the gut-brain axis reveal that communication between the gut and brain is predominantly gut-driven, highlighting its role in mood regulation and decision-making processes—a connection hinted at by the well-known expression “gut feeling.”
This presentation will explore these two micro worlds and their interaction. By drawing on insights from microbiology, neuroscience, and agricultural science, we aim to foster a deeper understanding of how regenerative agriculture practices can support soil health, and in turn, contribute to the cultivation of healthier food systems and human well-being. This approach highlights how everything in life is connected and shows the crucial role microbiomes play in keeping nature and our bodies in balance.

The gut microbiota modulates anastomotic healing in patients with colorectal cancer undergoing surgery

Manuela Santos
Université de Montréal/CRCHUM, Canada

Abstract:
Anastomotic leak (AL) is a major complication in colorectal surgery and significantly increases morbidity and mortality. Our objective was to investigate the role of gut microbiota in anastomotic healing. Preoperative fecal samples were collected from patients with colorectal cancer (CRC). Fecal microbiota transplantation (FMT) was performed in mice using samples from patients with and without AL, after which transplanted mice underwent colonic surgery. At day 6 after surgery, anastomotic healing, gut barrier integrity, and gut microbiota composition were analyzed. Bacteria of interest were isolated and assessed in vitro and in vivo. We found that, compared to mice transplanted with fecal microbiota from donors without AL, mice receiving fecal transplants from donors with AL displayed poorer anastomotic healing, increased gut permeability, and higher levels of colonic pro-inflammatory cytokines, resulting in higher AL rates. We identified a strain of Parabacteroides goldsteinii, which exerted a beneficial anti-inflammatory effect and improved anastomotic healing, and a deleterious Alistipes onderdonkii strain, which promoted inflammation and increased leakage. In conclusion, gut microbiota plays an important role in surgical colonic healing in patients with CRC, paving the way toward microbiota-targeted interventions to improve anastomotic healing and prevent AL.

Fabrication of a plant-based nutrition bar to enhance gut microbiome brain interactions and validation of effects on Zebra Fish (Danio Rerio)

Chandini Lokkashri Sai Balaji
University College Dublin, Ireland

Abstract:
University College DublinThe interconnection between the gut microbiome and brain function has garnered significant scientific interest, highlighting the impact of diet on cognitive and physiological well-being. This study presents the fabrication and development of a plant-based nutrition bar to enhance gut microbiome-brain interactions. Validation studies were conducted on Zebrafish (Danio rerio), which serves as an effective model due to its physiology and the feasibility of gut extraction for microbial analysis following controlled dietary interventions Utilising cost-effective, nutritionally rich ingredients, the formulation was optimised to support gut microbial diversity and neurotransmitter synthesis. Comprehensive nutritional, physical, and microbial analyses confirmed the bar's efficacy and safety.
The experimental phase involved subjecting zebrafish to varying doses of the nutritional bar, followed by extraction and bacterial colony identification. DNA sequencing revealed the presence of beneficial microbial strains known for their roles in triggering the synthesis of necessary neurotransmitter modulation. The results indicate a promising link between dietary intervention and improved gut microbiome composition, potentially leading to enhanced mental health outcomes.
While these findings provide compelling evidence supporting the role of dietary components in microbiome modulation, the scope for future exploration remains vast. Further studies are required to delineate the mechanistic pathways involved, optimise formulations for human consumption, and assess long-term impacts on cognitive function. This research underscores the immense potential for dietary innovations in therapeutic and preventive healthcare, paving the way for interdisciplinary advancements in nutrition, microbiology, and neuroscience.

Biography:

Chandini Lokkashri Sai Balaji holds a Master of Science in Biological and Biomolecular Science from University College Dublin and a Bachelor of Technology in Biotechnology from Sathyabama Institute of Science and Technology. A highly motivated bioscience enthusiast with a background in Molecular Biology and Microbiology, she is passionate about translating research into real-world impact. She developed a patented nutrition bar which is aimed at enhancing gut health and mental well-being. With hands-on experience across multiple disciplines, she is committed to advancing innovative solutions in biotechnology and is actively pursuing opportunities for further growth and impact.

The Challenge of Post-Acute Compliance with Infection Prevention and Control: Defying the Odds with a Fresh Outlook for Lasting Change

Joi McMillon

J.*A.D. Infection Control Experts, United States*

Abstract:

The post-acute nursing world presents many challenges for the prevention of healthcare acquired infections. CMS has minimum requirements of only 20 hours per week dedicated to infection prevention and control no matter the size and capacity of the building.

Many of the infection preventionists do not have the proper training and experience and are wearing many hats. Most function as the Assistant Director of Nursing and Staff Development Coordinator. Depending on the competing priorities in the facility, proper infection prevention often takes a backseat to patient issues, complaints and regulatory survey issues. This leaves the facility at a greater risk for outbreaks and extended length of stay for patients.

It is important to use a proactive approach to infection prevention and control and it requires proper surveillance of compliance with evidence-based practices, as well as role specific education in infection prevention and control.

To effectively manage infection prevention and control the infection preventionist must have the time to complete the risk assessments, root cause analysis, construction risk assessments and monitoring of compliance.

Proper infection prevention does not fall solely on the clinical departments such as nursing. Infection prevention and control is the responsibility of everyone in the healthcare facility. J.A.D. Infe4ction Control Experts has developed a way to proactively address these issues and develop a tailored blueprint for success.

Biography:

Joi A. McMillon, RN, BSN, MBA HA, CRRN, WCC, CJCP, HACP-CMS, CIC, is the founder and CEO of J.A.D. Infection Control Experts. With over 30 years of experience in infection control and prevention, she has established herself as a leader in the post-acute clinical setting, journey in healthcare began as a Certified Nursing Assistant, where she witnessed firsthand the devastating impact of healthcare-associated infections (HAIs). Rising through the ranks to become a Director of Nursing, Joi faced the relentless battle against infections daily. It was in these moments—looking into the eyes of patients and seeing their trust—that Joi found her calling.

Recognizing the need for innovation in infection control, Joi founded J.A.D. Infection Control Experts. Her vision? To create a company that would, set new standards in infection prevention

offer tailored solutions for healthcare facilities, empower professionals with data-driven strategies.

“At J.A.D., we’re more than service providers—we’re partners in your mission to protect every patient, staff member, and corner of your facility. Our commitment goes beyond meeting regulatory standards; we’re here to preserve life, maintain trust, and secure the future of healthcare facilities.”

Gut microbiome phylogeny of carp species from wild and aquaculture: A metagenomic analysis

Shrihari Ashok Pingle

Sangamner Nagarpalika Arts, D. J. Malpani Commerce and B. N. Sarda Science College , India

Abstract:

A metagenomic analysis of the gut microbiome of Indian Major Carp and Common carp from wild and aquaculture setting was carried out through 16S rDNA sequencing. The V3-V4 hypervariable regions of the 16S rDNA library of gut microbiome was amplified. DNA Sequencing was done using using Illumina MiSeq. Proteobacteria, Firmicutes, Cyanobacteria and Actinobacteria were the most dominant phyla as observed by the analysis of sequencing data carried out through the Quantitative Insights into Microbial Ecology pipeline. Cultured forms of carp showed high abundance of genera such as Bacillus, Sphingomonas, and Clostridium. This indicates that these genera may have role in the survival of cultured forms under considerable ecological stress of aquaculture. The gut microbiome of cultured forms shows more diversity as indicated by the αdiversity and β- diversity studies. The gut microbiome of the cultured forms shows great resemblance too. Bacillus spp. were absent in the gut microbiome of wild form, and Lactococcus spp. were observed in low abundance indicating the need to find alternatives for probiotics. The results from the present study can be used for further exploring the role of the gut microbiome in aspects such as growth, immunity and other physiological functions of the fish. This study can also be helpful in revisiting fish farm management keeping in mind the impact on gut microbiome.

Biography:

Shrihari Ashok Pingle has completed his PhD from Savitribai Phule Pune University, India in the area of fish gut microbiome. He is an Associate Professor in Zoology at Sangamner Nagarpalika Arts, D. J. Malpani Commerce and B. N. Sarda Science College, Sangamner, India. He is working on the task force of funding agencies of Government of India. With more than 16 years of teaching and research experience, he has published 14 papers in reputed journals and 21 text books. He has been serving as a reviewer of several reputed research journals.

Case report of a patient with gastrointestinal disease

Vera
MKNC, Russia

Abstract:
Patient R., aged 68, came to see a gastroenterologist at the MCRC named after A.S. Loginov. The patient complained of diarrhea up to 20 times a day, abdominal pain, bloating, after a coronavirus infection in 2021, standard therapy did not help. A preliminary diagnosis was made: neuroendocrine tumor of the gastrointestinal tract? Inflammatory bowel disease? However, instrumental examinations (endoscopy and colonoscopy with biopsy) did not confirm this theory. During the collection of complaints and anamnesis, it became known that the patient had a long-term, about 2 years of continuous antibiotic intake. The patient underwent genetics of the intestinal microbiota using the molecular NGS method. According to the results: reduced biodiversity, according to the indices - Shannon 3.5, Piel 0.3, the number of genera is 35. Of the dominant genera, the patient's Escherichia / Shigella, Bacteroides, Prevotella prevailed. Of the opportunistic bacteria, a high level of Escherichia was noted. Of the functional bacteria, the patient did not have Bifidobacterium and Lactobacillus. Noteworthy is the high titer of Methanobrevibacter - 1.04 (the average value in the population is 0.0001-0.005), which is associated with severe bloating of the patient. A large number of Fusobacterium nucleatum is noted - a bacterium from the oral cavity, which indirectly demonstrates a violation of the oral-intestinal barrier. An important indicator is Faecalibacterium_prausnitzii, which was absent in the intestine, and this is due to a violation of the intestinal mucosa protection, since it is a butyrate producer. According to the analysis of 18S rRNA, the patient has a high level of mycotic load. The patient was prescribed therapy - bacteriophages, probiotic and prebiotic correction, lasting at least 6 months. Currently, the patient continues treatment, noting a positive effect. The patient's stool has returned to normal, it is formed up to 2 times a day without impurities. In the future, after therapy, full-genome sequencing of the intestine will be carried out to determine the viral load and antibiotic resistance.
The study of specific bacterial taxa can contribute to the development of more effective diagnostic and therapeutic methods. This opens up new opportunities for studying the interaction between microbiota and disease, which can change the approach to treating patients with gastrointestinal diseases.

Single-Bacterium Sequencing: Decoding Microbial Heterogeneity in Host and Environmental Microbiomes

Jose Eluani
Microbiologist, Independent Innovation Initiative Houston, United States

Dr. Ling Dong
M20 Genomics, United States

Abstract:
Microbial communities exhibit profound functional heterogeneity, which population-level omics often overlook. We present a single-microbe RNA-seq method enabling high-resolution bacterial transcriptomics. This approach revealed antibiotic-resistant subpopulations in E. coli with distinct stress responses. To study host-microbe interplay, we developed a dual RNA-seq technology that simultaneously captures host and bacterial transcripts, uncovering host-induced ferroptosis during Acinetobacter baumannii infection. For complex microbiomes, we applied single-cell transcriptomics to gut and rumen ecosystems, identifying species-specific metabolic niches and adaptive strategies. Our low-input smGel-seq platform further enabled clinical sputum microbiome analysis, revealing pathogenic subpopulations linked to antibiotic resistance. These technologies also illuminated host regulation of bacterial lifestyles, such as Drosophila-driven commensalism in Serratia marcescens, and dynamic functional shifts in keystone species like Megamonas. Collectively, our work demonstrates how single-bacterium sequencing resolves microbial heterogeneity, host-microbe interactions, and ecological adaptations, offering new avenues for microbiome research and therapeutic discovery.

Keywords: single-microbe RNA-seq, microbial heterogeneity, host-pathogen interactions, antibiotic resistance, functional microbiome profiling.
As a complement to the above, this brief segment will introduce a cross-disciplinary initiative focused on collecting and harmonizing one million human microbiome profiles, particularly from individuals in early stages of metabolic syndrome and cancer. The initiative aims to foster collaboration among researchers and clinicians to enable AI-driven pattern recognition and early diagnostics through scaled, structured microbiome data.

Biography:
MBA Jose Eluani is a Microbiologist and PhD Candidate with over 20 years of experience in the pharmaceutical sector and 5 years in the food industry. He has promoted the application of probiotics supported by leading-edge AI technologies, with a background that spans academic research and international business. He currently leads an initiative focused on leveraging microbiome data for early diagnosis and health optimization.

Biography:
Dr. Ling Dong is the COO and co-founder of M20 Genomics, where she and her partners lead the development of next-generation sequencing technologies such as M20-seq. With over a decade of experience in life science research and leadership, she has driven innovation and commercial transformation across basic research, clinical projects, and microbiology studies in both industry and academia.

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