# 2025 MEETING GUIDE

ISAPP

International Scientific Association for PROBIOTICS and PREBIOTICS

Annual Scientific Meeting
Banff, Canada • July 15-17, 2025

# Welcome

On behalf of the ISAPP board, I'd like to welcome you to ISAPP's 2025 annual scientific meeting in Banff, Canada. This year's location will be marked by the awe-inspiring beauty of the Canadian Rockies. I was first introduced to Banff through the annual Banff Centre Mountain Film Festival World Tour which shows films and documentaries made around the world on mountain culture, sports, adventure, and exploration. The films have gorgeous cinematography and memorable storytelling. Although I don't plan to take up free climbing any time soon, it's easy to appreciate the dedication it takes to reach that goal.

Just at those mountain films are a source of motivation, so too is our life-long exploration of the biotic sciences. Within ISAPP this past year, we continued the forward momentum to provide insight and guidance on biotic research. Our projects have led to a number of key outputs over the past 12 months. These include publications addressing important current issues in the biotics fields – elucidating detailed criteria for prebiotics, recommendations for addressing the underexamined role of diet in biotic studies, taking a critical look at evidence for probiotic-mediated restoration of the microbiome after antibiotics, exploring the challenges and paths forward in postbiotic quantification, and synthesizing the latest understanding of the use of a biotics in animals. Another highlight was the ISAPP-organized panel discussing the concept and practicalities of the term gut health. We thank all of those who have collaborated with us over the past year for sharing in the advancement of the ISAPP mission.

As I reach the end of my first year as President of the Board of Directors, I want to extend gratitude to past ISAPP leadership for their efforts. I am so grateful for Dan Merenstein and his prior leadership in this position. He has been a great mentor and continues to provide guidance with great instincts and rapid responses. I also want to thank our Board of Directors who not only give hours of time each month, but also continue to be leaders in their fields. We on the board are particularly grateful for Eamonn Quigley whose term on the board is ending, but who has left an indelible mark of major contributions over the past 13 years. We welcome our two new board members Jens Walter and Hannah Holscher, both of whom will continue the excellence of the ISAPP mission. Importantly, all of this is possible because of our Executive Director, Marla Cunningham. Marla has been THE leader to meet the moment and has set ISAPP on a great trajectory for upcoming years.

Last, but not least, I hope you will join me in celebrating the ISAPP community. As participants in the annual meeting, you are strengthening this community by bringing diverse perspectives and distinct disciplinary expertise to climb new heights for biotic science for future generations.

**Maria Marco, ISAPP President**

# Welcome

Welcome to the ISAPP Annual Meeting in Banff, Canada!

This is an exciting time of the year for ISAPP, when our community gathers for connection, exchange and learning, and new ideas and collaborations begin.

ISAPP is made of people – and the ISAPP community is composed of a diverse group of leading scientists representing many disciplines, career stages and continents, from across academic, industry and public settings. Each year, a rotating group of academic experts join us to share novel work and advance discussion on important issues, along with scientists from ISAPP member companies - organisations leading the way in industrial research and the translation of biotic science to market. Representing the future of the field, a competitive selection process brings in a group of accomplished early career researchers from around the globe. It's always both illuminating and inspiring to hear about the collective work of the community in growing knowledge, rigour and utility of science in our field.

This year, the ISAPP board have put together a plenary program addressing some of most notable recent findings and progress from across the field of probiotics, prebiotics, postbiotics, synbiotics and fermented foods. In the interactive discussion groups, we will explore six important research questions for the field in small group settings, with academic and industry scientists sharing research advancements, implementation challenges and opportunities for the field. The panel session this year is focused on clinical translation of biotic science, bringing together insights and perspectives from key stakeholders on how to advance the implementation of science in this field by healthcare professionals. The premeeting programs provide an opportunity for industry member scientists and early career researchers to connect with each other and share knowledge, leveraging the unique experiences and perspectives of these two groups of scientists, leading to fertile discussions to fuel research, development and innovation. Amongst these and other scientific portions of the program, you will also find opportunities for social connection, fun, and time to both explore and gaze at the spectacular surrounds of our meeting venue.

On behalf of the ISAPP community, we thank you for joining us for our annual meeting. Your contributions, in presentations, posters or discussion groups, your enthusiasm and opinions and knowledge, all contribute to making this event a rewarding and inspiring experience for all.

Looking forward to connecting in Banff.

**Marla Cunningham, ISAPP Executive Director**


# 2025 ANNUAL MEETING PROGRAM

All program events will be held in the Kinnear Centre building at Banff Centre for Arts and Creativity unless otherwise noted below.

**Breakfast** is served in Vistas Dining Room, Sally Borden Building, 3rd Floor unless otherwise noted below.
*Abbreviations: IAC=Industry Advisory Committee (representatives of member companies); SFA=Students and Fellows Association*

## TUESDAY JULY 15

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|---|---|
| 07:30 - 13:00<br>*KC100 Galleria* | Registration desk open |
| **Pre-meeting program (Open only to IAC, SFA and Board of Directors)** | |
| 07:15 – 08:15<br>*KC105* | IAC member networking breakfast (Industry members only) |
| 08:30 – 09:30<br>*KC103* | **IAC Featured plenary session: The role of microbial communities in healthy ageing**<br>Elaine Holmes, Murdoch University, Australia & Imperial College London, UK<br>Sean Gibbons, Institute for Systems Biology, USA |
| 09:30 – 10:00 | Break |
| 10:00 - 11:30<br>*KC203* | **IAC/SFA Innovation workshops (separate sign-up required).**<br>**1: Non-gut microbiomes**<br>Shalome Bassett, Fonterra, New Zealand |
| *KC305* | **2: Mechanisms of action – From microbe to mechanism**<br>Jessica Van Harsselaar, Beneo, Germany |
| *KC303* | **3: The promise and potential of next-generation probiotics**<br>Patricia Sanz, University of Reading, UK |
| *KC301* | **4: Microbial consortia**<br>Dave Hourigan, University College Cork, Ireland |
| 11:30 - 12:15<br>*KC103* | **IAC and Board of Directors meeting** |
| *12:15 - 12:30* | *Move to rooms for working lunch* |
| 12:30 | Working lunch during discussion groups *(served in Galleria on 2nd and 3rd floors)* |
| 12:30 - 17:00 | **Discussion groups** (concurrent sessions) |
| *KC201* | **1: Role of microbially-derived compounds on fermented food and postbiotic health benefits**<br>Maria Marco, University of California, Davis, USA and Gabriel Vinderola, National University of Litoral and CONICET, Argentina |
| *KC203* | **2: Use of biotics in health and disease – towards optimizing the host response**<br>Eamonn Quigley, The Methodist Hospital and Weill Cornell School of Medicine, Texas, USA and Geoffrey Preidis, Baylor College of Medicine and Texas Children's Hospital, USA |
| *KC205* | **3: 'Phagebiotics'? Exploring the application of phage and virome interventions in health and disease**<br>Colin Hill, University College Cork, Ireland and Andrey Shkoporov, APC Microbiome, University College Cork, Ireland |

# 2025 ANNUAL MEETING PROGRAM

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| *KC301* | **4: Opportunities for biotics in precision nutrition**<br>Anisha Wijeyesekera, University of Reading, United Kingdom and Kelly Swanson, University of Illinois at Urbana-Champaign, Illinois, USA |
| *KC303* | **5: Exploring the integration of prebiotics in pharmaceutical applications**<br>Kristin Verbeke, Katholieke Universiteit Leuven, Belgium and Sarah Lebeer, University of Antwerp, Belgium |
| *KC305* | **6: Cesarean section delivery and gut microbiota – early colonization patterns, outcomes, and emerging interventions**<br>Hania Szajewska, The Medical University of Warsaw, Poland and Seppo Salminen, University of Turku, Finland |
| **17:00 - 19:00** | **Outdoor social activity** |
| **19:00 - 21:00**<br>*KC101 &*<br>*KC Terrace* | **Welcome reception** |

# WEDNESDAY JULY 16

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|---|---|
| 07:30 - 08:30<br>*KC100 Galleria* | Registration desk open |
| 08:30 - 08:35<br>*KC101/103/105* | **Welcome**<br>Maria Marco and Marla Cunningham |
| 08:35 - 09:05 | **Dietary fibers and immune health**<br>Paul de Vos, Maastricht University, The Netherlands |
| 09:05 - 09:35 | **Leveraging the gut environment for functional biosensor microbes**<br>Carolina Tropini, University of British Columbia, Canada |
| 09:35 - 10:00 | **The Sanders Award for Advancing Biotic Science 2025 Lecture:**<br>**Two decades of applied research for the advancement of biotic science**<br>Remco Kort, Vrije Universiteit Amsterdam, The Netherlands |
| 10:00 - 10:30<br>*KC100 Galleria*<br>*KC201/203* | Break & Poster Preview<br>*Refreshments served in galleria on 1st floor*<br>*Posters available for previewing on 2nd floor* |
| 10:30 - 11:00<br>*KC101/103/105* | **The scientific communication ecosystem: the responsibility of investigators**<br>Howard Bauchner, Boston University Chobanian & Avedisian School of Medicine, USA |
| 11:00 - 12:30 | **Expert Panel: Clinical translation of biotic science: How can we enhance impact for clinical practice?**<br>Howard Bauchner, Boston University Chobanian & Avedisian School of Medicine, USA<br>Dan Merenstein, Georgetown University, USA<br>Hania Szajewska, The Medical University of Warsaw, Poland<br>Geoffrey Preidis, Baylor College of Medicine and Texas Children's Hospital, USA<br>Kristina Campbell, Science writer, Canada<br>Kristie Leigh, Danone North America, USA<br>Kyle Sloan, Procter & Gamble, USA |
| 12:30 - 13:30 | Lunch break, *Vistas Dining Room, Sally Borden Building, 3rd Floor* |
| 13:30 - 14:30<br>*KC201/203* | **Poster session.** Poster presentations and SFA poster judging. Authors will be present for all posters. |
| 14:30 - 15:00<br>*KC101/103/105* | **Probiotics and postbiotics to regulate the immune system: what can we gain or lose from viability or inactivation?**<br>Haruki Kitazawa, Tohoku University, Japan |
| 15:00 - 15:30 | **Health benefits of fermented food: from bacterial genomes to dietary guidelines**<br>Guy Vergeres, Agroscope, Switzerland |

## 2025 ANNUAL MEETING PROGRAM

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| 15:30 - 16:00 | **Gut health: An ISAPP consensus definition effort**<br>Maria Marco, University of California, Davis, USA |
| 16:00 - 16:15 | **The Glenn Gibson Early Career Researcher Award 2025 Lecture:**<br>**Psychobiotics: unveiling the molecular basis of host mood regulation**<br>Peijun Tian, Jiangnan University, P. R. China |
| 16:15 - 16:30 | **The Gregor Reid Award for Outstanding Scholars in Developing Nations 2025 Lecture:**<br>**The Leke project: Mapping the vaginal microbiome and benefits of vaginal lactobacilli in Cameroon.**<br>Josiane Kenfack, University of Yaounde I, Cameroon |
| 16:30 - 17:30 | **Late Breaking News**<br>Chair: Bob Hutkins, University of Nebraska – Lincoln, USA |
| 17:30 - 18:00 | Break |
| *18:00 - 18:30* | *Buses to gala social event. Pick up outside PDC building.*<br>*Departure times: 17:50, 18:00, 18:25, 18:35* |
| **18:30 - 23:00** | **Gala social event,** *Banff Park Ranch* |

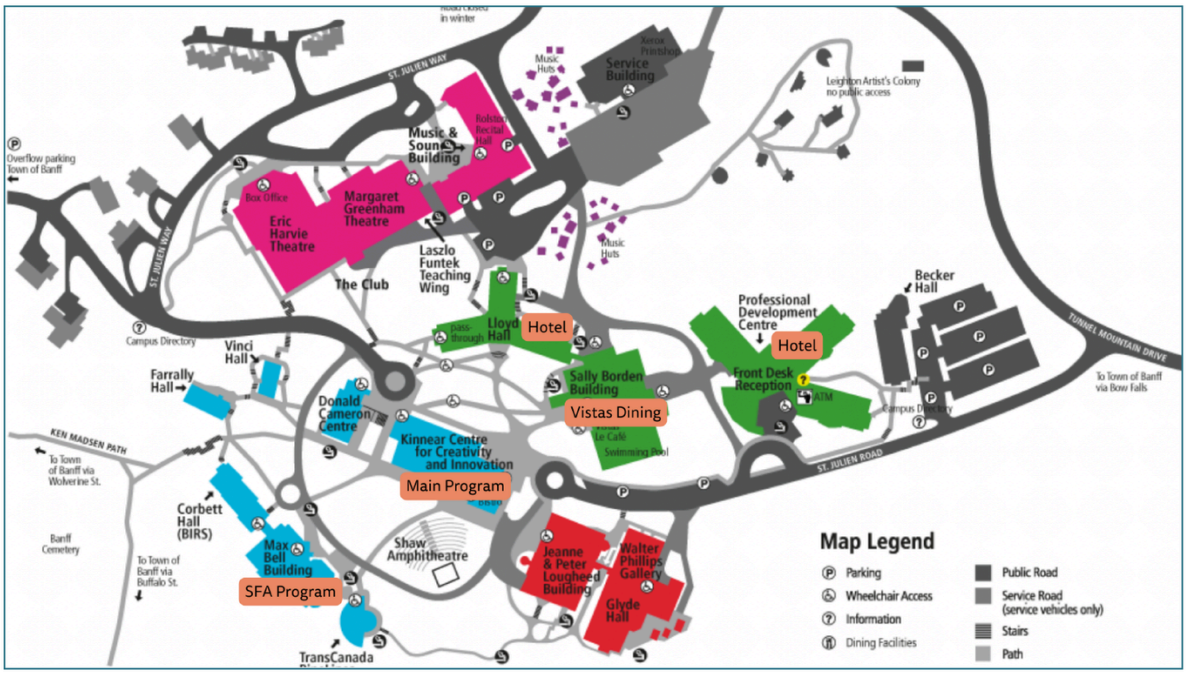
## THURSDAY JULY 17

| | |
|---|---|
| 09:00 - 09:15<br>*KC101/103/105* | **IAC highlight**<br>**Effects of a probiotic formula containing *Levilactobacillus brevis* KABP 052, *Lactiplantibacillus plantarum* KABP 051, and *Pediococcus acidilactici* KABP 021 on symptoms and quality of life in peri- and postmenopausal women (GynMeno trial).**<br>Maria Rodriguez-Palmero, AB Biotics, Spain |
| 09:15 - 09:30 | **IAC highlight**<br>**Towards EU health claims for prebiotics: A focus on scientific evidence and regulatory pathways**<br>Elaine Vaughan, Sensus/ILSI, The Netherlands |
| 09:30 - 09:45 | **SFA highlight**<br>**Prebiotic-like activity of cranberry extract: Modulating gut microbiota composition and enhancing intestinal barrier function in ex vivo and in vivo models**<br>Valentina Cattero, Laval University, Canada |
| 09:45 - 10:00 | **SFA highlight**<br>**Acetate and the gut-brain axis: A pilot study on mental health and metabolic outcomes**<br>Kait Al, Western University, Canada |
| 10:00 - 10:05 | **Announcement of poster award winners** |
| 10:05 - 10:35 | **Next generation probiotics for metabolic and liver health**<br>André Marette, Université Laval, Canada |
| 10:35 - 11:00 | Break |
| 11:00 - 12:30 | **Summary reports from Discussion groups**<br>SFA: **Students and Fellows Association report**<br>DG1: **Role of microbially-derived compounds on fermented food and postbiotic health benefits**<br>DG2: **Use of biotics in health and disease – towards optimizing the host response**<br>DG3: **'Phagebiotics'? Exploring the application of phage and virome interventions in health and disease**<br>DG4: **Opportunities for biotics in precision nutrition**<br>DG5: **Exploring the integration of prebiotics in pharmaceutical applications**<br>DG6: **Cesarean section delivery and gut microbiota – early colonization patterns, outcomes, and emerging interventions** |
| 12:30 | **Close** |

Washrooms are located on each level in the Kinnear Center building. Lactation room is in KC304.

# 2025 ANNUAL MEETING PROGRAM

Banff Centre map




Click here or visit www.banffcentre.ca/maps-directions for full campus map and directions.

# IAC Featured Plenary

**Tuesday July 15 - 08:30-09:30 Open only to IAC.**

**The role of microbial communities in healthy ageing**

Gut microbial communities play a vital role in healthy ageing by supporting a myriad of critical functions such as immune regulation, nutrient absorption, and integrity of the gut barrier. The composition of the gut microbiome can also influence inflammation levels and other age-related disorders that impact health and wellbeing as we age. In this session, our experts will share some of their key findings and insights in this exciting space.

**IAC Featured Plenary Speakers:**

**Elaine Holmes, Murdoch University, Australia & Imperial College London, UK**

Holmes is an ARC Laureate Fellow, former Premier's Fellow and Head of the Centre for Computational and Systems Medicine at Murdoch University. Her main research area focuses on applying metabolic profiling and computational modelling of biofluids and tissues to understand the impact of the gut microbiome on human health. She retains a position at Imperial College London where she focuses on precision nutrition and is a founder director of Melico, a startup company that operates in the personalised nutrition space and is a visiting professor at various International 'Universities. She has authored over 500 papers and books in metabolic profiling and chemometrics. She is a Fellow of the Academy of Medical Sciences and the Australian Academy of Science and has won several awards including the Royal Society of Chemistry Interdisciplinary Award.

**Sean Gibbons, Institute for Systems Biology, USA**

Sean Gibbons earned his PhD in biophysics from the University of Chicago in 2015. He completed his postdoctoral work at MIT in 2018. Sean is now an associate professor at the Institute for Systems Biology, in Seattle. His lab studies the ecology and evolution of microbial communities. In particular, Sean is interested in how host-associated bacterial communities influence the health and wellness of the host organism. His group designs computational and wet-lab tools for studying these complex systems. Ultimately, the Gibbons Lab aims to develop strategies for engineering the ecology of the gut microbiome to improve human health.

**Tuesday July 15 - 10:00-11:30 (concurrent workshops) Open only to SFA and IAC.**

Innovation is critical to tackling the many scientific and clinical challenges facing the biotics field today. This session enables Industry Advisory Committee (IAC) and Students and Fellows Association (SFA) members to share their respective insights from their research and development work on the cutting edge of innovation across four highly topical areas.

*Check your name badge for your workshop number.*

**Workshop 1: Non-gut microbiomes**
Chaired by Shalome Bassett, PhD, Fonterra, New Zealand

While traditional biotic research has primarily focused on the gut microbiome and its role in overall health and wellbeing, the body is also host to a variety of other microbiomes that likewise play important roles in health and disease and are fast-becoming important targets for biotic interventions and novel solutions. This session will focus on biotic applications for the skin, oral, vaginal, and respiratory microbiomes, emphasizing innovations for biotics beyond traditional gut-focused applications.

**Workshop 2: Mechanisms of action – From microbe to mechanism**
Chaired by Jessica Van Harsselaar, Beneo, Germany

Biotic interventions—including probiotics, prebiotics, and postbiotics—operate through a variety of mechanisms that influence microbial communities, host responses, and systemic health. While these categories have distinct definitions, they also share common pathways in how they modulate the gut ecosystem and impact physiological functions.

This session will explore the core principles underlying the mechanisms of action of biotics. We will discuss the key factors that drive biotic efficacy, including microbial viability, metabolite production, and host-microbe interactions. The discussion will help refine our understanding of how biotics exert their effects and identify gaps in current knowledge.

**Workshop 3: The promise and potential of next-generation probiotics**
Chaired by Patricia Sanz, University of Reading, UK

Next-Generation Probiotics (NGPs) are emerging as a transformative frontier in the field of biotics. These are microbial species that fulfill the general criteria for probiotics (e.g., conferring a health benefit on the host when administered in adequate amounts) but are often newly identified, lack a documented history of safe use in foods or supplements, and may include genetically engineered strains designed for targeted functions.

This workshop aims to spark dialogue around the scientific, regulatory, and translational aspects of NGPs, particularly in relation to human health challenges and the future of personalised interventions.

**Workshop 4: Microbial consortia**
Chaired by Dave Hourigan, University College Cork, Ireland

This session will explore commensal bacterial consortia and how their ecological dynamics can be harnessed to enhance microbiome modulation. The workshop will explore the composition of defined microbial consortia, interactions between members and nutritional dependencies. Well-defined commensal bacterial consortia have the potential to address the limitations of current probiotics and overcome challenges associated with personalised interventions.

**Tuesday July 15 - 12:30-17:00 (concurrent sessions) Open only to invited experts and IAC.**

**Group 1: Role of microbially-derived compounds on fermented food and postbiotic health benefits**
Maria Marco PhD, University of California, Davis, USA and Gabriel Vinderola PhD, National University of Litoral and CONICET, Argentina

Fermented foods and many postbiotics contain a wide range of microbially-derived compounds comprised of thousands of metabolites, enzymes, and cell-wall components not contained in the raw material. Although many of these compounds are known to induce immune, epithelial, and neural responses when provided individually or synthesized by members of the gut microbiome, there is little evidence showing how they contribute to health benefits conferred by fermented foods and postbiotics. However, the potential for those compounds to affect the host is evident, based on studies showing that β-galactosidase made by bacteria during yogurt production drives relief from lactose intolerance symptoms. This discussion group will evaluate what is known about individual metabolites present in fermented food and postbiotic preparations with regard to their physiological relevance and effects on the target host. We will examine recent findings on the structural and metabolic bioactive compounds present in bacteria and fungi, reflect on challenges to identify the health-modulatory roles of individual compounds in complex mixtures, and to control and optimize fermented foods and postbiotics for their delivery. A better understanding of these knowledge gaps may help further advance the science of fermented foods and postbiotics, paving the way for a wider popular use and contributing to nutritional recommendations.

Key aims
- Examine the potential for ingested metabolites made by microorganisms to benefit host health.
- Define the main compounds in fermented foods and postbiotics with health modulatory potential.
- Explore the influence of particular microbes and substrates on the metabolite profile of fermented foods, with a view to predicting and optimizing health benefits.
- Identify gaps in knowledge to guide future research

Key Questions
- Do fermented foods and postbiotics have health-promoting metabolites in common?
- Can individual compounds be singled-out as the main cause of health benefits from fermented foods and postbiotics?
- How may metabolite profiles vary between different preparations of fermented foods and postbiotics?
- Are health-promoting bioactive compounds in fermented foods and postbiotics substrate specific? Are there common metabolites shared across different fermented food and postbiotic types?
- What is the state of tools for predictions of the above, e.g. in silico tools?
- Is ingestion of bioactive compounds, also made by members of the gut microbiome (for example indole-3-lactic acid (ILA) and phenyllactic acid (PLA)), sufficient to achieve the desired host-modulatory effect?

Experts:
Shijie Cao, University of Washington, USA
Michael Gänzle, Universiy of Alberta, Canada
Carol Johnston, Arizona State University, USA
Haruki Kitazawa, Tohoku University, Japan
Guy Vergères, Education and Research EAER, Switzerland

**Group 2: Use of biotics in health and disease – towards optimizing the host response**
Chaired by: Eamonn Quigley MD, The Methodist Hospital and Weill Cornell School of Medicine, Texas, USA and Geoffrey Preidis MD, PhD, Baylor College of Medicine and Texas Children's Hospital, USA

While a variety of biotics have been the subject of clinical trials in humans and animals, in many cases the selection of product, dose and means of administration seemed to owe more to conjecture or convenience than science. This approach was not unreasonable when little was known of the structure and function of the gut microbiome or of its interactions with the host. The thesis that forms the basis of this discussion group is that, given tremendous progress in our understanding of the host response, a much more rational and informed process can now guide the precise selection of a biotic for a given indication. To achieve this goal, we plan to explore various determinants of the host response including, but not limited to the commensal microbiome and components of the host immune and neuro-endocrine responses as well as impacts on metabolic functions and the brain-gut axis.

Along the way we will identify targets that have the potential to be modulated by a biotic intervention and then review the evidence that biotics can actually modify these responses. The basic mechanisms and pathways whereby such modulations can occur will be explored,the accessibility and reproducibility of potential biotic targets will be critically evaluated and an attempt to prioritize targets in terms of their relevance to individual biotics and potential for translation to human studies performed. Looking to the future we will discuss emerging approaches for studying host-microbiome interactions (e.g., human-derived organoids, gut on a chip, machine learning approaches). Finally, and mindful of the challenges inherent to translation from bench to bedside in this area, we will attempt to develop recommendations for the future design of human studies with particular attention to choice of biotic product and human disease targets.

Experts:
Premysl Bercik, McMaster University, Canada
André Marette, Université Laval, Canada
Liam O'Mahony, APC, University College Cork, Ireland
Vanessa Sperandio, Univeristy of WI MMI, USA

**Group 3: 'Phagebiotics'? Exploring the application of phage and virome interventions in health and disease**
Chaired by: Colin Hill PhD, DSc, University College Cork, Ireland and Andrey Shkoporov PhD, APC Microbiome, University College Cork, Ireland

A recent ISAPP blog considered whether or not bacteriophage could be considered a member of the 'biotic' family (probiotics, prebiotics, postbiotics, etc). Phage as 'biotics' would of course include classical phage therapy for the treatment of infections, as has been used for almost a century, but also include other mechanisms by which phage could be used to improve human and animal health. This discussion group will explore the use of phage (or whole viromes) as tools to manipulate the bacteriome, as agents of horizontal gene transfer, as biomarkers of bacterial community composition or host health, or as agents to deliver DNA to in situ members of communities, etc. Experts will discuss the latest data from clinical and preclinical intervention studies as well as insights from biological and ecological studies of the virome and its role in host and microbiome health.

Experts:
Jean-Paul Pirnay, Queen Astrid Military Hospital, Belgium
Nathaniel Ritz, Institute for Systems Biology, USA
Torben Sølbeck Rasmussen, University of Copenhagen - Food Science, Denmark

**Group 4: Opportunities for biotics in precision nutrition**
Chaired by: Anisha Wijeyesekera PhD, University of Reading, United Kingdom and Kelly Swanson PhD, University of Illinois at Urbana-Champaign, Illinois, USA

Precision nutrition is growing in recognition as a more data-driven, individualised approach to nutrition counselling, where dietary recommendations are tailored to an individual's unique needs. Unlike traditional "one-size-fits-all" dietary guidelines, precision nutrition takes into account factors such as genetic and phenotypic characteristics, lifestyle and environmental factors, preferences, and health goals.

The gut microbiota is an integral component of the human phenotype, and recent advances in analytical technologies have furthered our understanding of host-gut microbiota interactions. Exploiting these mechanisms of action to develop biotic substances targeting specific microbes or metabolites/function, presents an exciting opportunity for biotics researchers to contribute to the precision nutrition effort. This discussion group will review the current status of precision nutrition, discuss the opportunities and potential for the development of targeted, precision biotic products, and conclude on the feasibility of the implementation of biotics substances in precision nutrition practice.

Experts:
Matthew Amicucci, one.bio, USA
Clara Cho, University of Guelph, Canada
Sean Gibbons, Institute for Systems Biology, USA
Elaine Holmes, Murdoch University, Australia & Imperial College London, UK
Bruce Y. Lee, PHICOR, USA
Sara Martini, University of Illinois Urbana-Champaign, USA
Kim Watson, University of Reading, UK

**Group 5: Exploring the integration of prebiotics in pharmaceutical applications**
Chaired by: Kristin Verbeke PhD, Katholieke Universiteit Leuven, Belgium and Sarah Lebeer PhD, University of Antwerp, Belgium

Background and Objectives:
Prebiotics, while commonly used in food and supplement industries, are underutilized in pharmaceutical applications, and more so in symbiotic combinations in live biotherapeutic products (LBPs). The addition of prebiotics in pharmaceutical products has potential to enhance therapeutic efficacy for specific diseases or clinical indications. In addition to being the active ingredient themselves, they can also serve as excipients promoting the survival and efficacy of probiotics, which could complement or even potentiate the action of probiotics and other LBPs.

The proposed discussion group will explore and discuss industrial and academic challenges, potential benefits, regulatory hurdles, and formulation innovations needed to advance prebiotics in pharmaceutical contexts.

Possible Discussion Points:
1. Why Are Prebiotics Rarely Incorporated into Pharmaceutical Applications?
    - Formulation Challenges? Pharmaceutical-grade prebiotics must meet rigorous standards for purity, stability, and consistency. The challenges are different from manufacturing LBPs under GMP conditions, but do not seem necessarily more complicated. Why, then, is pharmaceutical-grade production of prebiotics perceived as difficult or not clearly on the radar of academics and industry?
    - Regulatory Complexity: There may be regulatory ambiguity around prebiotics, particularly regarding their categorization and approval as therapeutics versus supplements. What specific regulatory challenges hinder the development of prebiotics as pharmaceutical agents, and how could these be addressed?
    - Market Demand and Incentives: Given the strong market for food-grade prebiotics, is there a lack of motivation to push prebiotics into the pharmaceutical space? Are there concerns around cost-benefit given that prebiotics are generally non-patentable, natural compounds?

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2. Defining Prebiotics' Role in Pharmaceutical and Therapeutic Contexts
    - Clinical Efficacy and Endpoints: To establish prebiotics as therapeutic agents, it's critical to define specific endpoints and mechanisms of action for specific clinical conditions and intended use. How can the field standardize clinical studies and efficacy measures to support prebiotics as a legitimate pharmaceutical category?
    - Patient Populations and Target Indications: Prebiotics could play a role in managing conditions such as metabolic disorders, immune modulation, and GI diseases. What specific patient populations and indications should be prioritized, and how might these influence regulatory and formulation strategies?

Input requested from ISAPP industry advisory committee
We welcome IAC members to suggest regulatory and market experts to actively join our group as experts.

Outcomes and Next Steps:
The group aims to work towards an overview or opinion paper which could include actionable steps to promote the integration of prebiotics in pharmaceutical applications. The exact content of this outcome and next steps will depend on the discussion at the annual meeting of ISAPP.

Experts:
Jonathan Chapman, Newcastle University, UK
Magali Cordaillat-Simmons, University Clermont Auvergne - IUT Aurillac, France
Karen Madsen, University of Alberta, Canada
Siobhan McCormack, NHS GP, UK
Jacques Ravel, University of Maryland School of Medicine, USA

**Group 6: Cesarean section delivery and gut microbiota – early colonization patterns, outcomes, and emerging interventions**
Chaired by: Hania Szajewska MD, PhD, The Medical University of Warsaw, Poland and Seppo Salminen PhD, University of Turku, Finland

This discussion group will address the important and timely topic of how cesarean section delivery affects early gut microbiota colonization, its impact on short- and long-term health outcomes, and emerging interventions to reduce potential negative effects.
Key themes include (subject to change):

- Early Gut Microbiota Colonization Patterns: How birth mode influences microbial exposure, the role of maternal microbiota, and the impact of hospital environments and antibiotics.
- Health Outcomes: Links between altered gut microbiota and immune system development, as well as long-term risks like allergies, asthma, and obesity.
- Post-C-Section Influences on Gut Microbiota Development: The role of feeding methods, dietary factors, and environmental exposures in microbiota restoration.
- Emerging Interventions: Innovative strategies such as vaginal seeding, maternal fecal microbiota transplantation, and the use of biotics.

Participants will discuss ways to bridge research and clinical practice, evaluate the feasibility and safety of interventions, and identify priorities for future research. This session aims to improve the understanding of the relationship between cesarean delivery and microbiota and to help shape future guidelines and strategies in this evolving field.

Experts:
Kjersti Aagaard, HCA Healthcare Texas and Boston Children's Hospital/Harvard Medical School, USA
Howard Bauchner
Jose C. Clemente, Mount Sinai, USA (virtual)
Eldin Jasarevic, University of Pittsburgh, USA
Katri Korpela, University of Helsinki , Finland (pre-recorded)
Daniel Merenstein, Georgetown University
Anne Salonen, Univeristy of Helsinki, Finland
Mary Ellen Sanders, Mary Ellen Sanders LLC, USA
Daniel Tancredi, University of California, Davis

SFA
ISAPP - STUDENTS AND FELLOWS ASSOCIATION

## Tuesday July 15 - 11:30 - 12:15 Talks (open only to SFA)

**Publishing in influential journals**
Howard Bauchner, Boston University School of Medicine, USA

## Tuesday July 15 - 13:00-14:30 Breakout Group Discussions (open only to SFA)

**Group 1. Probiotics and the concept of using beneficial microbes for health**
Sarah Ahannach, University of Antwerp, Belgium

**Group 2. Prebiotics and the concept of using beneficial substrates for health**
Breanna Metras, University of Minnesota, USA

**Group 3. Microbiota and related bioinformatic analysis**
Cathy Lordon, Teagasc, Ireland

## Tuesday July 15 - 15:00-16:00 Oral Presentations (open only to SFA)

**Designing the dream team: formulating probiotic consortium for maximum impact.**
Hina Maniya, RK University, India

**Developing a topical probiotic to prevent penile HIV acquisition**
Rachel Penney, University of Western Ontario, Canada

**Antiplasmodial Activity of Probiotic Limosilactobacillus fermentum YZ01 in Plasmodium berghei ANKA Infected BALB/c Mice**
Timothy Bamgbose, ICMR-National Institute of Malaria Research

**Dietary intake, gut microbiome and anxiety: multilevel insights from a cross-sectional study on highly anxious females aged 18-25.**
Melissa Basso, University of Surrey, United Kingdom

## Tuesday July 15 - 16:00 - 17:00 Plenary (open only to SFA)

**From X to YT: The role of scientists in the changing landscape of science communication**
Kristina Campbell, Science writer, Canada

**A meditation on useful suffering, empathy, the hazards of power, and the pursuit of fulfilment**
Sean Gibbons, Institute for Systems Biology, USA

**Paul de Vos, Maastricht University, The Netherlands**

Prof. Dr. Paul de Vos is an immunologist specializing in the impact of dietary molecules on immunity and disease prevention. His research spans over two decades, focusing on autoimmune diabetes, cell encapsulation, and the interaction between food components and immune health. He was a visiting scientist at the Joslin Diabetes Institute, Harvard Medical School, from 1997-1998. At the University Medical Center Groningen, he leads a multidisciplinary research group composed of immunologists, polymer chemists, and endocrinologists. His team has been at the forefront of studying dietary fibers such as pectins, beta-glucans, and fructans, demonstrating their direct interaction with immune receptors. Prof. de Vos has published over 300 peer-reviewed papers and holds seven patents on food components and health. He is a principal investigator at the Carbohydrate Competence Center (CCC) and a member of various international research consortia, including those funded by the Juvenile Diabetes Research Foundation (JDRF).

**Wednesday July 16 - 08:35-09:05**
**Dietary fibers and immune health**

Abstract: The human gut is not only essential for digestion, but also serves as the body's largest immune organ, housing nearly 80% of our immune cells. These cells form a highly organized network that interacts closely with the trillions of commensal bacteria living in our gut. This immune system must walk a fine line: it must tolerate beneficial bacteria that support metabolism and immunity, yet remain alert and responsive to potential pathogens and toxins. Specialized receptors allow gut immune cells to distinguish between friend and foe with remarkable precision.

Dietary fibers have emerged as key modulators of this system. They can either shape immunity indirectly by altering microbial fermentation products or act directly through interaction with receptors on immune cells. However, we have learned that not all fibers are equal. It is not simply the quantity of fiber, but rather the precise chemistry that determines its biological effect. Our work, supported by advanced analytical tools, has shown that specific structural features in carbohydrates are responsible for their immune-regulating properties.

For instance, the health benefits of human milk oligosaccharides (hMO) depend on their interaction with gut immune receptors, and their chemistry dictates how well they support barrier function. Similarly, we demonstrated that the methylation pattern of pectins is crucial in preventing inappropriate immune activation. We have also observed that responses to dietary fibers vary by age, gender, and health condition.

Altogether, our findings emphasize the importance of selecting and designing dietary fibers based on their molecular properties. By tailoring interventions to specific target groups, we can better support immune function and even counteract age-related immune decline. Precision nutrition based on fiber chemistry represents a promising path forward in improving public health through diet.

**Carolina Tropini, University of British Columbia, Canada**

Dr. Carolina Tropini is an Assistant Professor at the University of British Columbia in the Department of Microbiology and Immunology and the School of Biomedical Engineering, and a Canada Tier 2 Research Chair in Quantitative Microbiota Biology for Health Applications. In 2020 she was nominated a Paul Allen Distinguished Investigator, and she was the first Canadian to be awarded the Johnson & Johnson Women in STEM2D Scholar, which was granted in the field of Engineering. She is the inaugural Alan Bernstein Canadian Institute for Advanced Research (CIFAR) Fellow in the Humans & the Microbiome Program and a Michael Smith Foundation for Health Research Scholar. In 2019, she was nominated as a CIFAR Azrieli Global Scholar.

The Tropini lab is investigating how a disrupted physical environment due to altered nutrition or concurrent with intestinal diseases affects the microbiota and host at a multi-scale level. They are a cross-disciplinary group that incorporates techniques from microbiology, bioengineering and biophysics to create highly parallel assays and study how bacteria and microbial communities function, with the goal of translating the knowledge gained to improve human health.

Dr. Tropini conducted her Ph.D. in Biophysics at Stanford University. Her studies in the laboratory of Dr. KC Huang combined computational and experimental techniques to investigate bacterial mechanics and morphogenesis. In 2014 she received the James S. McDonnell Foundation Postdoctoral Fellowship Award, and she joined the laboratory of Dr. Justin Sonnenburg at Stanford. During her post-doc, Dr. Tropini applied her background in biophysics to study the impact of physical perturbations on host-associated microbial communities living in the gut.

**Wednesday July 16 - 09:05-09:35**

**Leveraging the gut environment for functional biosensor microbes**

Abstract: The human gut is a complex, dynamic ecosystem characterized by a diverse community of microbes that play critical roles in health and disease. However, despite the profound impact of physical forces like osmolality, pH, and oxygenation on microbial behavior, these factors remain underexplored in the context of microbiome research and therapeutic development. Given the gut's natural mosaic of localized niches, where distinct physical environments shape unique microbial communities, it is essential to understand how these forces influence microbiota structure and function.

Our work aims to harness the gut's physical landscape as a blueprint for engineering next-generation biosensor microbes. By integrating insights from physical microbiology with advanced synthetic biology, we are developing genetically engineered microbes capable of sensing and reporting on critical gut parameters. Our approach uses Bacteroides, a prominent and genetically tractable gut commensal, to build biosensors that detect environmental shifts.

In proof-of-concept studies, we engineered biosensors responsive to malabsorption conditions, demonstrating their ability to detect physiological changes in gut health through graded fluorescent outputs in both in vitro and in vivo models. These biosensors enabled near real-time, non-invasive monitoring of single-cell responses in a murine model of malabsorption, revealing the potential of gut-resident bacteria as diagnostic platforms for diverse gastrointestinal disorders.

By integrating biophysical understanding with cutting-edge genetic tools, this work highlights the potential of engineered gut microbes to transform our ability to monitor and manage gut health, bridging the gap between microbiome science and precision diagnostics.

## The Sanders Award for Advancing Biotic Science 2025 Lecture

**Remco Kort, Vrije Universiteit Amsterdam, The Netherlands**

Prof Dr Remco Kort is a microbiologist dedicated to advancing research on commensal bacteria and their impact on human health. He is a Full Professor of Microbiology at the Vrije Universiteit Amsterdam and ARTIS-Micropia Chair, where he develops innovative ways to engage the public with microbiology. As co-founder of the Yoba for Life Foundation, he has played a key role in introducing probiotic yogurt to communities in Uganda, Tanzania, and Ethiopia, supporting local health and entrepreneurship. His research spans microbiome interventions, microbial genomics, and fermented foods, and he has been instrumental in citizen science initiatives on vaginal and gut health. Beyond academia, he is an advocate for planetary health and co-developer of ARTIS-Micropia, the world's first microbe museum. He has authored over 100 scientific publications and the popular science book 'De Microbemens'.

**Wednesday July 16 - 09:35-10:00**

**Two decades of applied research for the advancement of biotic science**

Abstract: Over the past two decades, groundbreaking research has shaped the field of biotic science, transforming our understanding of its impact on health and society. This presentation highlights my involvement over the last two decades in this fascinating and emerging field of research and its societal applications. The Yoba for Life initiative, established to address nutritional and economic challenges in East Africa, exemplifies how locally produced probiotic yogurts can improve health and empower communities. By deploying a novel *Lactobacillus*-based starter culture[1] alongside educational programs, this initiative has enabled sustainable health and economic benefits across Uganda, Tanzania, and Ethiopia. In Amsterdam, ARTIS-Micropia—the world's first microbe museum—serves as an innovative bridge between science and society. By visualizing the unseen world of microbes, it inspires visitors to appreciate their crucial role in human and environmental health, enabling broader public engagement with microbiome science. In addition, participatory nutrition interventions like the GEEF study[2] stimulate public involvement to explore the interplay between diet and microbiota, promoting sustainable lifestyle changes. Lastly, citizen science has also informed interventions for vaginal health[3]. Research into *Lactobacillus crispatus*[4], a key bacterium in maintaining a balanced vaginal microbiome, has led to novel insights for the development of a multi-strain probiotic to prevent recurrence of bacterial vaginosis.

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**Howard Bauchner, Boston University Chobanian & Avedisian School of Medicine, USA**

Howard Bauchner, MD is a Professor of Pediatrics and Public Health at Boston University Chobanian and Avedisian School of Medicine. He served as the 16th Editor in Chief of JAMA and the JAMA Network between 2011 and 2021 and Editor in Chief of Archives of Disease in Childhood between 2003 and 2011. At BUSM, prior to JAMA, he was Vice-Chair of Research for the Department of Pediatrics and Chief, Division of General Pediatrics. He is a member of the National Academy of Medicine and an honorary fellow of the Royal College of Paediatrics and Child Health. He has been a Visiting Scholar at the National University of Singapore between 2022-2024 and has continued to write on issues such as conflict of interest, pre-print servers, drug-approval, open-science, and the role of AI in scientific publication.

At JAMA Howard focused on publishing important and novel research articles including randomized clinical trials, opinion pieces, and special communications, improving and expanding clinical content, using electronic/digital approaches to enhance communication, ensuring a commitment to innovation and increasing diversity. During his tenure followers on social media increased from ~13,000 to ~1,200,000 and the electronic table of contents was distributed to over 1,000,000 individuals each week. In print, via eTOC, and social media content published by JAMA reached over 1.5M physicians worldwide each week. Views (PDF and HTML) increased from 10M in 2011 to over 100M in 2020 (50% from outside the U.S.). Podcast downloads increased from 300,000 in 2014 to 6M and videos were viewed more than 16M times in 2020. The print journals were redesigned for the first time in over 20 years and the website updated twice. All 9 of the specialty journals were renamed (Archives of Pediatrics became JAMA Pediatrics, etc.), 4 new journals were launched – JAMA Oncology (2015), JAMA Cardiology (2016), and JAMA Network Open (2018); and JAMA Health Forum (2020/2021), the latter 2 are both fully open-access journals. Howard authored and recorded over 200 editorials and podcasts (including live-stream events) discussing issues such as open-science (data-sharing, pre-print servers, open access), conflict of interest, diversity in medicine, the interpretation of randomized clinical trials, mentoring, maintaining editorial standards during a pandemic, the language and reporting of race and ethnicity, scientific misconduct, authorship and team science, and numerous health policy issues, including healthcare as a right, waste in medicine, the cost of health care, health care disparities, and race, racism, equity, and poverty in medicine.

**Wednesday July 16 - 10:30-11:00**

**The scientific communication ecosystem: the responsibility of investigators**

Abstract: Many people participate in the communication of science, including investigators, institutions, federal agencies, and journals. The approach to communication now includes the printed page, videos, podcasts, and social media. Communication begins with investigators, and they have a responsibility to present their work without bias, and consistent with the primary goals of a study. In addition to investigators, "experts" are often asked to comment on science - they need to be aware of their biases, and not to overstate the quality of evidence supporting their views.

**Wednesday July 16 - 11:00-12:30**

## Expert Panel: Clinical translation of biotic science: How can we enhance impact for clinical practice?

Aiding the efficient and timely translation of research to practice is a challenge for all health sciences, and the field of biotic science is no exception. Clinical research on probiotics, prebiotics, postbiotics, synbiotics and fermented foods continues to grow year each year, creating a wide range of evidence-backed interventions with significant potential to improve patient health. At the same time, growing public and market interest in the concepts of gut health and the microbiome contribute at times to a landscape of misconception and hype.

Scientists from both industry and academic backgrounds are in a unique position to influence the successful translation of biotic research into clinical settings, through appropriate and clinically relevant research design, conduct and reporting, as well as communication and outreach efforts tailored to a clinical audience. This panel will explore the challenges and paths forward for clinical implementation of biotic science, including the identification of key research gaps, study quality issues, research interpretation and misinterpretation challenges, communicating to clinicians, and other barriers for translation.

The expert panel includes the following speakers:

**Howard Bauchner**
**Boston University Chobanian & Avedisian School of Medicine, USA**

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**Daniel Merenstein**
**Georgetown University, USA**

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**Hania Szajewska**
**Medical University of Warsaw, Poland**

See page 34 for bio

**Geoffrey Preidis**
**Baylor College of Medicine and Texas Children's Hospital, USA**

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**Kristina Campbell**
**Science writer, Canada**

Kristina Campbell (M.Sc.) is a science and medical writer who specializes in creating books and other scientific resources on the gut microbiome and biotics. She holds degrees from University of Toronto and University of British Columbia, and now lives in Victoria (Canada).

**Kristie Leigh, Danone North America, USA**

Kristie Leigh, RDN is the Director of Nutrition and Scientific Affairs at Danone North America. Since 2015 Kristie has been leading efforts to educate and valorize the science behind biotics, gut health, and plant-based nutrition. She plays a pivotal role in supporting Activia and DanActive, as well as plant-based brand Silk.

**Kyle Sloan, Procter & Gamble, USA**

Kyle Sloan is in Scientific Communication for Procter & Gamble's Digestive Wellness business. His focus is on bringing to life the science behind the products in easy to understand formats tailored to each audience: consumers, retailers and health care professionals. Previous work experiences include medical affairs and working as a retail pharmacist.

ISAPP

**Haruki Kitazawa, Tohoku University, Japan**

Dr. Haruki Kitazawa is the Dean of the Graduate School of Agricultural Science at Tohoku University (Japan). He earned his Ph.D. in 1993 from Tohoku University, focusing on the immunomodulatory functions of phosphopolysaccharides produced by lactic acid bacteria. He has been actively involved in international research collaborations, particularly with CERELA-CONICET (Argentina), exploring the potential of immunomodulatory probiotics and postbiotics. His outstanding contributions to the field are reflected in his authorship of over 300 internationally peer-reviewed publications on probiotics and postbiotics. His current research focuses on the immunoregulatory properties of probiotics, postbiotics and synbiotics via Gut-mucosal tissue axis. Additionally, he is pioneering in the development of advanced in vitro evaluation systems, utilizing diverse livestock cell lines to enhance the scientific understanding and application of probiotics and postbiotics in animal and human health.

**Wednesday July 16 - 14:30-15:00**

**Probiotics and postbiotics to regulate the immune system: what can we gain or lose from viability or inactivation?**

Abstract: The viability state of bacteria fundamentally distinguishes probiotics from postbiotics. The immunomodulatory postbiotics obtained through the heat treatment of live bacteria (HT postbiotics) have gained interest not only because of their ease of obtention compared with the purification of probiotic effector molecules, but also because of their potential to improve health in the growing populations of immunocompromised hosts. Research from the last decades has demonstrated that HT postbiotics can beneficially modulate immunity, in some cases in a similar way to that achieved by live microorganisms and in others to a lesser or greater extent. These findings may be associated to the distinct probiotic strains evaluated in the studies as well as the different inflammatory/infection contexts, animal/cell models, doses and specific heat treatments used. Therefore, the mechanisms by which probiotics and HT postbiotics differentially influence host immunity remain incompletely understood, partly due to limited comparative studies using the same bacterial strain under the same experimental conditions. On the other hand, the lack of *in vitro* systems that more accurately mimic the cellular and molecular interactions between probiotics or HT postbiotics and the host immune system has also delayed the understanding of the mechanisms involved in their beneficial effects. In this talk, first a review of the publications in which probiotic strains and their HT postbiotic derivatives were comparatively evaluated will be conducted, focusing on their interaction with the immune system and their equal or distinct capacity to confer the beneficial effects. In a second part, the development and implementation of a new *in vitro* system that could allow a more precise study of probiotic strains and their HT postbiotic derivatives will be described. This *in vitro* microfluidic co-culture system with swine intestinal epithelial cells (SIECs) coupled to integrated transcriptomic and metabolomic analyses revealed distinct cell responses shaped by the bacterial viability state when an immunomodulatory *Lactiplantibacillus plantarum* strain and the HT derivative where compared. The presentation will focus on the mechanistic insights gained from these findings and discuss their broader implications for optimizing probiotic and HT postbiotic strategies to support immune health.

Authors and affiliations: Kaho Matsumoto[1], Keita Nishiyama[1,2], Fu Namai[1,2], Julio Villena[2,3], Tomoyuki Hashimoto[4], Haruki Kitazawa[1,2]*.
[1]Food and Feed Immunology Group, Laboratory of Animal Food Function, Graduate School of Agricultural Science, Tohoku University, Sendai 980-8572, Japan. [2]Livestock Immunology Unit, International Education and Research Centre for Food and Agricultural Immunology (CFAI), Graduate School of Agricultural Science, Tohoku University, Sendai 980-8572, Japan. [3]Laboratory of Immunobiotechnology, Reference Centre for Lactobacilli (CERELA-CONICET), Tucuman 4000, Argentina. [4]Technology Research Laboratory, Shimadzu Corp., Kyoto, Japan.

**Guy Vergeres, Agroscope, Switzerland**

PD Dr Guy Vergères leads the research group Functional Nutritional Biology at Agroscope in Bern, Switzerland. He also leads WG3 of the COST Action "Promoting Innovation of fermented foods' (PIMENTO)" on the health benefits/risks of fermented foods. Guy Vergères teaches nutrigenomics at ETH-Zurich and the University of Lausanne. His translational research focuses on the nutritional properties of fermented foods making use of the recent advances in analytical strategies in food (foodomics) and nutrition (nutrigenomics) sciences. His research spans from the genomic selection of bacterial strains to produce fermented food with targeted composition to intervention studies in animal models and humans investigating the impact of food fermentation on metabolism and finally to observational studies aimed at determining the relationship between the intake of fermented foods or live microbes and human health.

**Wednesday July 16 - 15:00-15:30**

**Health benefits of fermented food: from bacterial genomes to dietary guidelines**

Abstract: Research into the health benefits of fermented foods is expanding rapidly, driven by both consumer interest and scientific advancements. Key developments in microbial genomics, foodomics, and nutrigenomics, along with the recognized influence of gut microbiota on health, have highlighted the potential of fermented foods as functional dietary components. However, understanding their effects on human physiology remains complex.

The FerFood.CH project adopts a translational approach to study fermented foods through *in silico*, *in vitro*, animal, and human studies. Bioinformatics tools were developed to analyze the annotated genomes from a culture collection containing over 12,000 isolates and to link the genomes of selected strains to the phenotypes of fermented milk products. Yogurt consumption by germ-free pregnant mice improves intestinal immunity of their offspring. In human crossover studies, fermented dairy modify postprandial metabolic responses, influenced by both product types and individual factors such as age and genetics. Finally, removing fermented foods from diets changes gut microbiota composition.

To better understand population-level effects, observational studies were conducted to quantify fermented food- and dietary microbe intakes and to link them to health outcomes. A food frequency questionnaire was also developed within the COST Action CA20128 (PIMENTO) to track the consumption of specific fermented foods and food groups. Additionally, biomarkers in blood and urine were identified that correlate with the intake of fermented foods and clinical endpoints.

The COST Action PIMENTO also undertook systematic reviews of clinical literature to objectively assess the benefits of fermented foods. This approach mirrors regulatory requirements for health claims by integrating data on food characteristics, mechanisms of action, and bioavailability. Taken together, research activities such as FerFood.CH and PIMENTO provide support, based on robust scientific evidence, for the inclusion of fermented foods and dietary microbes in national dietary guidelines.

**Maria Marco, University of California, Davis, USA**

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**Wednesday July 16 - 15:30-16:00**
**Gut health: An ISAPP consensus definition effort**

Abstract: The term *gut health* is increasingly used as a catch-all phrase by many stakeholders, including scientists, healthcare professionals, industry, and consumers to describe a wide range of health-related concepts. However, the term can be interpreted to encompass any number of health-promoting outcomes. An ISAPP panel comprised of experts across diverse medical and scientific fields was convened in September 2024 to address the current state of knowledge on the physiology, manifestation, application, and measurement of gut health. This talk will summarize the main findings of the expert panel, including a consensus definition, a comprehensive framework for application of the term across functional, subjective, and extrinsic domains, and clinically relevant and accessible metrics available to assess gut health.

**The Glenn Gibson Early Career Researcher Award 2025 Lecture**
**Peijun Tian, Jiangnan University, P. R. China**

Peijun Tian is an Associate Professor and Master's supervisor at the School of Food Science and Technology, Jiangnan University. He earned his Ph.D. in Food Science from Jiangnan University (January 2021) and was a visiting scholar at the APC Microbiome Institute, Ireland (September 2019–October 2020). He completed postdoctoral research at Jiangnan University, supported by the prestigious "National Postdoctoral Program for Innovative Talent" (top 1% in China). His research focuses on elucidating the interactions between gut microbiota and brain function, exploring the application of probiotics to mitigate stress, support neurodevelopment, and address neurodegenerative disorders. He has authored over 30 peer-reviewed articles, including three ESI Highly Cited Papers, with an H-index of 23 (Google Scholar, March 2025). In 2025, he was honored with the Glenn Gibson Early Career Researcher Award by the International Scientific Association for Probiotics and Prebiotics (ISAPP).

**Wednesday July 16 - 16:00-16:15**
**Psychobiotics: unveiling the molecular basis of host mood regulation**

Abstract: The microbiota–gut–brain axis has opened up a revolutionary perspective for brain health modulation and has led to the emergence of psychobiotics as an effective intervention strategy. Psychobiotics have been widely demonstrated to exert beneficial effects on mood regulation, social behavior, sleep, and even neurodevelopment, with increasing clarity regarding their mechanisms, targets, and host interactions. However, most existing studies remain fragmented, and the discovery of effective strains have mostly been discovered by chance. Moreover, there has been little effort to identify the shared microbiological traits among these strains — a critical step for the efficient selection and development of novel, more potent psychobiotics. In our previous work, through animal studies and clinical trials, we identified Bifidobacterium breve CCFM1025 as a strain with antidepressant properties. Using a gut organoid model, we established a dose–response analytical framework and screened multiple candidate effector molecules, including acetate, purines, and indole-3-lactic acid. Further employing gene editing and multi-omics approaches, we systematically revealed the bidirectional regulatory roles of these microbial metabolites on host mood (either promoting or inhibiting mood regulation). Our findings provide molecular and genetic evidence supporting the functional mechanisms of psychobiotics, paving the way for more targeted and efficient strain development.

## The Gregor Reid Award for Outstanding Scholars in Developing Nations 2025 Lecture

**Josiane Kenfack, University of Yaounde I, Cameroon**

Josiane Kenfack is a PhD student passionate about scientific research aimed at improving women's health through the advancement of studies of the vaginal microbiome and probiotics. Josiane is co-coordinator of a citizen science project in Cameroon, the LEKE project. This project was inspired by the Isala project (https://isala.be/en/) which aims to better understand the female microbiome while raising awareness about vaginal health and breaking taboos. Through the LEKE project, Josiane and colleagues have conducted field activities to explore vaginal and menstrual health and promote good practices with women and men in rural and urban areas. In her ongoing research, she is investigating beneficial lactobacilli that could serve as biotherapeutics or probiotics development to combat conditions such as bacterial vaginosis, HIV, and sexually transmitted infections which are still prevalent in Africa. while she co-coordinates in Cameroon the IMVAHA project which aims to determine the impact of different menstrual products on the vaginal microbiome.

**Wednesday July 16 - 16:15-16:30**

**The Leke project: Mapping the vaginal microbiome and benefits of vaginal lactobacilli in Cameroon.**

Abstract: The vaginal microbiome has gained increased attention in the last decades, with increasing documentation on the role in women's health and health of their families. Yet we lack an in-depth comprehension of the factors fostering a healthy vaginal ecosystem, slowing down the development of much-needed effective diagnostic and therapeutic approaches. Notably, there exists a substantial knowledge deficit regarding the vaginal microbiome in regions like Sub-Saharan Africa. Our research aims to bridge this gap by delving into the vaginal microbiome dynamics in Central Africa (Cameroon) using state-of-the-art microbiome analyses. This includes research on the ecological and metabolic benefits of vaginal lactobacilli based on the culture swabs, to select a few promising candidate strains that could be applied in live biotherapeutics or probiotics. Application areas of interest are HIV infection and bacterial vaginosis, which are both highly prevalent in Africa (28,5% - 52,4%). We started a sampling campaign in March 2023, with four distinct cohorts: healthy women residing in rural and urban areas, HIV-positive pregnant women, and HIV-negative pregnant women in Cameroon. Each participant contributed four vaginal swabs for comprehensive analysis: eNat swabs for microbiome sequencing, Eswab for culturomics and metabolomics, and two dry swabs (for vaginal pH measurement and bacterial vaginosis assessment using the Nugent score). Participants also filled in a survey on lifestyle, sociodemographic, reproductive, and sexual health. Our results showed bacterial vaginosis prevalence was 58,98%, which appear higher than studies in women from European descent. The microbiome sequencing data of women from rural and urban areas (107) showed that *Lactobacillus. crispatus* was the dominant taxa in only 13%, while this taxon on dominant in women from European descent. The most prevalent taxa were *Lactobacillus. iners* group (38.8%), *Prevotella* (22.4%), and *Bifidobacterium* (10.3%). However, the vaginal profile for women from rural areas showed more abundance of *Lactobacillus crispatus*. We are now analyzing survey data. Further analysis will be focused on lactobacilli as well as bacterial vaginosis-like bacteria. The aim will be to investigate the probiotic potential of our lactobacilli isolates lactobacilli, and its intraspecies diversity compared to lactobacilli isolated from Belgian women.

**IAC Highlight**

**Maria Rodríguez-Palmero, AB Biotics, Spain**

Maria Rodríguez-Palmero holds a PhD in nutritional sciences and Pharmacy from the University of Barcelona and has completed a Management Development Program at IESE Business School. She trained in nutrition and metabolism at the Pediatric Hospital of the Ludwig Maximilians University of Munich, Germany, supported by the Alexander von Humboldt Foundation. With over 25 years of experience in research and innovation within the pharmaceutical and food industries, her scientific interests focus on infant nutrition and probiotics. She currently serves as Director of the Medical Department at AB-BIOTICS, a biotechnology company dedicated to the research and development of probiotics for various health applications. Maria is the author of more than 50 scientific publications and conference communications, and she is an active member of several scientific societies.

**Thursday July 17 - 09:00-09:15**

**Effects of a probiotic formula containing *Levilactobacillus brevis* KABP 052, *Lactiplantibacillus plantarum* KABP 051, and *Pediococcus acidilactici* KABP 021 on symptoms and quality of life in peri- and postmenopausal women (GynMeno trial).**

Abstract:

Introduction

Falling estrogen levels are the main cause of menopausal symptoms, which can significantly impair women's quality of life [1]. Up to 86% of women report symptoms bothersome enough to seek medical care[2]. The estrobolome—a subset of the gut microbiota involved in estrogen metabolism—plays a key role in hormonal balance [3,4]. Emerging evidence suggests menopause is associated with estrobolome alterations, including reduced microbial diversity [5]. Modulating estrobolome activity through targeted probiotics may offer a natural strategy to alleviate menopausal symptoms. A recent trial showed that the probiotic blend Gyntima® Menopause may help slow estrogen decline via β-glucuronidase activity, contributing to estrobolome modulation[6]. This study evaluates its efficacy in symptom reduction and quality of life improvement.

Methods

This real-world, prospective, randomized, double-blind, placebo-controlled trial was conducted in Spain. Women aged 45–60 in peri- or early postmenopause (≤5 years) with Cervantes Scale score >38 were included. Participants received either Gyntima® Menopause (*L. brevis* KABP-052, *L. plantarum* KABP-051, *P. acidilactici* KABP-021; $1\times10^9$ CFU/day) or placebo once daily for 3 months. Study outcomes included changes in Menopause Rating Scale (MRS)-II, Utian Quality of Life Scale (UQoL) and Gastrointestinal Symptom Rating Scale (GSRS) scores evaluated monthly throughout the intervention period. For comparisons between groups, statistical analyses using generalized linear models adjusted for baseline, BMI, and physical activity were performed.

Results

A total of 221 women completed the study (per protocol population). Demographic characteristics, MRS-II, Utian QoL and GSRS scale scores were similar between probiotic and placebo groups at baseline. MRS-II total score was significantly reduced in the probiotic group compared to placebo (p=0.012, fully adjusted). UQoL scores improved significantly in the probiotic group compared to placebo (p=0.039). No significant differences were observed in GSRS scores. The product was well tolerated, with no serious adverse events and high participant satisfaction.

Conclusion

Gyntima® Menopause significantly reduced menopausal symptoms and improved quality of life over 3 months compared to placebo. These findings support the potential of targeted probiotic therapy as a safe, non-hormonal option for managing menopause-related symptoms.

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Authors and Affiliations:
Maria Rodriguez-Palmero[1], Claudia Prat[1], Jordi Espadaler-Mazo[1], Marta Perez[1], Bianca Bolatti[1], Silvia P. González[2].
[1]AB-BIOTICS SA (Part of Kaneka Corporation), Sant Cugat del Vallès, Spain
[2]HM Gabinete Velázquez, HM Hospitales, Madrid, Spain

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**IAC Highlight**
**Elaine Vaughan, Sensus/ILSI, The Netherlands**

Elaine Vaughan (BSc PhD) leads health science and regulatory affairs since 2014 for Sensus (Royal Cosun) where she conducts scientific research on the beneficial effects of prebiotic fibers and other plant-based ingredients on human health. Elaine studied microbiology as well as nutrition, cell biology and immunology, and obtained her PhD in molecular microbiology aspects of dairy cultures at University College Cork, Ireland. She has since led research in both industry and academia, including at Nestle Research Center-Switzerland, Unilever-the Netherlands, and as assistant professor at Wageningen University and Top Institute Food & Nutrition (TIFN), in various fields of research in probiotic / prebiotic /polyphenols food ingredients on impact on gut microbiome and health. Elaine represents Sensus at International Life Sciences Institute-Europe and other associations, and has published extensively in journals and edited one of the first books dedicated to gastrointestinal microbiology.

**Thursday July 17 - 09:15-09:30**
**Towards EU health claims for prebiotics: A focus on scientific evidence and regulatory pathways**

Abstract: The Prebiotic Task Force of the International Life Sciences Institute (ILSI) Europe plays a key role in advancing the scientific understanding of prebiotics and their health benefits. Comprising academic advisors and industry scientists, the Task Force works to provide robust scientific evidence supporting the development of prebiotic-containing foods and dietary supplements aimed at improving gut health and overall wellbeing. Last year, the Task Force published a comprehensive framework to address the regulatory challenges of establishing prebiotic health claims in the European Union (EU) and furthering scientific understanding of health benefits.

In the EU, health claims must demonstrate a direct cause-and-effect relationship between the food component and the physiological health benefit, such as supporting bowel habit.

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However, there is currently no guidance from the European Food Safety Authority (EFSA) on the scientific requirements for health claims related to the term 'prebiotic' as exists for physiological benefits, and it's considered to be an implied health claim. Ideally to establish a prebiotic health claim, a causal link should be drawn between specific microbiota changes and their associated health benefits.

An initiative organized by the ILSI Europe Prebiotic Task Force brought together academic, regulatory and industry scientists who took up the challenge of advancing the science and regulation of prebiotics, which has culminated in a roadmap for the development of a scientifically sound framework for prebiotic health claims with emphasis on Europe. This roadmap proposes the necessary scientific evidence, including clinical trials, to substantiate prebiotic claims. Moreover, the scientific status in the health benefit fields of digestion, metabolism, immunity, and cognition were reviewed with respect to their potential for health claims, and current gaps to achieve this. In the latter respect, there is an important role for molecular technologies, such as high-throughput sequencing, multiplex community sequencing, and metabolomics, as well as machine learning and artificial intelligence to further the science of prebiotics impact on health. Such approaches may facilitate the prediction of individual microbiota responses and be used to support effective clinical trials. These harmonized approaches can support the establishment of definitive links between microbiome modulation and specific health outcomes, together with high-quality randomized controlled trials and robust statistical approaches. Overall this study provides important insight into the regulatory and scientific path forward for prebiotic health claims, especially for Europe, which is essential for advancing the credibility of prebiotics and fostering their use in food products with scientifically substantiated health claims for consumers.

Authors and Affiliations:
Kieran Tuohy[1], Elaine E Vaughan[2*], Lucien F Harthoorn[3], Ellen E Blaak[4], Philip W J Burnet[5], Alessandro Busetti[6], Anirikh Chakrabarti[7], Nathalie Delzenne[8], Paul de Vos[9], Louise Dye[10], Damien Guillemet[11], Lesley A Houghton[12], Alwine F M Kardinaal[13], Cath Mersh[14], Kathy Musa-Veloso[15], Annegret Nielsen[16], Justyna Palasinska[17], Seppo Salminen[18], Gemma Walton[19], Naomi Venlet[20], Charlotte Hubermont[20], Georgia Chatonidi[20], Philip C Calder[21]

[1]School of Food Science & Nutrition, University of Leeds, Leeds, UK.
[2]Sensus (Royal Cosun), Roosendaal, The Netherlands.
[3]Clasado Ltd, Reading, UK.
[4]Department of Human Biology, NUTRIM, School of Nutrition and Translational Research in Metabolism, Maastricht University Medical Centre+, Maastricht, The Netherlands.
[5]Department of Psychiatry, University of Oxford, Oxford, UK.
[6]Metabolon Inc, Morrisville, NC, USA.
[7]Cargill R&D Centre Europe, Vilvoorde, Belgium.
[8]Woluwe Louvain Drug Research Institute, UCLouvain, Brussels, Belgium.
[9]Pathology and Medical Biology, University Medical Center Groningen, Groningen, The Netherlands.
[10]Institute for Sustainable Food, University of Sheffield, Sheffield, UK.
[11]Nexira, Rouen, France.
[12]Leeds Institute of Medical Research, University of Leeds, Leeds, UK.
[13]NIZO, Ede, The Netherlands.
[14]Cath Mersh Communications, Aarhus, Denmark.
[15]Intertek Health Sciences Inc., Mississauga, ON, Canada.
[16]Analyze & Realize GmbH, Berlin, Germany.
[17]Argenta Barcelona, Barcelona, Spain.
[18]Center for Food and Nutrition Research, Faculty of Medicine, University of Turku, Turku, Finland.
[19]Food and Nutritional Sciences, University of Reading, Reading, UK.
[20]ILSI Europe, Brussels, Belgium.
[21]School of Human Development and Health, Faculty of Medicine, United Kingdom and NIHR Southampton Biomedical, Research Centre, University Hospital NHS Foundation Trust and University of Southampton, Southampton, UK.

**SFA Highlight**
**Valentina Cattero, Laval University, Canada**

Valentina Cattero is a researcher in microbiome–nutrition interactions, recently graduated with a PhD in Plant Biology from Laval University (Québec), where she was affiliated with the Institute of Nutraceuticals and Functional Foods. Her work investigates the impact of cranberry-derived bioactives on gut microbiota composition and intestinal epithelial function, using both ex vivo and in vivo models. She combines microbiology, metabolomics, and transcriptomics to elucidate diet–microbiota–host mechanisms relevant to intestinal and systemic health. Valentina holds an MSc in Medicinal Natural Products and Phytochemistry from University College London and a BSc in Gastronomic Sciences from the University of Gastronomic Sciences in Italy. Her interdisciplinary background spans ethnobotany, functional foods, and science communication. She received Best Oral Presentation awards at the Food Bioactives and Health Conference (2022) and the International Conference on Polyphenols and Health (2024). She is dedicated to translating traditional plant knowledge into evidence-based strategies at the intersection of microbiota-driven research, nutrition, and plant bioactives.

**Thursday July 17 - 09:30-09:45**
**Prebiotic-like activity of cranberry extract: Modulating gut microbiota composition and enhancing intestinal barrier function in ex vivo and in vivo models**

Abstract:
Background: Proanthocyanidins (PAC) and oligosaccharides from cranberry exhibit multiple bioactive health properties and persist intact in the colon post-ingestion. Their interaction with the microbiome and the resulting effect on the gut epithelium remains inadequately understood. Methods: Six healthy participants underwent a two-week intervention with cranberry extract using the ex vivo TWIN-M-SHIME model, replicating the luminal and mucosal environments of the ascending and transverse colon. Fermentation effluents from four donors were incubated with murine intestinal organoids to assess gene expression related to epithelial differentiation, barrier integrity, and receptor signaling. Results: Cranberry extract supplementation significantly influenced gut microbiota ecology, altering bacterial metabolism. *Bifidobacterium adolescentis* flourished in the mucus of the ascending colon, accompanied by reduced Proteobacteria adhesion. The metabolism shifted from acetate to propionate and butyrate production, with a consistent butyrogenic effect across donors followed by the enrichment of several short-chain fatty acid producing bacteria and the formation of a consortium of key butyrogenic bacteria in the transverse colon mucus. Organoid incubations revealed increased expression of genes related to goblet cell differentiation, mucus production, intestinal barrier integrity, and metabolites receptors. Butyrate correlated with defensin regulation and GPR109a expression. Interestingly, effects stabilized after two weeks, suggesting microbiota and epithelial adaptation. Conclusions: Cranberry extract supplementation can beneficially modulate gut microbiota and epithelial function, supporting gut barrier integrity and overall gut health.

**SFA Highlight**
**Kait Al, Western University, Canada**

Dr. Kait Al is a postdoctoral fellow in the Department of Microbiology and Immunology at Western University, Ontario, Canada, working in the lab of Dr. Jeremy Burton. She is passionate about translational research and investigating the microbiome in clinically relevant, human-centered contexts. Throughout her doctoral and postdoctoral training, she has studied microbial influences and the potential of microbiome-modulating therapies for a wide range of conditions, including kidney stones, organ transplantation, cancer, and mental health. Currently, her research focuses on the role of short-chain fatty acids—particularly acetate—in metabolic health and disease. Outside the lab, she enjoys reading, exploring nature, and spending time with her dog, Bunsen.

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**Thursday July 17 - 09:45-10:00**

**Acetate and the gut-brain axis: A pilot study on mental health and metabolic outcomes**

Abstract: Mental illnesses affect 1 in 5 Canadians, most often mood and anxiety (M/A) disorders, which can require the use of psychotropic medications. However, these medications are commonly associated with weight gain and metabolic side effects. The gut microbiota plays a role in mental illnesses via the gut-brain axis, with short-chain fatty acids like acetate influencing both microbiota composition and metabolic outcomes. This study evaluated the feasibility of acetate supplementation (enteric coated high-potency apple cider vinegar powder) to beneficially alter the gut microbiota and mitigate metabolic side effects in individuals with M/A disorders. 11 participants, aged 16–35, who experienced weight gain on stable medication doses, underwent a 1-month baseline assessment, 3 months of acetate administration (3 caplets twice daily) and a 1-month follow-up observation period. Adherence was excellent and no product-associated adverse events occurred. While no significant weight reduction was observed, M/A symptoms significantly improved, as measured by validated instruments. 7 participants also had meaningful reductions in LDL cholesterol and/or triglycerides. 16S rRNA gene sequencing of gut samples from the first 5 participants revealed significant shifts in gut microbiota composition, including enrichment of beneficial species such as *Bifidobacterium* spp., *Lactiplantibacillus* spp., and *Akkermansia muciniphila*. These findings suggest that acetate use may be a feasible approach to improving mental health symptoms and metabolic profiles of some patients with M/A disorders on psychotropics. Future studies with larger sample sizes and extended follow-up are warranted to confirm these effects, identify subgroups of responders, and explore the intervention's clinical relevance.

**André Marette, Université Laval, Canada**

Dr. André Marette is a Professor of Medicine and researcher at the Heart and Lung Institute Hospital Center (IUCPQ), and at the Institute of Nutrition and Functional Foods (INAF) at Laval University. He holds a Valbiotis Research Chair in plant bioactives and metabolic liver diseases and a Pfizer Research Fund in the pathogenesis of insulin resistance and cardiovascular complications.

Dr. Marette is an international renowned expert on how nutrition and the microbiome modulate immunometabolic pathways involved in obesity and cardiometabolic diseases (CMD). He is investigating the metabolic impact of nutritional interventions and microbiome-based therapeutics (probiotics, prebiotics) using both clinical and pre-clinical studies, and uses various cellular models and molecular tools to discover novel disease biomarkers and mechanistic targets. Dr. Marette's research work has been published in over 330 papers, reviews and book chapters and also authored two books.

He has received several awards for his work including the prestigious Charles Best Award and Lectureship from the University of Toronto for his overall contribution to the advancement of scientific knowledge in the field of diabetes.

**Thursday July 17 - 10:05-10:35**

**Next generation probiotics for metabolic and liver health**

Abstract: There is growing evidence that changes in the gut microbiome contributes to the pathogenesis of obesity and associated chronic inflammatory diseases. Loss of commensal microbes can lead to intestinal inflammation and altered gut integrity thus promoting metabolic alterations and insulin resistance. Beneficial gut microbes were isolated from fecal samples and developed as first-generation probiotics with demonstrated health effects in several animal models of metabolic diseases and a limited number of proof-of-concept human trials. Despite the early promise of several fecal microbiota-based therapeutics, only few probiotics have been approved for clinical use and even less are currently developed as novel microbiome-based drugs. In this presentation, I will discuss new strategies to develop next generation probiotics and related microbiome therapeutics based on both fecal and non-fecal bacteria that are readily culturable (or not yet) and designed to improve metabolic and liver health in people with obesity and the metabolic syndrome.

# Late Breaking News

**Wednesday July 16 - 16:40- 17:30**

The Late Breaking News session provides an opportunity for ISAPP meeting delegates to share interesting data, perspectives, or developments in 5-minute talks. **Start times** are approximate for this fast-moving session.

Chaired by Bob Hutkins, University of Nebraska – Lincoln, USA

**16:40** William Chen: Fungal Precision Fermentation and Future Foods

**16:45** Elke Lievens: Binding the Unseen: Probiotics vs. Microplastics

**16:50** Kjersti Aagaard: Yum yum bubble gum...chewing gum for preterm birth prevention?

**16:55** Caroline Montelius: *L. plantarum* 299v reduces side effects of iron therapy in anemia

**17:00** Colin Hill: The microbiome: An actor or stage for biotic activity?

**17:05** Gabriel Vinderola: Latest guidance on categorising and quantifying postbiotics

**17:10** Tommy Auchtung: Improving lactose intolerance with *Bifidobacterium adolescentis* iVS-1

**17:15** Siobhan McCormack: Microbiome narratives for behaviour change

**17:20** Sabrina Green: Phage Support Ukraine, a project to combat multidrug-resistant bacteria

**17:25** Bruce Y. Lee: How to talk to the media about prebiotics, probiotics, postbiotics, and the microbiome

# Board of Directors

**Maria Marco, University of California, Davis, ISAPP President**

Dr. Maria Marco, PhD, is a Professor in the Department of Food Science and Technology at the University of California, Davis. She earned her bachelor's degree in microbiology at The Pennsylvania State University and her PhD in microbiology at the University of California, Berkeley. As a postdoc at NIZO food research in The Netherlands, she developed a love for lactic acid bacteria and the importance of these microorganisms in our foods and the digestive tract. Her postdoctoral studies led to the discovery that probiotics are metabolically active in the intestine and responsive to dietary intake. Dr. Marco started her lactic acid bacteria and gut health laboratory at UC Davis in 2008 and has built an internationally-recognized, NIH, USDA, and NSF funded research program on probiotics, fermented foods, and dietary modulation of the gut microbiome. Dr. Marco also consults with and has received funding from international foundations and companies to investigate how certain microbes in foods or supplements may benefit health. She is active with science communication activities such as the EATLAC project and is the instructor for two food microbiology courses. Dr. Marco received a UC Davis Graduate Program Advising and Mentoring Award in 2024. She received the American Society for Microbiology Distinguished Lecturer award in 2012 and is currently a fellow in the American Academy of Microbiology. Dr. Marco attended her first ISAPP meeting as a postdoc and participated as an invited expert before joining the ISAPP Board of Directors in 2019.

**Sarah Lebeer, University of Antwerp, ISAPP Vice President**

Prof. Sarah Lebeer, PhD, is a research professor at the Department of Bioscience Engineering of the University of Antwerp, Belgium. She has studied bioscience engineering, with a specialisation in cell and gene technology/food & health, and obtained her Master at KU Leuven (Belgium). In 2008, she obtained a PhD degree with a topic on the mode of action of gastro-intestinal probiotics in inflammatory bowel diseases and a scholarship in the team of Prof. Jos Vanderleyden (KU Leuven). After a postdoc on the interaction between lactobacilli, viruses, and mucosal immunology, in November 2011, she was offered a tenure-track position at the University of Antwerp. Since then, she is leading the Laboratory for Applied Microbiology and Biotechnology. In 2020, she was awarded an ERC Starting Grant that enables her to gain more in-depth knowledge of the evolutionary history and ecology of lactobacilli. This rationale was also an important driving force to revise the Lactobacillus genus taxonomy with a large international consortium. Within the ERC project, Sarah has also launched the Isala citizen-science project to gain new insights into the role of vaginal lactobacilli for women's health. Since 2018, Sarah is an academic board member of the International Scientific Association on Probiotics and Prebiotics. Communicating about beneficial microbes and probiotics for experts and laymen is an important inspiration for her daily work.

**Daniel Merenstein, Georgetown University, ISAPP Past President**

Dr. Daniel Merenstein, MD, is a Professor with tenure of Family Medicine at Georgetown University, where he also directs Family Medicine research. Dr. Merenstein has a secondary appointment in the undergraduate Department of Human Science, in the School of Health. Dr. Merenstein teaches two undergraduate classes, a research capstone and a seminar class on evaluating evidence based medical decisions. He has been funded by PCORI, NIH, USDA, foundations and industry. The primary goal of Dr. Merenstein's research is to provide answers to common clinical questions that lack evidence and improve patient care. Dr. Merenstein is a clinical trialist who has recruited over 2,000 participants for 10 probiotic trials since 2006. He is an expert on probiotics, on antibiotic stewardship in outpatient settings, and also conducts HIV research in a large women's cohort. He sees patients in clinic one day a week. Dan was nominated into the National Academy of Medicine (NAM) in 2024.

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**Anisha Wijeyesekera, University of Reading, ISAPP Secretary**

Dr. Anisha Wijeyesekera, PhD, is an Associate Professor in Human Microbiome and Metabolome Studies, and Director of Postgraduate Research Studies in the Department of Food and Nutritional Sciences at the University of Reading, UK. She obtained her BSc (Hons) in Biomedical Sciences from the University of Durham (UK), MSc in Bioinformatics from the University of Exeter (UK), and PhD in Biochemistry from Imperial College London (UK). Her research interfaces analytical chemistry with microbiology and nutrition and applies 'omics technologies coupled with bio/chemoinformatics data analysis, for functional assessment of the human microbiota and to gain better insight into host-gut microbiota interactions. Dr. Wijeyesekera's research utilises in vitro laboratory model systems for studying the gut microbiota, as well as running human studies to capture information relating to microbial composition and function in vivo. She has wide ranging experience in the application of these analytical approaches in a number of research projects spanning the life course. These include pregnancy studies, infant early life, identifying signatures associated with disease outcome and in response to nutritional intervention in children, young and older adults, mining metabolite patterns associated with diet, microbiome and ageing that contribute to health status in large-scale human epidemiology studies, as well as stratified medicine clinical research projects. The ultimate aim of her research is to identify potential targets for therapeutic modulation through dietary intervention (in particular, prebiotics, probiotics and fermented foods), and capturing the impact of such interventions on gut and overall human health. Dr. Wijeyesekera's research portfolio includes projects funded by research councils, charities/societies, and the food industry. Dr. Wijeyesekera joined the ISAPP Board of Directors in 2021. She is also a member of the Academic Board for the Royal Society of Chemistry's Community of Analytical Measurement Sciences, and the London Metabolomics Network Committee.

**Kelly Swanson, University of Illinois, ISAPP Treasurer**

Prof. Kelly Swanson, PhD, is Director of the Division of Nutritional Sciences and the Kraft Heinz Company Endowed Professor in Human Nutrition at the University of Illinois Urbana-Champaign. He is also an Excellence in Nutrition Fellow of the American Society for Nutrition (ASN). His laboratory studies the effects of nutritional intervention on health outcomes, identifying how nutrients impact host physiology and gut microbiota, with primary emphasis on gastrointestinal health and obesity in dogs, cats, humans, and rodent models. Much of his lab's work has focused on dietary fibers, prebiotics, probiotics, synbiotics, and postbiotics. Over the past 2 decades, he has established an internationally recognized research program, highlighted by over $27 million in research support, 170 invited lectures at scientific and professional meetings, 275 peer-reviewed journal articles, and 18 research and teaching awards. He has trained over 55 graduate students and post-doctoral fellows, hosted 18 international visiting scholars, and mentored over 40 undergraduate research projects. In addition to research, Kelly teaches a couple classes each year to undergraduate and graduate students and has been named to the university's 'List of Teachers Ranked as Excellent by Their Students' over 35 times. He also serves on advisory boards for many companies in the human and pet food industries as well as non-profit organizations, including the Institute for the Advancement of Food and Nutrition Sciences (IAFNS).

**Karen Scott, Rowett Institute, University of Aberdeen**

Prof. Karen Scott, PhD, is a Professor of Research in the Gut Microbiology Group at the Rowett Institute, University of Aberdeen. She leads a research team investigating the (molecular) mechanisms by which key members of the gut microbiota interact with the diet and host, at different life-stages. The fermentation products of gut bacteria contribute to gut health and are differentially expressed on different substrates, including prebiotics. In vitro bacterial growth studies utilising the Rowett's large culture collection of gut anaerobes illustrate niche-specific processes and bacterial interactions, identifying strains with potential for development as probiotic/live biotherapeutic products. Utilisation of pure culture, co-culture, and mixed culture fermentor incubations combined with bioinformatic genome analysis, are essential to match genotype and phenotype and fully understand what happens in the complex gut ecosystem. This work is enhanced by the co-development of a system to understand interactions between anaerobic bacteria and human epithelial cells. Karen has numerous highly cited publications and has attracted multiple research council and commercially funded grants.

**Seppo Salminen, University of Turku**

Prof Seppo Salminen, PhD, is a Professor at the Faculty of Medicine and director of the Functional Foods Forum, University of Turku, Finland. He has been visiting professor at RMIT University, Melbourne, Australia, and BOKU University, Vienna Austria. His main research interests are probiotics, prebiotics, and intestinal microbiota modulation as well as functional foods and health and regulatory issues in novel foods and health claims. He has been active in the International Life Sciences Institute Europe, the International Dairy Federation, and the International Scientific Association for Probiotics and Prebiotics (past President and current Board Member). He received his MS at Washington State University (USA) in 1978, MSc from the University of Helsinki in 1979, and PhD from the University of Surrey (United Kingdom) in 1982. He has around 500 journal articles and several textbooks and book chapters and he has received several international awards including the ISF-Institute Pasteur Metchnikoff Price, Swiss Price on Modern Nutrition and the Grand Prix du Yoplait.

**Eamonn Quigley, Houston Methodist Hospital and Weill Cornell Medical College**

Dr. Eamonn M M Quigley MD FRCP FACP MACG FRCPI MWGO is David M Underwood Chair of Medicine in Digestive Disorders and Chief of the Division of Gastroenterology and Hepatology at Houston Methodist Hospital. A native of Cork, Ireland, he graduated in medicine from University College Cork. He trained in internal medicine in Glasgow, completed a two-year research fellowship at the Mayo Clinic, and training in gastroenterology in Manchester, UK. He joined the University of Nebraska Medical Center in 1986 where he rose to become Chief of Gastroenterology and Hepatology. Returning to Cork in 1998 he served as Dean of the Medical School and a PI at the Alimentary Pharmabiotic Center. He served as president of the American College of Gastroenterology and the WGO and as editor-in-chief of the American Journal of Gastroenterology. Interests include IBS, gastrointestinal motility and the role of gut microbiota in health and disease. He has authored over 1000 publications and has received awards and honorary titles world-wide. Married for over 40 years to Dr Una O'Sullivan they have 4 children and 5 grandchildren. Interests outside of medicine include literature, music and sport and rugby, in particular; Dr Quigley remains a passionate supporter of Munster and Irish rugby.

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**Hania Szajewska, The Medical University of Warsaw, Department of Paediatrics**

Prof. Hania Szajewska, MD, PhD, is Professor and Chair of the Department of Paediatrics at the Medical University of Warsaw. Among her various functions, she served as the Editor-in-Chief of the Journal of Pediatric Gastroenterology and Nutrition; a member of the Council, and then as the General Secretary of the European Society for Paediatric Gastroenterology, Hepatology and Nutrition (ESPGHAN); the Secretary of the ESPGHAN Committee on Nutrition. Most recently, she joined the Board of Directors of the International Scientific Association for Probiotics and Prebiotics (ISAPP). Prof. Szajewska has broad interests in paediatric nutrition but her research focuses on the effects of early nutritional interventions on later outcome (especially food allergy); and the gut microbiota modifications such as with various biotics (probiotics, prebiotics, synbiotics, postbiotics). She is or has been actively involved in several European Union-funded research projects. She is an enthusiastic advocate for the practice of evidence-based medicine. She has co-authored over 400 PubMed-indexed publications, which have been cited more than 24,000 times, with an H-index of 83.

**Daniel Tancredi, University of California, Davis**

Prof. Daniel J. Tancredi, PhD, is Professor in Residence of Pediatrics in the University of California, Davis School of Medicine. He has over 25 years of experience and over 300 peer-reviewed publications as a statistician collaborating on a variety of health-related research. A frequent collaborator on probiotic and prebiotic research, he has attended all but one ISAPP annual meeting since 2009 as an invited expert. In 2020, he joined the ISAPP Board of Directors. Colin Hill and Daniel co-host the ISAPP Podcast Series "Science, Microbes, and Health". On research teams, he develops and helps implement effective study designs and statistical analysis plans, especially in settings with clusters of longitudinal or otherwise correlated measurements, including cluster-randomized trials, surveys that use complex probability sampling techniques, and epidemiological research. He teaches statistics and critical appraisal of evidence to resident physicians; graduate students in biostatistics, epidemiology, and nursing; and professional scientists. Dan grew up in the American Midwest, in Kansas City, Missouri, and holds a bachelor's degree in behavioral science from the University of Chicago and masters and doctoral degrees in mathematics from the University of Illinois at Chicago. He lives in the small Northern California city of Davis, with his wife Laurel Beckett (UC Davis Distinguished Professor Emerita), their Samoyed dogs Simka and Milka, and near their two grandkids.

**Gabriel Vinderola, Dairy Products Institute, Faculty of Chemical Engineering (UNL)**

Dr. Gabriel Vinderola, PhD, graduated from the Faculty of Chemical Engineering at the National University of Litoral (Santa Fe, Argentina) in 1997 and obtained his Ph.D. in Chemistry in 2002 at the same University. He is presently Principal Researcher at the Dairy Products Institute (CONICET-UNL) and Adjoint Professor at the Biotechnology and Food Technology Department of the Faculty of Chemical Engineering (National University of Litoral). He participated in the development of the first commercial cheese carrying probiotic bacteria from Latin America, released in the market in 1999. In 2011, he was awarded the prize in Food Technology for young scientists, by the National Academy of Natural, Physic and Exact Sciences from Argentina. His interests are technological and microbiological aspects of lactic acid bacteria, bifidobacteria, fermented foods, and probiotics. He has joined several research groups in Brazil, Canada, Spain, Italy, France, Germany, and Finland. He has co-edited the fifth (2019) and the sixth (2024) editions of the book Lactic Acid Bacteria: Microbiological and Functional Aspects. He is engaged in communication of science to the general audience.

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**Kristin Verbeke, KU Leuven**

Prof. Kristin Verbeke, Pharm, PhD, graduated from the KU Leuven, Belgium as a pharmacist in 1991. She obtained a PhD in Pharmaceutical Sciences at the Laboratory of Radiopharmaceutical Chemistry in 1995 and subsequently spend a postdoctoral period in developing radioactively labelled compounds. In 2002, she was appointed at the department of gastroenterology of the Medical Faculty of the Leuven University where she became involved in the use of stable isotope labelled compounds to evaluate gastrointestinal functions. Within the University Hospitals Leuven, she is responsible for the clinical application of diagnostic 13C- and H2-breath tests. Her current research interest specifically addresses the microbial bacterial metabolism in the human colon. Her team has developed several analytical techniques based on mass spectrometry and stable isotope or radioisotope technologies to evaluate several aspects of intestinal metabolism and function in humans (transit time, intestinal permeability, carbohydrate fermentation, protein fermentation, metabolome analysis). Collaborative research has allowed showing an aberrant bacterial metabolism in patient groups with end stage renal failure, inflammatory bowel diseases, irritable bowel disorders and alcohol abuse. These collaborations all have resulted in high quality peer-reviewed papers. In addition, she showed the impact of dietary interventions (modulation of macronutrient composition, pre- or probiotic interventions) on the microbial metabolism and its impact on health. As a PI, she acquired grant support from the university and different funding bodies and successfully completed these projects. Similarly, she supervised several PhD projects that all resulted in the achievement of a PhD degree. Her research resulted in over 200 full research papers. Together with colleague Prof. J. Delcour, she was the beneficiary of the W.K. Kellogg Chair in Cereal Sciences and Nutrition (2010-2020). She is the president of the Belgian Nutrition Society, the vice-chair of the Leuven Food Science and Nutrition Center, and the co-chair of the Prebiotic task force at ILSI Europe. Furthermore, Kristin Verbeke is the editor of the journal Gut Microbiome and member of the editorial board of Gastrointestinal Disorders.

**Geoffrey Preidis, Baylor College of Medicine and Texas Children's Hospital**

Dr. Geoffrey A. Preidis, M.D., Ph.D., Associate Professor of Pediatrics at Baylor College of Medicine in Houston, Texas, is a board-certified Pediatric Gastroenterologist with basic and translational research expertise in nutrition-sensitive mechanisms that regulate intestinal and liver physiology, growth, and development. Based at Texas Children's Hospital, which contains the largest neonatal intensive care unit in the United States, Dr. Preidis explores how the intestinal microbiome develops in extreme prematurity and how probiotics might be used to reduce the risk of necrotizing enterocolitis, sepsis, feeding intolerance, growth failure, and death in this vulnerable population. His biomedical research career began during undergraduate studies at Harvard University. He developed an interest in Neonatal Gastroenterology while in the Medical Scientist Training Program at Baylor College of Medicine. He completed internship and residency training in Pediatrics, as well as fellowship training in Pediatric Gastroenterology, Hepatology & Nutrition, at Baylor College of Medicine.

# Board of Directors

**Hannah Holscher, University of Illinois Urbana-Champaign**

Dr. Hannah Holscher is an Associate Professor of Nutrition at the University of Illinois Urbana-Champaign, where she also serves as Associate Director of the Personalized Nutrition Initiative and holds affiliations with the Division of Nutritional Sciences, the Carl R. Woese Institute for Genomic Biology, and the National Center for Supercomputing Applications. Her research integrates clinical nutrition, microbiome science, and computational biology to explore how diet influences human health. She has authored more than 90 peer-reviewed publications and leads multidisciplinary research projects supported by government agencies, foundations, commodity boards, and private industry. Dr. Holscher has held leadership roles within the American Society for Nutrition and serves on the editorial boards of The Journal of Nutrition and Nutrition Research.

**Jens Walter, University College Cork, APC Microbiome Ireland**

Jens Walter serves as the Professor of Ecology, Food, and the Microbiome at University College Cork and the APC Microbiome Ireland. His expertise lies at the interface of evolutionary ecology of the gut microbiome and human nutrition. His research focuses on the evolutionary and ecological processes that have shaped host-microbiome symbiosis and the translation of basic microbiome science into therapeutic and nutritional strategies. Dr. Walter and his collaborators have pioneered the application of ecological theory to elucidate ecological and nutritional factors that shape gut microbiomes and have achieved targeted modulations of microbiomes via dietary strategies and live microbes. Prof. Walter has published >140 peer-reviewed publications (google scholar H-index 69, >23,000 citations) and is a 'highly cited researcher' according to the Web of Science group.

**Marla Cunningham, ISAPP Executive Director**

Marla Cunningham is the Executive Director of ISAPP. Prior to 2023, Marla was an industry scientist within the ISAPP community and brings over 20 years of experience in the probiotic, prebiotic, and natural products industry, working across innovation, clinical research, product development, regulatory compliance, and education. She trained as a healthcare practitioner in complementary medicine and has written and presented extensively for clinical audiences on the implementation of biotic-related science. Marla has broad scientific literacy across the fields of biotic substances, microbiome, gut health, nutrition, and human physiology, and brings a passion for harnessing science to deliver beneficial changes in health for our community and our planet.

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# Industry Advisory Committee Representatives

**Shalome Bassett, Senior IAC Representative 2024-2025**

Dr. Shalome Bassett, PhD, is Manager of the Probiotic Biosciences team based at Fonterra's Research and Development Centre in Palmerston North, New Zealand. Shalome is a molecular microbiologist with a diverse background in microbial research, having worked for over 30 years in various research, science management and technology development roles across academia, government, and the food industry. Over the past six years, she has established and led Fonterra's Probiotics Discovery and Kowbucha™ Research Programmes, where she's been responsible for developing new commercial probiotic strains for human health as well as a viable on-farm solution for reducing methane in cattle, respectively. In the past, she's also dabbled in various gut pathogens, plant microbiology (with PhD research on symbiotic fungal endophytes of forages) and the development of vaccines against bovine tuberculosis. Her current interests lie in the interactions between probiotic strains, diet and genetic background, and the gut microbiome for improved health outcomes. Shalome loves being able to build new collaborations and relationships and to communicate science to a wide range of people in a way that interests and excites them.

**Jessica Van Harsselaar, Junior IAC Representative 2024-2025**

Jessica Van Harsselaar works as a Manager Nutrition Science at the BENEO-Institute, where she is responsible for global scientific research programs related to BENEO's prebiotic dietary fibers. Jessica is a nutrition scientist, specializing in prebiotic research and the gut microbiota. Her research focus is on prebiotics, gut health, the gut-brain axis, and nutrition across different life stages. With more than eight years of experience in the field, Jessica plays a pivotal role in translating complex scientific findings into meaningful, evidence-based applications that support BENEO's innovation and communication strategies. She has contributed to several peer-reviewed publications, including studies demonstrating the beneficial effects of prebiotics on microbiota composition and emotional well-being.

Currently, Jessica represents the Industry Advisory Committee of the International Scientific Association for Probiotics and Prebiotics (ISAPP), where she actively fosters dialogue between academia and industry. She is passionate about advancing scientific understanding and supporting collaborative efforts that push the boundaries of microbiome science and its role in nutrition.

Jessica has served as Junior IAC advisor to the ISAPP Board for the past year and moves into the Senior IAC representative position for 2025-2026.

ISAPP

# SFA Executive Committee

**David Hourigan, APC Microbiome Ireland, SFA President**

Research Interests: My research is centered around the role of bacteriocins, which are small ribosomally encoded antimicrobial peptides produced by bacteria, and their subsequent role within the microbiome. My research focuses on exploiting their effectiveness as selective antibacterial agents to curate the microbiota to tackle AMR and climate change. Interests include functional, ecological, and evolutionary genomics, microbial ecology, and bacterial competition.

**Patricia Sanz Morales, University of Reading, UK, SFA Vice President**

Current research: I am interested in understanding the prebiotic effects of human milk oligosaccharides (HMOs) in adult gut microbiomes, with a particular focus on Irritable Bowel Syndrome (IBS). I combine in vitro and in vivo approaches to assess the influence of HMOs on the gut microbiome through metabolic and microbial profiling, and subsequent impact on human health. I hope to provide some clarity on the potential of HMOs as therapy option in IBS through this work.

**Cathy Lordan, PhD, Teagasc and APC Microbiome Ireland, SFA Past President**

Current Research: My research is based on human milk oligosaccharides (HMOs), found in breast milk, and their impact on the early life gut microbiota, with a specific focus on Bifidobacterium. I am looking at how HMOs impact both composition and functional potential of the infant microbial community, including the metabolites they produce as a result of HMO availability.

**Brendan Daisley, PhD, University of Guelph, SFA Local Organiser**

Research Interests: I am interested in how probiotic science can be applied to favourably impact human, wildlife, and overall planetary health. A major focus of my current work is to elucidate mechanisms by which beneficial strains of bacteria can directly and/or indirectly improve immunity, detoxification of pesticides, and the nutritional status of honey bees. Through this work, I hope to contribute to a sustainable future by developing a framework of how microbial-based solutions can be used to support the health of important pollinator insects that are critical to the global food supply.

**Breanna Metras, University of Illinois Urbana Champaign, SFA Treasurer**

Research Interests: I love researching the relationship between nutrition/food and the gut microbiome. My PhD work at the University of Illinois Urbana-Champaign focused on the composition and impact of kefir on the gut microbiome of mice, dogs, and humans. I am continuing this work at the U of M, while also using bioinformatics to better understand the interplay between food and the gut microbiome. I hope my data can contribute to dietary databases and serve as a focal point for future policy and regulation of fermented foods in the USA. My work as a dietitian and researcher has informed my path and I hope to share our findings with all audiences, from academics to non-scientists.

ISAPP

# SFA Executive Committee

**Sarah Ahannach, PhD, University of Antwerp, Belgium, SFA Director of Outreach and Community Engagement**

Research interests: I am interested in the deeper understanding of women's microbiome and how microbial management and cutting-edge microbiome analyses can improve women's health and safety. A major focus of my work is studying the inner workings of the vaginal ecosystem (Isala project), vitamin-producing bacteria, and applying microbiome analysis to forensics with a focus on sexual assault cases (GeneDoe project). I hope to contribute to knowledge on the stability and dynamics of the female microbiome by presenting novel understandings for future intervention studies to unravel underlying mechanisms; the development of probiotics and biotherapeutics; and for developing novel tools that could be used in diagnostics and criminal investigations.

**Rounak Chourasia, PhD, National Agri-Food and Biomanufacturing Institute (iBRIC-NABI), India, SFA Secretary**

Current Research: My research centers on investigating protein-rich, plant-based fermented foods as valuable sources of bioactive compounds with the potential to deliver targeted health benefits. A key focus of my work is the generation of bioactive peptides during fermentation and the exploration of how peptide chemistry influences their gastrointestinal stability and functional properties. By leveraging microbial bioprocesses, I aim to contribute to the development of a sustainable food ecosystem, positioning fermented foods as affordable, globally accessible sources of functional proteins.

**Ellen Murray, PhD, APC Microbiome Ireland, Ireland, SFA Director of Communications and Development**

Current Research: I am interested in the effects of postbiotics on the human microbiome. My current research is an industry-partnered project that focuses on harnessing the microbiome to improve health and wellbeing. This collaboration aims to develop novel postbiotic solutions, focusing on the gut-brain axis, for unmet health needs. During my PhD, I explored the therapeutic and diagnostic potential of phage-derived enzymes called endolysins.

**Poster 1 SFA**

**Unveiling the vaginal microbiome shift in iatrogenic menopause: Insights from breast cancer therapy-induced changes**

Menopause is a universal biological transition that affects approximately half of the world's population, marking a significant phase in a woman's life. Despite its prevalence, the impact of menopause on women's health and well-being is often underestimated, leading to a range of physical and emotional challenges that can disrupt the quality of life. Furthermore, there is a notable gap in research and effective solutions to manage these symptoms, highlighting the need for increased awareness and resources to support women during this critical time. One common manifestation are genitourinary symptoms of menopause (GMS; such as vaginal dryness and irritation), which can be linked to changes in the vaginal microbiome; however, only a limited amount of research has been conducted in this area. GMS is also prevalent among women with a history of breast cancer, yet the onset of these symptoms during breast cancer treatment remains poorly understood. In this study we aimed to elucidate changes in the vaginal microbiome associated with iatrogenic menopause induced by breast cancer therapies. We conducted a longitudinal prospective trial involving 60 premenopausal breast cancer patients (median age 42.9 years, SD 6.8), from whom we collected vaginal microbiome samples at baseline (V1) and at 3 (V2) and 6 months (V3) post-treatment initiation. The vaginal microbiome was assessed through 16S rRNA gene sequencing and qPCR, alongside measurements of vaginal pH and menopausal status via serum oestrogen levels. Clinical evaluations were performed using validated instruments, including the vaginal and vulvar assessment scales. Preliminary analysis of data from 17 participants revealed that all but one experienced induced menopause through ovarian function suppression. Notably, after V1, no participant exhibited a vaginal pH below 5.0. The results indicate a shift towards a larger vaginal microbiome diversity post-menopause, characterized by decreased dominance of Lactobacillus species and an increased presence of Gram-negative bacteria such as *Prevotella*, *Anaerococcus* and *Gardnerella*. Clinically, signs of vaginal and vulvar atrophy were evident as early as 3 months post-menopause, with subsequent increases in composite scores indicating worsening symptoms at V2 and V3. Our study highlights a significant reduction in *Lactobacillus* spp. and an associated increase in vaginal microbiome diversity following iatrogenic menopause. Our findings underscore the urgent need to explore oncologically safe interventions to alleviate GSM-related discomfort for patients undergoing BC treatment-induced menopause. This research will help enhance our understanding of the development of menopause and its effects on the vaginal microbiome, thereby equipping women with strategies to manage these symptoms, such as microbiome modulation or other therapeutic or preventative solutions.

Authors and affiliations (presenter underlined): Sarah Ahannach (Lab of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp, Antwerp, Belgium and U-MaMi Centre of Excellence, University of Antwerp, Antwerp, Belgium), Nynke Willers (KU Leuven, Department of Oncology, Leuven, Belgium and AZ Sint Blasius, Department of Senology, Dendermonde, Belgium), Tim van Rillaer (Lab of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp, Antwerp, Belgium), Ilke de Boeck (Lab of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp, Antwerp, Belgium), Paul Enzlin (Institute for Family and Sexuality Studies, Department of Neurosciences, KU Leuven, Leuven, Belgium), Patrick Neven (KU Leuven, Department of Oncology, Leuven, Belgium and Department of Gynaecologic Oncology, UZ Leuven, Leuven, Belgium), Sileny N. Han (KU Leuven, Department of Oncology, Leuven, Belgium and Department of Gynaecologic Oncology, UZ Leuven, Leuven, Belgium), Sarah Lebeer (Lab of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp, Antwerp, Belgium and U-MaMi Centre of Excellence, University of Antwerp, Antwerp, Belgium)

**Poster 2 SFA**

**Exploring the prebiotic potential of commercial cellobiose: in vitro and in vivo approaches**

The gut microbiome is critical for host health, with prebiotics like fructooligosaccharides (FOS), galactooligosaccharides (GOS), and inulin-type fructans (ITFs) enhancing *Bifidobacterium* growth, linked to immune function. However, their effect on *Lactobacillus* varies, highlighting the need for selective modulation. Cellobiose, a cellulose-derived disaccharide, is a promising candidate for targeted modulation of beneficial Lactobacillus strains and may be ideal for synbiotic formulations to refine microbiome management.

In this study, in vitro fermentations were first conducted using human faecal inocula from three healthy donors (D1, D2, and D3) to evaluate the effects of cellobiose and oligofructose P95 (FOS). Cellobiose fermentation resulted in the highest mean butyrate production (15.6 ± 3.2 mM) and total SCFA levels (59.6 ± 4.2 mM) at 48 hours. In contrast, oligofructose P95 led to the highest mean acetate (51.3 ± 3.7 mM) and propionate (14.8 ± 2.1 mM) production over the same period. Microbial analysis revealed a consistent decrease in the relative abundance of Proteobacteria across all treatments. Cellobiose fermentation specifically promoted increases in *Bifidobacterium* and *Lactobacillus* populations at 24 hours ($P<0.05$), while oligofructose P95 significantly stimulated the growth of Bacteroides and Firmicutes within the first 8 hours ($P<0.05$).To further confirm the selection fermentation of cellobiose, a subsequent in vivo study involving 36 healthy participants over four weeks is designed to assess cellobiose's prebiotic efficacy through detailed metabolite and bacterial profiling.

Findings suggest that cellobiose has potential as a new prebiotic, further investigation should focus on its dose-response and interactions with other prebiotics.

Authors and affiliations (presenter underlined): Manxi Huang (University of Reading, Reading UK), Peter Jackson (University of Purdue, Indiana USA), Afroditi Chatzifragkou (University of Reading, Reading UK), Bob Rastall (University of Reading, Reading UK)

**Poster 3 SFA**

**Human Milk Oligosaccharides for Irritable Bowel Syndrome: Preliminary Findings from a Crossover Randomised Controlled Trial**

Background: Irritable Bowel Syndrome (IBS) is a highly prevalent disorder of gut-brain interaction with significant morbidity and is a major public health/economic concern. Our in vitro (gut models) evidence has suggested human milk oligosaccharides (HMOs) as a potential prebiotic treatment for IBS symptoms. HMOs may modulate the gut microbiota and influence gut–brain signalling, offering a novel therapeutic approach.

Objective: This study aimed to evaluate the efficacy of a HMO blend in reducing symptom severity scores (SSS) in forty adults with IBS, compared to placebo (maltodextrin), as assessed by a validated IBS-SSS questionnaire. Secondary outcomes included characterisation of gut microbial composition via 16S rRNA gene sequencing and metabolic profiling of stool samples using nuclear magnetic resonance (^1H-NMR) spectroscopy and gas chromatography–mass spectrometry (GC-MS).

Methods: In this double-blind, placebo-controlled, 2×2 crossover trial (NCT06281600), 45 IBS participants (17 IBS-M, 15 IBS-D, 7 IBS-C and 6 IBS-U) were randomised to receive either a HMO blend or placebo (maltodextrin) for four weeks, followed by a four-week washout period, and then crossed over to the alternate intervention for another four weeks. Each participant attended four study visits: two baseline assessments (prior to each intervention phase) and two post-intervention assessments. At each visit, stool and urine samples were collected, and participants completed validated symptom and quality-of-life questionnaires.

Results: Paired T-tests confirmed the effectiveness of the washout period, with a significant return to baseline IBS-SSS scores between intervention phases ($P < 0.05$), validating the crossover design. The IBS-SSS data were normally distributed; therefore, a linear mixed model was used to assess treatment effects. Preliminary analysis showed a significant reduction in IBS-SSS following Treatment B ($P < 0.05$), but not Treatment A. Treatment allocation remains blinded.

Preliminary 16S rRNA sequencing data revealed that Treatment A, was associated with a significant increase in Bifidobacterium spp. relative abundance ($P < 0.05$), suggesting a microbiota-modulating effect during this intervention phase.

Conclusion: Preliminary findings indicate that the two interventions have differential effects on IBS symptom severity and gut microbiota composition, including changes in Bifidobacterium spp. abundance (which were not associated with improved symptomology). Further analyses are ongoing.

Authors and affiliations (presenter underlined): Sanz Morales, P. (The University of Reading, Whiteknights, Reading, UK) , Wijeyesekera, A. (The University of Reading, Whiteknights, Reading, UK), Boulangé, C.L. (Nestlé Institute of Health Sciences, Nestlé Research, Société Produits Nestlé, Switzerland), Gibson, G.R (The University of Reading, Whiteknights, Reading, UK).

**Poster 4 SFA**

**Developing a topical probiotic to prevent penile HIV acquisition**

A high abundance of anaerobic bacteria on the penis is associated with local inflammation and increased HIV risk. Circumcision results in a drastic decrease in strict anaerobes, reduced inflammation, and a reduction of HIV risk of about 60%. Six species of anaerobic bacteria are associated with HIV seroconversion, inflammation and immune cells (BASIC). Uncircumcised males often have a high burden of BASIC species, but those who do not have BASIC species, have a lower HIV risk. We hypothesized that these males have bacteria capable of inhibiting the growth of the BASIC species, and that these bacteria could be used in a topical probiotic to decrease one's susceptibility to HIV. We aimed to identify penile bacteria able to inhibit the BASIC species growth without damaging the penile epithelium. Penile swabs were collected from 12 uncircumcised men and were cultured on a variety of different media types. To date, 38 unique bacterial species were isolated that span across 23 genera. Deferred and simultaneous antagonism assays were used to identify isolates that inhibit the growth of BASIC species. These isolates were co-cultured with keratinocytes isolated from foreskin tissue and soluble E-Cadherin was quantified as a measure of epithelial damage. Five isolates were able to inhibit the growth of Peptostreptococcus anaerobius, a BASIC species: Cutibacterium acnes, Streptococcus anginosus, Enterococcus faecalis, Corynebacterium glucuronolyticum and Finegoldia magna. When co-cultured with keratinocytes, C. acnes and S. anginosus did not induce soluble E-cadherin release. C. acnes and S. anginosus can inhibit the growth of a bacterial species associated with increased HIV risk and do not damage foreskin epithelial cells, making them the most promising probiotic candidates.

Authors and affiliations (presenter underlined): Rachel Penney (University of Western Ontario, London, ON), Shirley Constable (University of Western Ontario, London, ON), Wongsakorn Kiattiburut (University of Western Ontario, London, ON), Kait Al (University of Western Ontario, London, ON), Matthew Razvi (University of Western Ontario, London, ON), Jeffrey Campbell (London Health Sciences Centre, London, ON), Jeremy Burton (University of Western Ontario, London, ON) and Jessica Prodger (University of Western Ontario, London, ON)

**Poster 5 SFA**

**Isala citizen-science study: navigating the vaginal microbiome's metabolic landscape**

To better understand the composition and functional activity of the vaginal microbiome in healthy women, we launched the Isala citizen science project in Flanders. Self-sampled vaginal swabs were provided for high-throughput genomic analysis and bacterial isolation. A subset of 257 samples, selected on the participant's age, infection history and contraceptive use, were subjected to untargeted metabolomics analysis, using HILIC and qTOF mass spectrometry. The majority of variance in the data could be explained by the dominant microbial taxa, rather than lifestyle factors. Distinct metabolic signatures were observed in profiles dominated by less optimal species, such as *Prevotella* and *Gardnerella*, compared to Lactobacillaceae. A targeted analysis of 83 bioenergetic and immunomodulatory metabolites (incl. amino acids, vitamins, quinones, and neurotransmitters) highlighted significant associations with microbial composition. Specifically, health-associated *L. crispatus* profiles, were enriched in anti-inflammatory compounds, including orotate and various indole derivatives. Remarkably, flavin mononucleotide (FMN), the active form of vitamin B2, showed a strong correlation with *L. crispatus* abundance ($R^2 = 0.014$, $p < 0.001$). Genome mining and in vitro analyses of vaginal isolates from the Isala cohort revealed a high potential for vitamin B2 production. These findings, combined with the well-established health benefits of vitamin B2, have led to the initiation of VIAB2L, an oral intervention study exploring the therapeutic potential of vitamin B2 producing lactobacilli in supporting female (vaginal) health. This comprehensive approach to understanding the vaginal microbiome's metabolic landscape opens new avenues for microbiome-targeted interventions in women's health.

Authors and affiliations (presenter underlined): Caroline E.M.K. Dricot (University of Antwerp, Antwerp, Belgium), Denise Medeiros Selegatob (European Molecular Biology Laboratory, Heidelberg, Germany), Thies

Ghermanna (University of Antwerp, Antwerp, Belgium), Isabel Errergersa (University of Antwerp, Antwerp, Belgium), Sandra Condoria (University of Antwerp, Antwerp, Belgium), Sarah Ahannach (University of Antwerp, Antwerp, Belgium), Eline Cauwenberghs (University of Antwerp, Antwerp, Belgium), Michael Zimmerman (European Molecular Biology Laboratory, Heidelberg, Germany), Sarah Lebeer (University of Antwerp, Antwerp, Belgium).

**Poster 6 SFA**

**Colocalization of bacteriocin production with DNA uptake systems across prokaryote genomes**

Bacteriocin production is a widespread trait among bacteria and has been shown to have a role in bacterial competition in complex communities. Lanthipeptides are a class of modified bacteriocins that can have both antibacterial and signalling activities and rely on a number of genes encoding production, modification, regulation and immunity. This study aimed to investigate whether class II lanthipeptide gene clusters co-locate with other encoded apparently unrelated functions. A total of 1,412 verified lanthipeptide bacterial gene clusters (BGCs) were analysed for their co-localization with other functions over a 40kb span. We found that genes involved in phage defence were among the most commonly located close to the bacteriocin BGCs. This phenomenon was found in many genera, such as *Paenibacillus larvae* and *Corynebacterium matruchotii* ATCC 33806, that have restriction modification (RM) systems. Anti-phage-defence proteins were also found in 1.2% of sampled regions and these include the anti-restriction protein ArdA. Genes related to bacterial competence were also discovered close to bacteriocin genes in genera such as *Bacillus, Enterococcus and Streptococcus*. This over-representation of genes encoding DNA defence systems and systems associated with the uptake of exogenous DNA near class II lanthipeptide gene clusters suggests an evolutionary rationale whereby killing and lysing functions are linked to DNA uptake and horizontal gene transfer. The presence of anti-CRISPR proteins and RM-systems also suggests convergence of genetic systems that perpetuate their own survival through mutually-beneficial genomic co-localisation. This, coupled with recent evidence showing co-transcription of ribosomally-synthesised peptides and phage defence systems, suggests that the production of antimicrobial peptides forms part of a broader system where bacterial antagonism and competition is linked to horizontal gene transfer.

Authors and affiliations (presenter underlined): David Hourigan (APC Microbiome Ireland and School of Microbiology, University College, Cork, Ireland), Colin Hill (APC Microbiome Ireland and School of Microbiology, University College, Cork, Ireland), R . Paul Ross (APC Microbiome Ireland and Teagasc, Cork, Ireland).

**Poster 7 SFA**

**Cassava (Manihot esculenta) cultivars: chemical composition, prebiotic activity scores, and impact on the colonic microbiota of celiac individuals**

This study aimed to investigate the potential prebiotic properties of cassava cultivars from Northeast [Ourinho (OUR) and Doce mel] and South [IPR-Upira (UPI) and Baiana] of Brazil using in vitro fermentation systems. The cassavas were assessed for their chemical composition, and two cultivars (OUR and UPI) were selected and submitted to in vitro gastrointestinal digestion. The effects on probiotic growth (Lactobacillus acidophilus, Lacticaseibacillus casei, and Bifidobacterium animalis), metabolic activity, and prebiotic activity scores were determined. Finally, the impact on the fecal microbiota of celiac individuals was evaluated using the 16S rRNA gene. OUR cultivar showed higher concentrations of resistant starch, lactic and formic acids, and K, Na, and Zn. Furthermore, it presented inulin, xylohexaose, nystose, and xylobiose. UPI cultivar showed higher total dietary fiber, sugars, phenolics, amino acids, and Cu and Mn concentrations. Furthermore, it presented inulin, raffinose, xylobiose, and mannose. These cultivars increased the proliferation rates of L. casei, L. acidophilus, and B. animalis, with more significant effects than FOS. Also, they showed positive prebiotic activity scores. Finally, they promoted increased relative abundance of Bifidobacteriaceae, Enterococcaceae, and Lactobacillaceae in the fecal microbiota of celiac individuals while decreased Lachnospirales, Bacteroidales, and Oscillospirales. In conclusion, cassava cultivars caused positive changes in the metabolic activity and composition of the human intestinal microbiota of celiacs. OUR and UPI cultivars from Brazil could be considered potential prebiotic ingredients for functional foods and dietary supplements.

Authors and affiliations (presenter underlined): Tatiana Colombo Pimentel (Federal Institute of Paraná, Paranavaí, Paraná, Brazil), Isis Meireles Mafaldo (Federal University of Paraíba, João Pessoa, Paraíba, Brazil), Lais Matias Araújo (University of Brasília–UnB, Brasília, DF, Brazil), Lucélia Cabral (University of Brasília–UnB, Brasília, DF, Brazil), Carlos Eduardo Barão (Federal Institute of Paraná, Paranavaí, Paraná, Brazil), Melline Fontes Noronha (Loyola University Chicago, Maywood, IL, USA), Jesse Rodrigo Fink (Federal Institute of Paraná, Palmas, Brazil), Thatyane Mariano Rodrigues de Albuquerque (Federal University of Paraíba, João Pessoa, Paraíba, Brazil), Marcos dos Santos Lima (Federal Institute of Sertao de Pernambuco, Petrolina, Pernambuco, Brazil), Hubert Vidal ( Université Claude Bernard Lyon-1, Pierre Bénite, France), Marciane Magnani (Federal University of Paraíba, João Pessoa, Paraíba, Brazil)

**Poster 8 SFA**

**Endolysins for Microbiome Editing – LysH1 is a Novel *Enterococcus faecium* Phage Endolysin with Activity Against *Ruminococcus gnavus* in a Simplified Human Gut Consortium.**

The human microbiome plays an important role in human health and disease. In recent years, a number of studies have associated changes in the composition of the gut microbiome with inflammatory bowel disease (IBD). One microbe that has been implicated in IBD is *Ruminococcus gnavus* (aka *Mediterraneibacter gnavus*). Transient blooms of *R. gnavus* in the human gut correlate with increased inflammatory symptoms in patients. Interventions that could deplete *R. gnavus* without causing significant collateral damage could prove useful as a possible therapy. Endolysins are phage-derived peptidoglycan hydrolases that could be promising in this context. Here, we identified, cloned, and expressed a novel *Enterococcus faecium* bacteriophage lysin, LysH1. Structural analysis of this endolysin revealed a two-domain structure composed of a catalytic domain and a previously uncharacterised domain. We constructed a green fluorescent protein hybrid fusion that allowed us to functionally characterise this unknown domain as a cell wall binding domain. This is the first instance of experimental characterisation of the cell wall binding domain of an *E. faecium* endolysin. Testing full-length LysH1 against a panel of strains revealed that it has cross-species lytic activity against *R. gnavus*. This activity was further analysed in liquid culture of *R. gnavus*, where LysH1 demonstrated significant killing ability. Due to the strong lytic activity of LysH1 against *R. gnavus*, its potential as a novel therapeutic was assessed in a simplified human intestinal microbiota (SIHUMI) model. LysH1 was shown to target *R. gnavus* in this defined population, without impacting the other members of the consortium. This suggests that LysH1 could be a therapeutic candidate for the depletion of *R. gnavus* in patients with IBD.

Authors and affiliations (presenter underlined): Ellen Murray (APC Microbiome Ireland and School of Microbiology, University College, Cork, Ireland), Natalia S. Ríos Colombo (APC Microbiome Ireland, Cork, Ireland), David Hourigan (APC Microbiome Ireland and School of Microbiology, University College, Cork, Ireland), R . Paul Ross (APC Microbiome Ireland and Teagasc, Cork, Ireland), Colin Hill (APC Microbiome Ireland and School of Microbiology, University College, Cork, Ireland).

**Poster 9 SFA**

**Ancestral Allies: Ultra-deep sequencing of Amazonian hunter-gathers yields insights into beneficial functions and novel probiotic candidates**

The gut microbiomes of indigenous hunter-gatherer populations offer a window into ancestral host-microbe relationships of humans, yet remain vastly underexplored. Here, we applied a hybrid metagenomic sequencing approach to comprehensively characterize stool samples of n=9 Yanomami individuals from an uncontacted hunter-gatherer group residing in the remote Amazon rainforest. Compared to Illumina short-read approaches, Nanopore long-read sequencing dramatically improved assembly continuity and enabled the recovery of over 1,700 medium- to high-quality metagenome-assembled genomes (MAGs)—more than tripling the number recovered from the same samples with short reads. A large proportion of these genomes represent previously undescribed species, underscoring the deep reservoir of uncultured microbial diversity within non-industrialized populations. These novel lineages, shaped by ecological and lifestyle factors distinct from industrialized settings, may possess unique adaptations relevant to host health and resilience—positioning them as promising candidates for future probiotic discovery. To contextualize these findings, we conducted a large-scale meta-analysis comparing our data to over 500 previously sequenced gut metagenomes from industrialized and non-industrialized populations. This analysis revealed distinct taxonomic and functional signatures associated with lifestyle, including microbial taxa and pathways consistently absent or depleted in

industrialized cohorts. Many of these "missing microbes" and their encoded functions may play protective roles in metabolic regulation, immune development, and barrier integrity—areas of increasing concern given the global rise in chronic inflammatory and metabolic diseases. Incorporating our MAGs into a custom KRAKEN2 reference database also improved classification accuracy for non-industrial microbiomes. Altogether, our findings highlight the value of long-read metagenomics combined with comparative population-scale analysis for uncovering key microbial functions lost in modern environments and informing therapeutic strategies rooted in evolutionary microbiome restoration.

Authors and affiliations (presenter underlined): Brendan A. Daisley (Department of Molecular and Cellular Biology, University of Guelph, Guelph, Canada), David A. Good (Department of Molecular and Cellular Biology, University of Guelph, Guelph, Canada), Sarah J. Vancuren (Department of Molecular and Cellular Biology, University of Guelph, Guelph, Canada), Panuya Athithan (Department of Molecular and Cellular Biology, University of Guelph, Guelph, Canada), Simone Renwick (Larsson-Rosenquist Foundation Mother-Milk-Infant Center of Research Excellence (MOMI CORE), The Human Milk Institute (HMI), University of California, San Diego, La Jolla, CA), Aleksander Kostic (Department of Microbiology and Immunology, Harvard Medical School, Boston), Emma Allen-Vercoe (Department of Molecular and Cellular Biology, University of Guelph, Guelph, Canada).

**Poster 10 SFA**

**Inulin-MCT Microcapsules: A Novel Approach to Treat Metabolic and Inflammatory Diseases**

High-fat diets (HFDs), known drivers of obesity, are increasingly associated with low-grade chronic inflammation, a hallmark of metabolic disorders and gastrointestinal diseases such as Inflammatory Bowel Disease (IBD). A critical underlying cause of these conditions is perturbation of the gut microbiome. This study evaluates the therapeutic potential of inulin-coated medium-chain triglyceride (InuMCT) microcapsules, produced via spray drying, in mitigating HFD-induced metabolic and inflammatory disturbances through targeted microbiome modulation. InuMCT microcapsules were fabricated using spray drying, and their particle size and matrix structure were characterized using scanning electron microscopy (SEM) and confocal microscopy. Sprague Dawley rats were divided into four groups: normal diet, HFD, HFD supplemented with inulin, and HFD supplemented with InuMCT. After 21 days, body weight, fecal 16S rRNA gene sequencing, metabolic markers (blood glucose, triglycerides, HDL cholesterol), and serum tumor necrosis factor-alpha (TNF-α) levels were assessed. InuMCT significantly improved gut microbial diversity, increasing α-diversity in HFD-fed rats by 78%. The growth of commensal bacteria, such as Bifidobacterium and Blautia, was up by up to 12-fold. InuMCT also mitigated diet-induced weight gain and improved blood glucose and HDL cholesterol by up to 23%. Additionally, diet-induced TNF-α levels were reduced 77%. SEM and confocal imaging confirmed successful encapsulation of MCT within the inulin shell, enabling targeted delivery to the colon and maximizing anti-inflammatory action.

This study highlights InuMCT microcapsules as a promising multifunctional therapy for managing HFD-induced metabolic and inflammatory disturbances. InuMCT offers a dual approach to restoring gut health and mitigating disease progression. Future research will focus on evaluating its long-term efficacy and potential as an adjuvant therapy for chronic metabolic and gastrointestinal diseases.

Authors and affiliations (presenter underlined): Amin Ariaee (University of South Australia), Dr Hannah Wardill (University of Adelaide), Prof. Georgina Hold (University of New South Wales, Microbiome Research Centre), Prof. Clive Prestidge (University of South Australia), Dr. Paul Joyce (University of South Australia).

**Poster 11 SFA**

**Antiplasmodial Activity of Probiotic *Limosilactobacillus fermentum* YZ01 in *Plasmodium berghei* ANKA Infected BALB/c Mice**

Malaria remains a significant global health challenge, with the deadliest infections caused by *Plasmodium falciparum*. In light of the escalating drug resistance and the limited effectiveness of available vaccines, innovative treatment approaches are urgently needed. This study explores the potential of the probiotic *Limosilactobacillus fermentum* YZ01, isolated from traditionally fermented kindirmo milk, to modify host responses to *Plasmodium berghei* ANKA infection. Twenty-five male BALB/c mice were grouped and administered various treatments, including probiotic-enriched yogurt alone or in combination with antibiotics. Parameters assessed included gut lactic acid bacteria (LAB) composition, parasitaemia

progression, survival rates, and immune response dynamics over a 21-day post-infection period. The probiotic treatment significantly altered gut microbiota, evidenced by increased LAB counts and modulated immune responses, by enhancing IgM and IL-4 production while reducing IFN-γ levels. Mice receiving prolonged probiotic treatment exhibited delayed parasitaemia onset, reduced mortality rates, and a more robust immune response compared to control groups. These outcomes suggest that probiotic intervention not only tempers the pathological effects of malaria but also enhances host resilience against infection. This study underscores the role of gut microbiota in infectious disease pathogenesis and supports probiotics as a promising adjunct therapy for malaria management.

Authors and affiliations (presenter underlined): Timothy Bamgbose (ICMR-National Institute of Malaria Research, Sector 8, Dwarka, New Delhi, India), Afshana Quadri (ICMR-National Institute of Malaria Research, Sector 8, Dwarka, New Delhi, India), Anupkumar R. Anvikar (ICMR-National Institute of Malaria Research, Sector 8, Dwarka, New Delhi, India), José de la Fuente (Department of Veterinary Pathobiology, Center for Veterinary Health Sciences, Oklahoma State University, Stillwater, OK 74078, USA), Alejandro Cabezas-Cruz (ANSES, INRAE, Ecole Nationale Vétérinaire d'Alfort, UMR BIPAR, Laboratoire de Santé Animale, Maisons-Alfort, F-94700, France).

**Poster 12 SFA**

**The Leke project: Mapping the vaginal microbiome and benefits of vaginal lactobacilli in Cameroon**

The vaginal microbiome has gained increased attention in the last decades, with increasing documentation on the role in women's health and health of their families. Yet we lack an in-depth comprehension of the factors fostering a healthy vaginal ecosystem, slowing down the development of much-needed effective diagnostic and therapeutic approaches. Notably, there exists a substantial knowledge deficit regarding the vaginal microbiome in regions like Sub-Saharan Africa. Our research aims to bridge this gap by delving into the vaginal microbiome dynamics in Central Africa (Cameroon) using state-of-the-art microbiome analyses. This includes research on the ecological and metabolic benefits of vaginal lactobacilli based on the culture swabs, to select a few promising candidate strains that could be applied in live biotherapeutics or probiotics. Application areas of interest are HIV infection and bacterial vaginosis, which are both highly prevalent in Africa (28,5% - 52,4%). We started a sampling campaign in March 2023, with four distinct cohorts: healthy women residing in rural and urban areas, HIV-positive pregnant women, and HIV-negative pregnant women in Cameroon. Each participant contributed four vaginal swabs for comprehensive analysis: eNat swabs for microbiome sequencing, Eswab for culturomics and metabolomics, and two dry swabs (for vaginal pH measurement and bacterial vaginosis assessment using the Nugent score). Participants also filled in a survey on lifestyle, sociodemographic, reproductive, and sexual health. Our results showed that the vaginal pH of all our participants (178) was on average 5.05. This result is higher than that obtained by other researchers on women of European ancestry (4.5). Bacterial vaginosis prevalence was 58,98%, which both appear higher than studies in women from European descent. The microbiome sequencing data of women from rural and urban areas (107) showed that *Lactobacillus crispatus* was the dominant taxa in only 13%, while this taxon on dominant in women from European descent. The most prevalent taxa were *Lactobacillus. iners* group (38.8%), *Prevotella* (22.4%), and *Bifidobacterium* (10.3%). However, the vaginal profile for women from rural areas showed more abundance of *Lactobacillus crispatus*. We are now analyzing survey data. Further analysis will be focused on lactobacilli as well as bacterial vaginosis-like bacteria. The aim will be to investigate the probiotic potential of our lactobacilli isolates lactobacilli, and its intraspecies diversity compared to lactobacilli isolated from Belgian women.

Authors and affiliations (presenter underlined): Marie Josiane Kenfack Zanguim (University of Yaoundel, Yaounde, Cameroon), Sandra Condori (University of Antwerp, Antwerp, Belgium), Monica Ticlla (University of Antwerp, Antwerp, Belgium), Martial Kenfack (Center of Research on Emerging and Reemerging Disease, Biotechnology Center, Yaounde, Cameroon), Tatiane Elomo (Center of Research on Emerging and Reemerging Disease, Biotechnology Center, Yaounde, Cameroon), Maria Pinedo-Bardales (), Micheal Besong (University of Yaoundel, Yaounde, Cameroon), Hillary Tene (University of Yaoundel, Yaounde, Cameroon), Reine Seumko'o (University of Yaoundel, Yaounde, Cameroon), Jude Bigoga (University of Yaoundel, Yaounde, Cameroon), Rose Megnekou4, Sarah Ahannach (University of Antwerp, Antwerp, Belgium), Livo Esemu (University of Yaoundel, Yaounde, Cameroon), Sarah Lebeer (University of Antwerp, Antwerp, Belgium).

**Poster 13 SFA**

**Assessing the Microbial Accuracy of Commercially Fermented Beverages in the United States**

Sugar-sweetened beverages are the leading source of added sugar in the American diet, contributing to adverse health outcomes such as metabolic syndrome and diabetes. Fermented beverages such as kefir, kombucha, probiotic sodas, and probiotic supplement drinks are frequently marketed as healthier alternatives to sugar-sweetened beverages, appealing to health-conscious consumers due to their health halo and the perceived benefits of microorganisms. According to Market Research Future, sales of fermented foods and beverages are projected to reach $4.37 billion USD in 2024, with an average consumer growth rate of 6% within the next year. It is unknown how many of these fermented beverage products contain significant amounts of added sugar, potentially aligning them closely with traditional sugar-sweetened beverages. To better understand the microbial communities and diversity of these beverages, two lots of 29 (7 kombucha, 10 kefir, 9 probiotic sodas, 2 water kefir, and 1 tepache) commercially fermented beverages, and a Greek yogurt (control), were purchased throughout Hennepin County, Minnesota USA. Products were centrifuged to concentrate solid matter and underwent DNA extraction and the full length of the 16S was sequenced using LoopSeq (ATIVI long read sequencing). Sequencing data will be processed with QIIME2. Products will be evaluated for microbial label accuracy, diversity metrics, and microbial variability by product category. This project aims to understand the microbial profiles and diversity of commercially produced fermented drinks.

Authors and affiliations (presenter underlined): Breanna Metras, Abigail Johnson, Janet Pettit, Lisa Harnack

**Poster 14 SFA**

**Boosting the respiratory tract microbiome: *Lacticaseibacillus casei* LAMBR2 as promising Live Biotherapeutic Product for respiratory health.**

The upper respiratory tract (URT) microbiome acts as a critical gatekeeper for airway health, forming a barrier against pathogens and modulating immune responses. Disturbances in the respiratory microbiome are associated with airway diseases such as chronic, and viral infections. Modulation of this microbiome using lactic acid bacteria as live biotherapeutic products (LBPs) seems a promising therapeutic approach. Strains isolated from the URT, adapted to this highly specialized ecosystem, offer several advantages.

In this study, we investigated *Lacticaseibacillus casei* AMBR2, a strain isolated from the healthy URT, for its potential as an LBP for the respiratory tract. Following extensive in vitro characterization, the strain demonstrated a strong safety profile, antimicrobial activity against bacterial and viral URT pathogens, immunomodulatory effects, and enhancement of the airway epithelial barrier. To assess its clinical applicability, *L. casei* AMBR2 was tested in two proof-of-concept trials: in 20 healthy volunteers using a nasal spray with spray-dried bacteria and 78 COVID-19 outpatients using a multi-strain throat spray (placebo-controlled) with lyophilized bacteria.

Both trials confirmed the safety of *L. casei* AMBR2 and its ability to temporarily colonize the URT, suggesting strong adaptation to this niche. COVID-19 patients receiving the Lactobacillaceae spray showed a trend toward lower SARS-CoV-2 viral loads (2/30, 6.7% positive) compared to the placebo group (7/27, 26% positive). These findings position *L. casei* AMBR2 as a promising LBP candidate for respiratory health due to its multifactorial mode of action, with broad application potential. Its safety profile and formulation insights support rapid development, warranting further clinical Phase 1/2 studies.

Authors and affiliations (presenter underlined): Ilke De Boeck (University of Antwerp, Antwerp, Belgium & aMylla, company in formation, Belgium), Eline Cauwenberghs (University of Antwerp, Antwerp, Belgium), Irina Spacova (University of Antwerp, Antwerp, Belgium), Dominique Schols (KU Leuven, Rega Institute, Leuven, Belgium), Gaëlle Boulet (aMylla, company in formation, Belgium), Peter Hellings (KU Leuven & University Hospitals Leuven, Leuven, Belgium), Olivier Vanderveken (University of Antwerp & Antwerp University Hospital, Antwerp, Belgium), Sarah Lebeer (University of Antwerp, Antwerp, Belgium & aMylla, company in formation, Belgium).

**Poster 15 SFA**

**Impact of colon-delivered riboflavin versus riboflavin-overproducing Limosilactobacillus reuteri on the female intestinal and vaginal microbiota**

Riboflavin (vitamin B2) is an essential vitamin with antioxidant effects that plays a critical role in women's health, including reproductive health, hormonal balance, pregnancy and child development. Besides dietary sources and supplements, microbially produced riboflavin seems a promising strategy to both meet women's riboflavin needs and beneficially modulate microbial ecosystems (doi: 10.1038/S41522-024-00579-5). In the Isala project (n = 3,345), *Limosilactobacillus reuteri* AMBV339 was isolated from the vagina of a healthy woman. The strain demonstrated an overproduction of riboflavin and exhibited anti-pathogenic, epithelial barrier-enhancing and immunostimulatory properties in vitro. Riboflavin may promote stability and cross-feeding in the gut, particularly the colon, as well as modulate the gut microbiome. However, its role in vivo, including in the vagina, remains unclear. To investigate the role of riboflavin when colon delivered versus produced by orally delivered *L. reuteri* AMBV339, a randomized, placebo-controlled, double-blind clinical trial was set up in 200 healthy women. Here, the impact of colon-delivered and microbially produced riboflavin is compared to placebo and a combination of both delivery methods for their impact on fecal and vaginal microbiota composition and activity. Blood, urine, vaginal and fecal samples are collected to study the microbiome, metabolome, safety and immune response throughout the study. In addition, survey data is used to analyze general health parameters. Currently, samples are being processed for analysis. Altogether, this study will provide new insights into the role of colon-delivered riboflavin for gut and vaginal microbiome dynamics and the potential for *L. reuteri* AMBV339 as a probiotic for gut and vaginal health.

Authors and affiliations (presenter underlined): Eline Cauwenberghs (Laboratory of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp, Antwerp, Belgium ), Isabel Erreygers (Laboratory of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp, Antwerp, Belgium ), Sarah Ahannach (Laboratory of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp, Antwerp, Belgium ), Tim Van Rillaer (Laboratory of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp, Antwerp, Belgium ), Caroline E.M.K. Dricot (Laboratory of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp, Antwerp, Belgium), Thies Gehrmann (Laboratory of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp, Antwerp, Belgium ), Annelies Breynaert (Natural Products & Food Research and Analysis (NatuRA), Department of Pharmaceutical Sciences, University of Antwerp, Antwerp, Belgium), Jonas Wittwer Schegg (DSM Nutritional Products AG, Kaiseraugst, Switzerland), Mehdi Sadaghian (DSM Nutritional Products AG, Kaiseraugst, Switzerland), Anneleen Spooren (DSM Nutritional Products AG, Kaiseraugst, Switzerland), Nina Hermans (Natural Products & Food Research and Analysis (NatuRA), Department of Pharmaceutical Sciences, University of Antwerp, Antwerp, Belgium), Veronique Verhoeven (Department of Family Medicine and Population Health (FAMPOP), University of Antwerp, Antwerp, Belgium), Sarah Lebeer (Laboratory of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp, Antwerp, Belgium )

**Poster 16 SFA**

**The Effect of a Probiotic Yoghurt on Gut Microbiome, Low-Grade Inflammation And Weight Status of Obese South African Women**

The prevalence of obesity and its associated comorbidities, such as low-grade chronic inflammation and altered gut microbiome profiles, is a growing public health challenge in South Africa. The study investigates the impact of a probiotic-enriched yogurt on the gut microbiome, systemic inflammation, and the effects of these enriched-gut microbiome on the weight status of obese South African women. Probiotic-enriched yogurt was prepared using LGG (*Lactobacillus rhamnosus* GG) and BB-12 (*Bifidobacterium animalis subsp. lactis*). The probiotic yogurt sample was analyzed at day 0 and 7 to ensure the concentrations are beyond the recommended levels. Using a randomized controlled trial design, participants consumed either probiotic yogurt or a placebo (plain yogurt) for 12 weeks, with assessments conducted at baseline and post-intervention. Gut microbiome composition was analyzed using next-generation sequencing, while markers of inflammation (e.g., C-reactive protein, interleukins) and weight-related parameters (BMI, waist circumference) were measured using standard protocols. Preliminary results suggest that probiotic yogurt consumption leads to significant modulation of the gut microbiota, marked by increased abundance of beneficial bacteria, reduced inflammatory markers, and modest weight improvements. This study

highlights the potential of functional foods as an adjunctive strategy for managing obesity and its metabolic consequences in vulnerable populations.

Authors and affiliations (presenter underlined): James Elegbeleye (Department of Consumer and Food Sciences, University of Pretoria, Pretoria, South Africa), Gabriela Maria Lourenco (Department of Consumer and Food Sciences, University of Pretoria, Pretoria, South Africa), Adeline Pretorius (Department of Consumer and Food Sciences, University of Pretoria, Pretoria, South Africa), Elna Buys (Department of Consumer and Food Sciences, University of Pretoria, Pretoria, South Africa)

**Poster 17 SFA**

**Maternal Mediterranean Diet Benefits Offspring Gut Microbiome and Neurodevelopment Features via the Gut–Brain–Immune Axis**

This study examined how maternal Mediterranean diet (MD) during gestation and nursing protects offspring against Western diet (WD)-induced impairments in gut microbiome (16S sequencing), fecal/serum/brain metabolomes (global NMR metabolomics), and neurodevelopment via the gut–brain–immune axis (Western blots; human microglial cell exposures to mice serum). C57BL/6 mice breeders were fed WD or MD and the offspring were randomized and weaned to WD or MD for 10-wks, forming four mother–infant groups (WDWD, MDWD, WDMD, MDMD). Beta-diversity differed significantly ($p=0.001$) between MD- and WD-weaned pups, and MD at any life stage significantly ($p<0.01$) modulated the microbiome vs. WDWD, upregulating SCFA-producing taxa (Intestinimonas, Roseburia) and suppressing WD-linked taxa (*Enterococcus, Enterobacteriaceae, Erysipelatoclostridium, Streptococcus*). Compared to WDWD group, prenatal MD, regardless of post-weaning diet (MDWD or MDMD), led to persistent fecal–serum–brain metabolomic arrays, viz. elevated fecal propionate (associated with intestinal gluconeogenesis); serum 3-hydroxybutyrate, acetate, succinate, glutamine, citrate, and creatine (associated with mitochondrial biogenesis, fatty acid oxidation, ketosis); and brain myo-inositol, serine, and taurine (associated with neurotransmission, membrane integrity). Prenatal MD also improved neurodevelopmental features via gut-brain axis by ameliorating intestinal morphology (longer villi, higher villi length/crypt depth ratio), elevating microglial BDNF, and reducing MCP-1 levels in gut, blood, and brain (esp. in MDMD). Overall, maternal MD during gestation/nursing fostered healthier neonatal microbiome ontogenesis, promoted beneficial taxa and metabolites, and mitigated WD-induced neurodevelopmental deficits via the gut-brain-immune axis.

Authors and affiliations (presenter underlined): Saurabh Kadyan (Florida State University, Florida, USA), Gwoncheol Park (Florida State University, Florida, USA), Leila Khalili (Florida State University, Florida, USA), Moses Mayonu (Florida Institute of Technology, Florida, USA), Bo Wang (Florida Institute of Technology, Florida, USA), Gloria Salazar (Florida State University, Florida, USA), and Ravinder Nagpal (Florida State University, Florida, USA)

**Poster 18 SFA**

***In vitro* fermentation insights into infant gut microbiota responses to 2'-fucosyllactose and/or galacto-oligosaccharides**

The early life gut microbiota is an important contributor to the development of the infant at this crucial stage of life. Several species of infant-associated *Bifidobacterium* have demonstrated an ability to directly metabolise human milk oligosaccharides (HMO) such as 2'fucosyllactose (2'-FL) as well as complex carbohydrates such as galacto-oligosaccharides (GOS). This study aimed to evaluate in vitro the temporal compositional changes in an early life microbial community when supplemented with 2'-FL, GOS or in combination (GOS+2'-FL). Stool samples from infants aged 1 to 8 weeks were collected to form a representative infant microbial community. Anaerobic in vitro faecal fermentation experiments were performed using the various carbohydrate substrates and a carbohydrate-free control. Samples were obtained at 0, 6 and 24 hours. The pH was measured, and DNA was extracted for subsequent shotgun metagenomic sequencing. Species-level taxonomic classification and functional potential were determined to assess the microbial changes that occurred. The pH decreased in all cases but more so in scenarios where a carbohydrate was present. *Bifidobacterium* remained the dominant genus when a carbohydrate was available. At 24 hours the relative abundance of *Bifidobacterium* was slightly higher in the presence of GOS alone compared to the other test substrates. Similarly, alpha diversity analysis revealed that all carbohydrate-supplemented groups had a lower diversity at 6 and 24 hours (i.e., reflective of a

*Bifidobacterium*-dominated community) compared to the control, which is more desirable in the infant microbiota. GOS alone had the lowest alpha diversity at the end of fermentation. At species level *Bifidobacterium breve*, whose HMO-utilisation ability is relatively limited, remained the most abundant species highlighting its ability to persist in the early life microbiota.

Authors and affiliations (presenter underlined): Cathy Lordan (Teagasc Food Research Centre, Moorepark, Fermoy, Co. Cork, Ireland and APC Microbiome Ireland, Cork, Ireland), Aoife Roche (APC Microbiome Ireland, Cork, Ireland and School of Microbiology, University College Cork, Cork, Ireland), Dianne Delsing (FrieslandCampina, Amersfoort, The Netherlands), Arjen Nauta (FrieslandCampina, Amersfoort, The Netherlands), Andre Groeneveld (FrieslandCampina, Amersfoort, The Netherlands), Ellen Looijesteijn (FrieslandCampina, Amersfoort, The Netherlands), John MacSharry (APC Microbiome Ireland, Cork, Ireland and School of Microbiology, University College Cork, Cork, Ireland), Paul D. Cotter (Teagasc Food Research Centre, Moorepark, Fermoy, Co. Cork, Ireland and APC Microbiome Ireland, Cork, Ireland), Douwe van Sinderen (APC Microbiome Ireland, Cork, Ireland and School of Microbiology, University College Cork, Cork, Ireland).

**Poster 19 SFA**

**Dietary intake, gut microbiome and anxiety: multilevel insights from a cross-sectional study on highly anxious females aged 18-25.**

Emerging evidence highlights diet's role in modulating anxiety through the gut-brain axis, with microbial metabolites mediating diet-microbiome-brain interactions. Our study identified gut bacteria (*Tyzzerella, Faecalibacterium, Roseburia*) as potential mediators of diet's impact on anxiety (Basso *et al.*, 2024). However, mechanisms linking gut microbiome to dietary responses remain underexplored, emphasizing the need for precision nutrition to improve anxiety outcomes. To address this, we investigated diet-microbiome-anxiety interactions in young, highly anxious females (N = 46, age: 18–25y), considering the higher anxiety prevalence in females and sex- and age-specific effects. Long-term diet quality was assessed via HEI-2020 (FFQ), and short-term intake via four 24-hour recalls capturing food processing levels, food, and nutrient intake. Multiple Factor Analysis identified four dietary patterns. Self-collected stool samples were sequenced using shotgun metagenomics to profile microbiome diversity (Shannon index), taxonomic composition, and metabolic capability (KEGG modules). Anxiety was measured using the STAI-State scale and a PCA-derived distress score. Participants with lower HEI-2020 scores, characterized by decreased fibres, whole fruits and grains, and higher refined grains and saturated fats intake, exhibited higher anxiety and distress scores. Ongoing analysis applies regularisation methods to refine dietary predictors and investigates microbiome diversity, composition, and KEGG modules as mediators and moderators of diet-anxiety interactions. These findings advance our understanding of the diet-gut-microbiome-mental health axis, highlighting dietary and microbiome modulation as cost-effective precision medicine targets for improving mental health outcomes.

Authors and affiliations (presenter underlined): Melissa Basso (University of Surrey, Guildford, Surrey, United Kingdom), Chantelle Winder (University of Sheffield, Sheffield, United Kingdom), Falk Hildebrandt (Quadram Institute Bioscience, Norwich, United Kingdom), David Baker (Quadram Institute Bioscience, Norwich, United Kingdom), Ralph Manders (University of Surrey, Guildford, Surrey, United Kingdom), Matteo Barberis (University of Surrey, Guildford, Surrey, United Kingdom), Kathrin Cohen Kadosh (University of Surrey, Guildford, Surrey, United Kingdom).

**Poster 20 SFA**

**The milk-enriched infant gut microbiome drives functional capacity for both breast feeding and weaning**

The human gut microbiota is established through various factors after birth from a sterile state. During breastfeeding, *Bifidobacterium* sp., the main consumer of milk glycans, constitutes a major component of the gut microbiota. During the transition of the gut microbiota to weaning, bacteria that degrade plant fiber rapidly emerge, and the ratio of bifidobacteria decreases. To sustain bifidobacteria during this transition, two different strains of *Bifidobacterium longum* subsp. *longum* YK1048 and *B. bifidum* YK1043 were isolated from the feces of breastfed infants using a medium containing milk glycoconjugates as the sole carbon source. Both strains exhibited high growth with non-fucosylated milk oligosaccharides or whey protein phospholipid concentrate (WPPC), a glycan-rich byproduct of cheesemaking. During growth on WPPC,

both strains demonstrated high expression of a suite of glycosyl hydrolases (GHs); however, the involved GHs differed in their targeting of O- and/or N-glycosylated glycans. Surprisingly, growth of *B. longum* YK1048 on WPPC also resulted in the expression of various arabinofuranosidases and external galactanases, activities utilized by bifidobacteria to degrade plant polysaccharides. These observations suggest that milk glycans prepare gut taxa for the weaning transition to plant food substrates and may facilitate the persistence of beneficial bifidobacteria throughout weaning.

Authors and affiliations (presenter underlined): You-Tae Kim (University of California, Davis, CA), Saumya Wickramasinghe (University of California, Davis, CA), Aidong Wang (University of California, Davis, CA), Sierra Durham (University of California, Davis, CA), Randall Robinson (University of California, Davis, CA), Daniela Barile (University of California, Davis, CA), David A. Mills (University of California, Davis, CA), Linh Nguyen (University of Alberta, Edmonton, Alberta, Canada), Amr El-Hawiet (University of Alberta, Edmonton, Alberta, Canada), John S. Klassen (University of Alberta, Edmonton, Alberta, Canada)

**Poster 21 SFA**

**Effects of soluble corn fiber consumption on cognitive function and gastrointestinal microbiota**

Objectives: This study evaluated the effects of soluble corn fiber (SCF) consumption on cognition and the gastrointestinal (GI) microbiota and metabolome, with pre-defined aims to investigate GI microbiota-dependent mechanisms linking SCF to cognitive performance.

Methods: This randomized, double-blind, crossover trial included 42 healthy adults (45-75y) who consumed maltodextrin (CON, 22g/d) or SCF (18g/d) for 4 wks, with a 4-wk washout in a counterbalanced order. Outcome assessments included cognitive control, GI microbiota, and metabolome, with exploratory in vitro and genomic analyses identifying species and genes facilitating SCF fermentation in the full cohort and select responders (n=3) and non-responders (n=3). Results: SCF consumption improved reaction times (RT) for congruent ($P<0.01$) and incongruent ($P<0.01$) flanker tasks. Faster congruent RT was correlated with higher fecal acetate ($\rho=-0.33$, $P=0.048$) and propionate ($\rho=-0.36$, $P=0.03$). SCF also enriched *Parabacteroides* abundance ($Q<0.01$), which correlated with acetate ($\rho=0.34$, $P=0.04$) and propionate ($\rho=0.27$, $P=0.1$). In vitro culturing demonstrated P. distasonis (Pd) growth (log OD600/hr) with SCF comparable to glucose and maltodextrin. Differential analysis of predicted metagenome found enriched carbohydrate metabolism pathways following SCF consumption ($Q<0.05$), MaAsLin revealed 2,701 differentially associated KEGG orthologs (KO), including carbohydrate-active (CA) KOs ($Q<0.05$). Shotgun metagenomic confirmed CA genes linked to Pd. Conclusion: SCF consumption improved attentional inhibition and increased *Parabacteroides* abundance. In vitro culturing confirmed Pd utilization of SCF. Acetate and propionate correlated with Parabacteroides and inversely with congruent RT. Funding: Tate&Lyle Ingredients Americas LLC.

Authors and affiliations (presenter underlined): David Alvarado (University of Illinois at Urbana-Champaign, Illinois, USA), Tori Holthaus (University of Illinois at Urbana-Champaign, Illinois, USA), Shelby Martell (University of Illinois at Urbana-Champaign, Illinois, USA), David Revilla (University of Illinois at Urbana-Champaign, Illinois, USA), Rhea Sarma (University of Illinois at Urbana-Champaign, Illinois, USA), Marco Atallah (University of Illinois at Urbana-Champaign, Illinois, USA), Naiman Khan (University of Illinois at Urbana-Champaign, Illinois, USA), Hannah D. Holscher (University of Illinois at Urbana-Champaign, Illinois, USA).

**Poster 22 SFA**

**Exploring the host-gut microbiota-related Polyamine Metabolism in MASLD development and treatment**

Metabolic dysfunction-associated steatotic liver disease (MASLD) is the most prevalent liver disorder globally. Dysregulation of the gut-liver axis plays a role in MASLD pathogenesis. Polyamines have been linked to MASLD development and progression in liver, but their role in gut remains unclear. This study explored polyamine metabolism in MASLD pathogenesis and its modulation by advanced microbiome therapeutics (AMTs) in mice. MASLD development was evaluated in C57BL/6J mice fed a high-fat, high-sugar diet for 8 (n=8), 12 (n=8), and 16 (n=8) weeks. After 14 weeks on this diet to induce MASLD, all mice switched to a standard diet for 7 weeks. During this period, intervention groups received gelatine cubes containing 10^9 CFU of *E. coli* Nissle expressing either aldafermin (n=6) or Insulin-like Growth Factor 1 (n=6).

Control groups received 10^9 CFU/gelatine cube of unmodified *E. coli* Nissle (n=6) or with no treatment (n=6). Untargeted metabolomics in plasma, liver, cecum, colon lumen contents and transcriptomics analysis in ileum and proximal colon tissues were performed. In MASLD model, increased levels of spermine, spermidine, and acetylputrescine were observed along with decreased acetylspermidine and diferuolyl putrescine in colon and cecum. AMTs administration reduced acetylputrescine and increased putrescine in colon and cecum. AMTs also upregulated polyamine-related genes (ornithine decarboxylase 1, solute carrier family 18 A1, and specificity protein 1) and fatty acid degradation and cytochrome P450 metabolism-related pathways in ileum, while downregulated steroid hormone biosynthesis, ribosome, and serotonergic synapse pathways in colon. These suggests that polyamine metabolism in gut contributes to MASLD pathogenesis, and AMTs can positively influence it.

Authors and affiliations (presenter underlined): Ambrin Farizah Babu (University of Eastern Finland, Kuopio, Finland; Afekta Technologies Ltd., Kuopio, Finland), Valeria Iannone (University of Eastern Finland, Kuopio, Finland); Johnson Lok (University of Eastern Finland, Kuopio, Finland); Giuseppe D'Auria (Sequencing and Bioinformatics Service, Foundation for the Promotion of Health and Biomedical Research of Valencia Region, FISABIO, Valencia, Spain; CIBER in Epidemiology and Public Health (CIBERESP), Instituto de Salud Carlos III, Madrid, Spain); Ruben Vazquez-Uribe (Technical University of Denmark, Kgs. Lyngby, Denmark; Center for Microbiology, VIB, Leuven, Belgium); Kati Hanhineva (University of Eastern Finland, Kuopio, Finland; Afekta Technologies Ltd., Kuopio, Finland, University of Turku, 20014 Turku, Finland); Hani El-Nezami (University of Eastern Finland, Kuopio, Finland; University of Hong Kong, Hong Kong, China); Morten Otto Alexander Sommer (Technical University of Denmark, Kgs. Lyngby, Denmark); Marjukka Kolehmainen (University of Eastern Finland, Kuopio, Finland); Carlos Gómez-Gallego (University of Eastern Finland, Kuopio, Finland).

**Poster 23 SFA**

**Synergistic interaction of *Akkermansia muciniphila* and mucin-degrading Bacteroides in Inflammatory bowel diseases**

Inflammatory bowel diseases (IBDs) are postulated to arise from a combination of host genetic susceptibility and environmental factors including diet and intestinal microbiota. We previously reported that feeding a fiber free diet to ex-germfree mice colonized with a synthetic microbiota containing 14 species (SM14) triggers lethal colitis when mice lack the IBD-associated cytokine, Interleukin-10 (IL-10). Il-10-/- mice colonized with a version of the synthetic microbiota lacking 4 species known to possess mucin-degrading abilities exhibited lower inflammation and significantly better survival, demonstrating a disease-promoting role of mucin-degrading bacteria. To test the roles of individual mucin degraders, we added them back to the synthetic microbiota either individually or in pairwise combinations. The presence of two mucin-degrading species (*Akkermansia muciniphila and Bacteroides thetaiotaomicron*) accelerated disease development with similar timing as the full SM14. Colonizing germfree IL-10-/- mice with just these two species also resulted in rapid disease development, suggesting that a combination of two species is both necessary and sufficient for rapid inflammation in this model. Another mucin-degrading *Bacteroides* (*B. caccae*) did not accelerate disease development as measured by survival when it was present within the community of non-mucin-degraders. However, when this species was present in the same community with *A. muciniphila* it caused significantly decreased survival, albeit slightly longer time-to-death than observed with the full SM14 or the community harboring *Akkermansia muciniphila* and *Bacteroides thetaiotaomicron together*. This work demonstrates that multiple combinations of mucin degrading bacteria are capable of acting synergistically during IBD pathogenesis and that diet and host genetic factors can unmask conditional pathogenic qualities of commensal gut anaerobes. Future work will focus on genetic analysis of the bacterial functions involved (e.g., mucin-degrading enzymes), mechanisms of synergy between mucin-degrading bacteria and determining if similar synergistic combinations occur in IBD patients that might contribute to disease occurrence.

Authors and affiliations (presenter underlined): Qinnan Yang (Department of Microbiology and Immunology, University of Michigan, Ann Arbor, MI, USA), Sadie Schaus (Department of Microbiology and Immunology, University of Michigan, Ann Arbor, MI, USA), Gabriel V. Pereira (Department of Microbiology and Immunology, University of Michigan, Ann Arbor, MI, USA), Nichlos Pudo (Department of Microbiology and Immunology, University of Michigan, Ann Arbor, MI, USA), Emily Madlambayan (Department of Microbiology and Immunology, University of Michigan, Ann Arbor, MI, USA), Eric C. Martens (Department of

Microbiology and Immunology, University of Michigan, Ann Arbor, MI, USA).

**Poster 24 SFA**

**Individual intestinal motility responses to acute whole-grain prebiotic ingestion mediates post-prandial nutrient metabolism: a single-blind randomized controlled clinical trial**

Background: Whole grains offer an array of prebiotic fibers and support cardiometabolic and digestive health. Yet, it is unclear whether these benefits are driven by differences in intestinal motility—the process coupling nutrient digestion and absorption to their postprandial appearance in circulation. This single-blind randomized crossover trial tested whether diet-induced shifts in intestinal motility mediate postprandial metabolism. Methods: Equal numbers of male and female participants (N=34, aged 20–59) underwent acute whole-grain (WG) and refined-grain (RG) bread feeding with a one-week washout between bread arms. Within each arm, intestinal motility metrics (transit time, pressure, pH) and blood metabolites (glucose, HDL, LDL, triglycerides) were tracked in tandem. Intestinal motility was surveyed using ingestible electronic capsules until stool sample collection. Blood metabolites were assessed over an 8-hour postprandial period. Results: WG reduced blood glucose over time (Time: $p>0.0001$, Diet: $p=0.0003$) and tended to lower colonic pressure ($p=0.09$), which positively correlated with total cholesterol ($r=0.40$, $p=0.02$). WG prolonged whole-gut transit time in females ($p = 0.03$), driven by a sex-by-diet (bread type) interaction in colonic transit time ($p = 0.01$). These findings were supported by a negative correlation between colonic transit time and stool consistency in females ($r = -0.78$, $p=0.0003$). Discussion: These data indicate that sex-by-diet interactions modulate intestinal motility in a sex-dependent manner, which may mediate postprandial glucose and cholesterol concentrations. We hypothesize these interactions are driven by gut microbial synthesis of amine compounds that confer inhibitory enteric nervous system activity in response to prebiotic ingestion.

Authors and affiliations (presenter underlined): Benjamin A. Levine (University of Illinois at Urbana-Champaign, IL, USA), Jordan E. Rindels (University of Illinois at Urbana-Champaign, IL, USA), Brett R. Loman (University of Illinois at Urbana-Champaign, IL, USA).

**Poster 25 SFA**

**Acetate and Gut-Brain Axis Modulation: A Pilot Study on Mental Health and Metabolic Outcomes**

Mental illnesses affect 1 in 5 Canadians, most often mood and anxiety (M/A) disorders, which can require the use of psychotropic medications. However, these medications are commonly associated with weight gain and metabolic side effects. The gut microbiota plays a role in mental illnesses via the gut-brain axis, with short-chain fatty acids like acetate influencing both microbiota composition and metabolic outcomes. This study evaluated the feasibility of acetate supplementation (enteric coated high-potency apple cider vinegar powder) to beneficially alter the gut microbiota and mitigate metabolic side effects in individuals with M/A disorders. 11 participants, aged 16–35, who experienced weight gain on stable medication doses, underwent a 1-month baseline assessment, 3 months of acetate administration (3 caplets twice daily) and a 1-month follow-up observation period. Adherence was excellent and no product-associated adverse events occurred. While no significant weight reduction was observed, M/A symptoms significantly improved, as measured by validated instruments. 7 participants also had meaningful reductions in LDL cholesterol and/or triglycerides. 16S rRNA gene sequencing of gut samples from the first 5 participants revealed significant shifts in gut microbiota composition, including enrichment of beneficial species such as *Bifidobacterium* spp., *Lactiplantibacillus* spp., and *Akkermansia muciniphila*. These findings suggest that acetate use may be a feasible approach to improving mental health symptoms and metabolic profiles of some patients with M/A disorders on psychotropics. Future studies with larger sample sizes and extended follow-up are warranted to confirm these effects, identify subgroups of responders, and explore the intervention's clinical relevance.

Authors and affiliations (presenter underlined): Kait F. Al (Department of Microbiology and Immunology, Western University), Michael Warren (Department of Psychiatry, Western University), David Walton (School of Physical Therapy, Western University), Colleen O'Connor (Brescia School of Food and Nutritional Sciences, Western University), Lisa Cameron (Pathology and Laboratory Medicine, Western University), Michael Wammes (Department of Psychiatry, Western University), Jeremy Burton (Department of Microbiology and Immunology, Western University), Elizabeth Osuch (Department of Psychiatry, Western University).

**Poster 26 SFA**

**Cranberry Extract Supplementation Modulates Gut Microbiota and Intestinal Epithelium in Ex Vivo and In Vivo Models**

Background: Proanthocyanidins (PAC) and oligosaccharides from cranberry exhibit multiple bioactive health properties and persist intact in the colon post-ingestion. Their interaction with the microbiome and the resulting effect on the gut epithelium remains inadequately understood. Methods: Six healthy participants underwent a two-week intervention with cranberry extract using the ex vivo TWIN-M-SHIME model, replicating the luminal and mucosal environments of the ascending and transverse colon. Fermentation effluents from four donors were incubated with murine intestinal organoids to assess gene expression related to epithelial differentiation, barrier integrity, and receptor signaling. Results: Cranberry extract supplementation significantly influenced gut microbiota ecology, altering bacterial metabolism. *Bifidobacterium adolescentis* flourished in the mucus of the ascending colon, accompanied by reduced Proteobacteria adhesion. The metabolism shifted from acetate to propionate and butyrate production, with a consistent butyrogenic effect across donors followed by the enrichment of several short-chain fatty acid producing bacteria and the formation of a consortium of key butyrogenic bacteria in the transverse colon mucus. Organoid incubations revealed increased expression of genes related to goblet cell differentiation, mucus production, intestinal barrier integrity, and metabolites receptors. Butyrate correlated with defensin regulation and GPR109a expression. Interestingly, effects stabilized after two weeks, suggesting microbiota and epithelial adaptation. Conclusions: Cranberry extract supplementation can beneficially modulate gut microbiota and epithelial function, supporting gut barrier integrity and overall gut health.

Authors and affiliations (presenter underlined): Valentina Cattero (Institute of Nutrition and Functional Foods (INAF), Faculty of Agriculture and Food Sciences, Laval University, Quebec City G1V0A6, Quebec, Canada, Centre Nutrition, Santé et Société (NUTRISS), INAF Laval University, Quebec City G1V 0A6, Quebec, Canada), Charlène Roussel (Institute of Nutrition and Functional Foods (INAF), Faculty of Agriculture and Food Sciences, Laval University, Quebec City G1V0A6, Quebec, Canada, Centre Nutrition, Santé et Société (NUTRISS), INAF Laval University, Quebec City G1V 0A6, Quebec, Canada, Excellence Research Chair on the Microbiome-Endocannabinoidome Axis in Metabolic Health, Laval University, Quebec City G1V 0A6, Quebec, Canada), Jacob Lessard-Lord (Institute of Nutrition and Functional Foods (INAF), Faculty of Agriculture and Food Sciences, Laval University, Quebec City G1V0A6, Quebec, Canada, Centre Nutrition, Santé et Société (NUTRISS), INAF Laval University, Quebec City G1V 0A6, Quebec, Canada), Thomas Mayer (Institute of Nutrition and Functional Foods (INAF), Faculty of Agriculture and Food Sciences, Laval University, Quebec City G1V0A6, Quebec, Canada, Centre Nutrition, Santé et Société (NUTRISS), INAF Laval University, Quebec City G1V 0A6, Quebec, Canada, Excellence Research Chair on the Microbiome-Endocannabinoidome Axis in Metabolic Health, Laval University, Quebec City G1V 0A6, Quebec, Canada), Alain Veilleux (Institute of Nutrition and Functional Foods (INAF), Faculty of Agriculture and Food Sciences, Laval University, Quebec City G1V0A6, Quebec, Canada, Centre Nutrition, Santé et Société (NUTRISS), INAF Laval University, Quebec City G1V 0A6, Quebec, Canada, Excellence Research Chair on the Microbiome-Endocannabinoidome Axis in Metabolic Health, Laval University, Quebec City G1V 0A6, Quebec, Canada), Denis Roy (Institute of Nutrition and Functional Foods (INAF), Faculty of Agriculture and Food Sciences, Laval University, Quebec City G1V0A6, Quebec, Canada, Centre Nutrition, Santé et Société (NUTRISS), INAF Laval University, Quebec City G1V 0A6, Quebec, Canada), Yves Desjardins (Institute of Nutrition and Functional Foods (INAF), Faculty of Agriculture and Food Sciences, Laval University, Quebec City G1V0A6, Quebec, Canada, Centre Nutrition, Santé et Société (NUTRISS), INAF Laval University, Quebec City G1V 0A6, Quebec, Canada)

**Poster 27 SFA**

**Engineered Bacillus subtilis as lactate converting probiotics to modulate host glucose metabolism**

Systemic elevation of lactate:pyruvate ratios is implicated in various acute and chronic disease states including metabolic disorders such as obesity and diabetes. Specifically, the accumulation of lactate systemically and in adipose tissue has been linked to the induction of adipose tissue inflammation and the development of insulin resistance. Recent evidence suggests that lactate is freely exchanged between tissues, systemic circulation, and the gut, allowing bidirectional modulation between the gut microbiota and peripheral organs. Inspired by these findings, we have engineered the spore-forming probiotic strain *B. subtilis* PY79 to produce Lactate Oxidase, enabling intestinal delivery of this therapeutic enzyme through oral probiotics which convert systemic lactate to pyruvate. After strain optimization, we first showed that oral administration of engineered PY79 spores to the gut of C57BL/6J mice reduced elevations in blood

lactate in two different mouse models involving exogenous challenge or pharmacologic perturbation without disrupting gut microbiota composition, liver function, or immune homeostasis. Next, we conducted a series of studies showing that treatment of mice with engineered spores promoted improvements in regulation of energy balance through glucose metabolism, and alleviation of adipose tissue proliferation during metabolic disease. Taken together, our studies offer a safe and practical probiotic strategy to address metabolic dysfunction through remediation of elevated lactate:pyruvate ratios by conversion of lactate in the gut, while also providing a new approach to help understand the role of systemic lactate:pyruvate ratios in the regulation of host metabolism and associated pathological processes.

Authors and affiliations (presenter underlined): Noah Hutchinson (University of Michigan, Ann Arbor MI, USA), Mengdi Yang (Northeastern University, Boston MA, USA), Ningyuan Ye (University of Michigan, Ann Arbor MI, USA), Jiahe Li (University of Michigan, Ann Arbor MI, USA).

**Poster 28 SFA**

**Targeted microbiome editing using a novel bacteriophage-derived endolysin with lytic activity against *C. difficile***

Introduction: *C. difficile* infection (CDI) is one of the leading causes of antibiotic-associated diarrhea and ~25% of patients treated for CDI are likely to develop recurrent infection. Bacteriophage-derived endolysins are peptidoglycan hydrolases that degrade the peptidoglycan layer in bacterial cell walls, ultimately leading to cell lysis. These enzymes specifically kill their specific prey without damaging non-target bacterial species. A novel bacteriophage-derived endolysin, CWH2, was identified as a potential antibiotic alternative for the treatment of CDI. Methods: Recombinant engineering techniques were used to express and purify CWH2 from *Clostridium* phage phiMMP01. Briefly, the gene sequence for CWH2 was codon optimized for expression in E. coli and cloned into the pET28b+ plasmid before transformation into *E. coli* BL21(DE3) cells as the final expression vector. Purified CWH2 was obtained from *E. coli* BL21(DE3) cells using sonification and the ÄKTA start chromatography system. The host range of CWH2 was evaluated against multiple Clostridioides spp. and commensal intestinal bacteria. The lytic activity of CWH2 was assessed in monoculture and mixed microbial community experiments. Results: CWH2 has a narrow host range confined to mainly *Clostridioides* spp. In monoculture experiments, CWH2 retains optimal lytic activity following treatment in up to 55$^{o}$C for 1 hour and can reduce *C. difficile* APC 43 cultures by over 60% in turbidity reduction assays. Discussion: CWH2 provides a viable alternative to conventional antibiotics for treating CDI. The specificity of CWH2 and strong lytic activity against *C. difficile* offers a new approach for targeted microbiome editing to eradicate pathogens while preserving surrounding microbiome integrity.

Authors and affiliations (presenter underlined): Ceylon Simon (School of Microbiology, University College Cork, APC Microbiome Ireland, University College Cork, Cork, Ireland), Ellen Murray (School of Microbiology, University College Cork, APC Microbiome Ireland, University College Cork, Cork, Ireland), R. Paul Ross (School of Microbiology, University College Cork, APC Microbiome Ireland, University College Cork, Cork, Ireland), Colin Hill (School of Microbiology, University College Cork, APC Microbiome Ireland, University College Cork, Cork, Ireland)

**Poster 29 SFA**

**Targeted vaginal probiotics with Lactobacillus crispatus based on their unique antimicrobial specialized peptides**

The female urogenital tract is an environment characterized by high rates of antibiotic use with only few innovations. *Lactobacillus crispatus* is a crucial member of the vaginal microbiota. However, besides a key role for lactic acid, its underlying mechanisms remain elusive, pausing its therapeutic development. Here, we show a tailored approach combining genomic, phenotypic and microbiome data of a large vaginal bacterial repository (https://isala.be), focusing on their antimicrobial potential, allowing the prioritization of strains of interest. This approach is largely based on genome-trait matching of specialized antimicrobial biosynthetic gene clusters and phenotypic activities against key urogenital pathogens linked with microbiome compositional data. These analyses pointed at not only species- and strain-specific gene clusters for ribosomally produced and post-translationally modified peptides (RiPPs) and bacteriocins, but also uncovered a link between community composition and biosynthetic potential of isolated *L. crispatus* strains, showing a clear distinction between isolates obtained from *L. crispatus*-dominated communities in comparison to more diverse communities. We showcase the potential of our platform by the discovery of a

previously undescribed lanthipeptide gene cluster. Heterologous expression and biochemical analyses point at a pore-forming antifungal lanthipeptide. The producer strain and purified peptide were able to significantly prolong survival in a preclinical model infected with pathogens. Together, our data stimulate the screening of *L. crispatus* strains based on their specific antimicrobial potential for application as probiotic for women's health and beyond.

Authors and affiliations (presenter underlined): Jelle Dillen (Laboratory of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp), Thibaut Maeyens (Laboratory of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp), Tom Eilers (Laboratory of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp), Eveline Vriens (Laboratory for Biomolecular Discovery and Engineering, VIB-KU Leuven Center for Microbiology and KU Leuven Department of Biology), Leonore Vander Donck (Laboratory of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp), Isabel Erreygers (Laboratory of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp), Peter A. Bron (Laboratory of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp), Stijn Wittouck (Laboratory of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp), Joleen Masschelein (Laboratory for Biomolecular Discovery and Engineering, VIB-KU Leuven Center for Microbiology and KU Leuven Department of Biology), Sarah Lebeer* (Laboratory of Applied Microbiology and Biotechnology, Department of Bioscience Engineering, University of Antwerp)

**Poster 30 IAC**

**Exploiting distinctive genomic features in New Zealand lactic acid bacterial isolates for novel candidate probiotic discovery.**

The accumulation of evidence supporting the positive effects of probiotics in human health has led to a growing need to identify novel probiotic strains for diverse indications. This study aimed to assess the genomic distinctiveness of lactic acid bacteria (LAB) isolates from New Zealand compared to the rest of the world, to facilitate novel probiotic candidate discovery. Over 500 LAB strains from over 50 different species, and isolated from various sources, were retrieved from the Fonterra Culture Collection (Palmerston North, New Zealand). Genome sequencing was performed using Illumina™, PacBio™ and Oxford Nanopore™ technologies combined on a case-by-case basis. Where possible, both short and long reads were used to conduct a hybrid genome assembly. For comparative analysis, available genome sequences for the species analysed were obtained from the RefSeq database. Genomic relatedness was assessed by multiple complementary approaches, including pangenome clustering, average nucleotide identity computation, and phylogeny reconstruction based on k-mer identities. The sequencing and data processing approach employed in this study generated high-quality genome assemblies, with complete circular chromosomes and plasmids sequences for the majority of the isolates analysed. Genomic relatedness and diversity analysis revealed the distinct genomic nature of many of the New Zealand isolates compared to the geographically diverse RefSeq genomes, with significantly distinct clusters for the former being identified in numerous LAB species. These included species widely known for their probiotic applications and safety of use, such as *Lacticaseibacillus rhamnosus*, *Lacticaseibacillus paracasei*, *Lactiplantibacillus plantarum*, *Lactobacillus acidophilus* and *Limosilactobacillus fermentum*. By identifying genetic distinctiveness inherent to LAB isolates from New Zealand, we shed new light on a potentially rich and relatively untapped source of new candidate probiotic strains with presumably distinct functional characteristics. Future work will determine the functional properties corresponding to the distinctiveness identified, supporting a bioinformatics-driven candidate selection for downstream *in vitro* and *in vivo* assessment of probiotic applications.

Authors and affiliations (presenter underlined): Eduardo L. de Almeida[1], Shalome A. Bassett[2], James Dekker[2], Paul W. O'Toole[3,4]
[1]Fonterra Microbiome Research Centre, University College Cork, Cork, Ireland
[2]Fonterra Research & Development Centre, Palmerston North, New Zealand
[3]APC Microbiome Ireland, University College Cork, Cork, Ireland
[4]School of Microbiology, University College Cork, Cork, Ireland
Corresponding Author: James Dekker
Corresponding Author Email: james.dekker@fonterra.com.

**Poster 31 IAC**

***In vitro* fermentation characteristics of acacia fiber (Everwell Fiber ®) using canine and feline fecal inocula.**

Everwell Fiber™, known for its prebiotic effects in humans, has not been studied in pets. This project evaluated the fermentability profile of this fiber compared to cellulose, inulin, and pectin, on canine and feline gut microbiota using an *in vitro* fermentation system, as well as to study its effects on short-chain fatty acid (SCFA) and gas production. Fecal samples were collected from healthy adult dogs (n=3) and cats (n=3) and pooled to serve as inoculum. Aliquots of fermentation media were collected at 0, 6, 12, and 18 hours to measure pH, SCFA, gas production, and microbiota populations. Fiber and blank Balch tubes, containing 10 mL of sterile *in vitro* fermentation media were aseptically inoculated with 1.5 mL of diluted feces. Each fiber substrate (115 mg/tube) was incubated in triplicates at 39°C for 0, 6, 12, or 18 h, with periodic mixing to mimic gut movements. Blank-corrected data were analyzed using the PROC GLIMMIX procedure of SAS with the main effects being fiber and time, with the fiber*time interaction also being tested. In the canine study, Everwell Fiber™ , inulin, or pectin had a greater ($P \leq 0.01$) decrease in pH than cellulose. Pectin and inulin had a greater ($P < 0.01$) increase in gas production than Everwell Fiber™ and cellulose. A greater ($P < 0.01$) increase in acetate, propionate, butyrate, and total SCFA was observed in Everwell Fiber™ , inulin, and pectin compared to cellulose. Bacterial alpha diversity analysis showed that bacterial richness (observed features; $P=0.03$) and diversity (Shannon diversity; $P=0.02$) were highest after 18 hours. Everwell Fiber™ had a greater ($P \leq 0.01$) number of observed features and Shannon Index than other fibers, indicating a higher bacterial richness and diversity. In the feline study, total gas production increased, while the pH decreased. These changes occurred at different rates depending on fiber source. Everwell Fiber™ was not different ($P > 0.05$) from cellulose in gas production but exhibited a greater decrease ($P \leq 0.05$) in pH after 12 h. Everwell Fiber™ had a greater ($P \leq 0.05$) increase in SCFA production than cellulose after 12 h and 18 h, which was driven by greater ($P \leq 0.05$) increases in acetate and propionate production. Everwell Fiber™ and cellulose had a greater ($P < 0.05$) increase in bacterial richness and diversity over time than pectin and inulin. Overall, these studies showed that Everwell Fiber™ results in a different fermentation profile and impacts intestinal microbiota differently and promoted higher bacterial richness and diversity while keeping levels of gas production low.

Authors and affiliations (presenter underlined):
All Authors: Elena Vinay[1].Vanessa M. De La Guardia-Hidrogo[2], Sofia M. Wilson[2], Elizabeth L. Geary[2], Laura L. Bauer[2], Ryan N. Dilger[2,3], and Kelly S. Swanson[2,3,4]. Mathieu Millette[5]
Organizations: [1]Kerry, Beloit, Wisconsin, USA,[2]Department of Animal Sciences, University of Illinois Urbana-Champaign; [3]Division of Nutritional Sciences, University of Illinois Urbana-Champaign; [4]Department of Veterinary Clinical Medicine, University of Illinois Urbana-Champaign., Kerry (Canada), Quebec, Canada.

**Poster 32 IAC**

**Bacillus Coagulans Unique IS2 Improves Stool Characteristics In Healthy Adults With Infrequent Bowel Movements: A Randomized, Double-Blind, Placebo-Controlled Trial**

Objectives: Over 60 million Americans are affected by digestive conditions and diseases leading to decreased quality of life and increased risk of various diseases. Most research examining probiotic efficacy has been conducted in specific patient populations, rather than a generally healthy population. Specifically, *Bacillus coagulans* Unique IS2 (Unique IS2) has improved stool frequency, stool consistency, and gastrointestinal (GI) symptoms in participants with constipation, irritable bowel syndrome, or diarrhea. Therefore, this randomized, double-blind, placebo-controlled trial investigated the efficacy of Unique IS2 on stool characteristics and GI symptoms in generally healthy adults.

Methods: Following a 2-week run-in, 144 healthy adults (18-65 years; BMI: 18.5-34.9 kg/m$^2$) with an average of ≥3 to <7 weekly complete spontaneous bowel movements (CSBM) were randomized to either Unique IS2 (2 billion Colony Forming Units/day) or placebo for 4 weeks. The primary outcome was the change in bowel movement (BM) frequency after 4 weeks. Secondary outcomes included change in stool consistency (Bristol Stool Form Scale), GI symptoms and quality of life (Gastrointestinal Quality of Life Index), gut microbiota composition (16S rRNA sequencing), and the proportion of CSBM to total BM.
Results: After 4 weeks of supplementation with Unique IS2 there was a significant increase in BM frequency compared to baseline ($P = 0.037$). Stool consistency significantly improved after each week in the Unique IS2 group (all $P < 0.05$) and was significantly improved compared to a placebo after 4 weeks ($P = 0.018$). These

improvements were likely related to a significant improvement in hard stool incidence (P = 0.001). No effects of Unique IS2 supplementation were demonstrated on GI symptoms and quality of life, gut microbiota composition, or proportion of CSBM to total BM.

Conclusions: Our results suggest that Unique IS2 improves stool characteristics in generally healthy individuals with hard stools and poor stool quality over a supplementation period of 4 weeks. Further research is needed to confirm the probiotic potential of Unique IS2 in healthy populations.
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Authors and affiliations (presenter underlined): Leila M. Shinn[1], Alison Kamil[1], Ashley LeMoire[2], Rebecca Replogle[1], Lois Lin[2], Adam P. Kuttenkeuler[2], Joshua Baisley[2], Jun Wang[2], Stephanie-Anne Girard[2], Stephanie Recker[2], Anthony Bier[3]
[1]PepsiCo, Inc. Chicago, IL USA
[2]Nutrasource Pharmaceutical and Nutraceutical Services, Inc. Guelph ON, Canada
[3] Apex Trials, Guelph ON, Canada

**Poster 33 not available**
**Poster 34 not available**

**Poster 35 IAC**
**Title: Probiotic *Bifidobacterium bifidum* strains desialylate MUC13 and increase intestinal epithelial barrier function**

Probiotic bacteria including Bifidobacterial species have the capacity to improve intestinal health, but the underlying molecular mechanisms are often not understood. Bifidobacteria are considered keystone species but have a relatively low abundance in the adult intestinal tract. Bifidobacterium colonization depends on degradation of host-derived carbohydrates, including human milk oligosaccharides and mucin-associated oligosaccharides. Specific Bifidobacterium strains can enhance intestinal barrier integrity and improve symptoms of gastrointestinal disorders. We previously reported that the transmembrane mucin MUC13 localizes to the apical and lateral membrane and regulates epithelial tight junction strength. Here, we screened probiotic bacterial strains for their capacity to modulate MUC13 and enhance intestinal barrier function. Of these probiotic bacteria, a *Bifidobacterium bifidum* strain uniquely degraded the MUC13 *O*-glycosylated extracellular domain. Further characterization of two probiotic *B. bifidum* strains (W23 and W28) and the type strain 20456 demonstrated that the W23 and W28 strains adhered strongly to the apical surface, had high sialidase activity, penetrated the mucus layer, and enhanced epithelial barrier integrity. These results underscore the strain-specific properties of these specific *B. bifidum* strains that most likely contribute to their probiotic effects in the intestinal tract.

Authors and affiliations (presenter underlined): Elke Lievens[1], Celia Segui-Perez[2], Liane Z. X[2]. Huang, Fernanda L. Paganelli[1], & Karin Strijbis[2]
[1] Winclove Probiotic BV, Amsterdam, The Netherlands
[2] Utrecht University, Utrecht, The Netherlands

**Poster 36**
**Exploring the Gut-Lung Axis in Pigs: Effects of Intestinal Microbiota and Postimmunobiotics on the resistance to PRRSV Infection**

Objective: The gut-lung axis has emerged as a significant area of research, revealing the interplay between the gut microbiota and respiratory health. Studies in humans and mice models demonstrated that the intestinal microbiota can modulate immune responses in the lungs, reducing the susceptibility to respiratory infections. The gut-lung axis has been less explored in pigs. This study aimed to a) investigate the effects of gut microbiota on the susceptibility to porcine reproductive and respiratory syndrome virus (PRRSV) infection in pigs and b) to evaluate the ability of Beneficial microbes with immunomodulatory capacities (immunobiotics) and their non-viable forms (postimmunobiotics) to modulate alveolar macrophages response through the gut-lung axis.

Methods: a) The gut microbiota of PRRSV-infected and non-infected pigs was analyzed with 16S rRNA sequencing. In a second set of experiments, the infection rate was quantified via qPCR in primary cultures of alveolar macrophages from pigs with and without microbiota. b) The influence of the immunobiotic strain *Lactobacillus delbrueckii* "E" on alveolar macrophages (PAM-KNU cell line) response to PRRSV infection was evaluated in vitro. Alveolar macrophages were stimulated with conditioned mediums obtained from porcine intestinal epithelial cells (INV1-3) and intestinal macrophages (IPIM-3) stimulated with heat-killed E or its purified DNA or RNA. Viral replication was assessed after 24 hours and the expressions of *IFN-β, IFN-γ, Mx1, OAS1, IL-1β, IL-6, A20, IL-10*, and *IL-27* were evaluated at various time points (0, 6, and 24 hours) using quantitative PCR.

Results: Significant alterations in the gut microbiota of PRRSV-infected pigs were observed in comparison with non-infected animals, with a marked reduction in alpha diversity. Viral load was significantly higher in pigs lacking microbiota, indicating a protective role of the gut microbiome against PRRSV. *In vitro* experiments showed that the conditioned medium obtained from intestinal epithelial cells and macrophages co-cultures stimulated with DNA from the strain E significantly reduced PRRSV replication in alveolar macrophages. The antiviral effects of the conditioned medium were related to improved expressions of *IFN-β* and *OAS1*, and down-regulation of *A20* in alveolar macrophages infected with PRRSV.

Conclusions: These findings suggest that the gut microbiota is crucial for an effective immune response in the lungs to protect the porcine host against PRRSV infection. Immunobiotic derived factors like the DNA of the strain *L. delbrueckii* E can be used to modulate the gut-lung axis, enhancing antiviral immunity through the stimulation of alveolar macrophages.

Authors and affiliations (presenter underlined): Luciano Arellano-Arriagada[1,3], Kohtaro Fukuyama[1,2], Fu Namai[1,2], Wakako Ikeda-Ohtsubo[1,2] , Keita Nishiyama[1,2], Leonardo Albarracin[2,3], Julio Villena[2,3], Haruki Kitazawa[1,2] (Tohoku University[1], CFAI[2], CERELA-CONICET[3]) Tohoku University, Laboratory of Animal Food Function

**Poster 37**

**Evaluation of Enriched Brewers' Spent Grains from Fermentation with Probiotic Bacteria as Potential Functional Food Ingredients**

Brewers' spent grains (BSGs) are nutritious food processing by-products generated in the brewing industry. In this study, in vitro digestion-fermentation was employed to examine fermented BSG using probiotic bacteria as functional food ingredients. Insoluble fibers in BSG were converted into soluble fibers after fermentation, giving an increase from 6.13 ± 0.42 to 9.37 ± 0.53 mg/100 g BSG. After in vitro digestion of unfermented and fermented BSG, various nutritional components were found to be higher in fermented BSG. After fermentation with probiotic bacteria, various short-chain fatty acids namely acetic acid, propanoic acid, and butyric acid were produced at higher amounts for fermented BSG. As for gut microbiota profile, differential genera such as Bacteroides and Ruminococcus were detected, showing different effects on the intestinal microbiota. This study demonstrates the potential of using microbial fermentation of underutilized BSG to serve as potential functional food ingredients.

Authors and affiliations (presenter underlined): Prof. William Chen, Endowed Professor in Food Science & Technology, Nanyang Technological University Singapore

**Poster 38**

**Exploration of the human duodenal microbiome in the development of the metabolic syndrome**

The human gut microbiome is a complex ecosystem of microorganisms living along the digestive tract. Growing evidence supports the key role of many intestinal bacteria in the regulation of immunometabolic processes that are involved in the development of obesity and related metabolic diseases such as type 2 diabetes. While knowledge of the human fecal microbiome, which mainly reflects bacteria found in the distal gut (colon), has progressed tremendously in the last decade, the bacteria inhabiting the upper digestive system (the small intestine) and their impact on metabolic health remain elusive. Indeed, the limited access to the upper intestinal segments of the intestine (e.g. duodenum, jejunum) makes it difficult to explore in humans. As our understanding of the gut microbiome grows, a question still arises: are the

analyses of the fecal microbiome sufficient to really assess the role and impact of the gut microbiome on human metabolic health?

Objective: Identify key bacterial taxa in the human duodenum and determine their potential impact on the development of metabolic syndrome (MetS).

Methods: Biopsies of 2 sections of the duodenum from 20 participants with normal metabolic parameters and 20 participants with features of the MetS were collected via upper endoscopy and inoculated onto more than 10 different culture media with appropriate contaminationaware protocols. The identification of the bacteria was performed by mass spectrometry using MALDI-TOF.

Results: At the genus level, several bacteria were identified from the duodenum samples including *Actinomyces, Neisseria, Rothia, Dietzia, Gemella, Kocuria, Streptococcus,* and *Veillonella*. We found that several bacterial species isolated from the duodenum are also commonly found in the oral cavity. Interestingly, bacteria from the metabolically healthy subjects are different from those found in the metabolically impaired participants. We observed more species of *Streptococcus* in the healthy group than in the MS group. The genus *Kocuria* was only identified in the MetS group. Bacterial screens will first be performed using the nematode *Caenorhabditis elegans* followed by studies in healthy and obese diabetic mice to determine the role of these bacteria in the regulation of gut and metabolic health. Conclusion: This project will contribute to a better understanding of the role of duodenal bacteria in health and in the pathogenesis of MetS in humans. Identification of bacteria enriched in the duodenum of healthy individuals may pave the way to a new potential class of probiotic bacteria for human gut and metabolic health.

Authors and affiliations (presenter underlined): Marilou Lavoie[1,2,3], Maria Lebeuf[1,3], Geneviève Pilon[1,3], André Tremblay[3], Patrick Couture[4], Valéry Lemelin[4], Frédéric Raymond[3], André Marette[1,2,3]
1-Québec Heart and Lung Institute Research Center, Université Laval, Québec, Canada;
2-Department of Medicine, Faculty of Medicine, Université Laval, Québec, Canada;
3-Institute of Nutrition and Functional Foods, Université Laval Québec, Canada;
4-CHUQ research center, Université Laval, Québec, Canada.

**Poster 39**

**Consumption of Fermented Foods Products by Adult Canadians: Trends and Opportunities**

Growing evidence suggests that consuming fermented foods (FFs) can lead to beneficial health outcomes. However, there is limited information by the Canadian population and a lack of established dietary recommendations for FF intake. To address this gap, an online survey was conducted to explore how Canadians utilize FFs and which factors influence their consumption. The objective was to identify consumption trends and potential opportunities for education, research, and development. A total of 4,045 responses from Canadians aged >18 years were obtained using age and sex quotas to reflect national demographic statistics. Overall, 25.7% of respondents reported consuming all 18 listed FF products at least once. The most consumed products were cheese (95.7%) and yogurt (93.2%), while fermented fish (38.9%) and fermented cereals and grains (40.2%) were the least consumed. FF intake was influenced by age, sex, income, and education level, with lower consumption observed among individuals over 51 years of age, those with lower income or education levels, and those who do not consider health benefits when choosing foods. Taste was the main motivator for consumption, except for kefir, fermented vegetables, kombucha, and plant-based yogurt/kefir, which were primarily consumed for perceived health benefits. Home fermentation remains uncommon, with 90% relying on commercial products. However, younger and more educated individuals were more likely to ferment foods like vegetables and yogurt at home. While most Canadians expressed openness to trying new FFs, common barriers included aversion to unfamiliar tastes or smells, limited product availability, and a lack of information. Importantly, two-thirds of respondents expressed interest in learning more about FFs, and nearly half believed this information should be included in Canada's Food Guide. This study highlights key trends and barriers in fermented food consumption among Canadians, revealing gaps in knowledge, access, and perceived benefits. These findings underscore the need for clear dietary guidance and targeted educational initiatives to improve awareness, acceptance, and integration of fermented foods into the Canadian diet. They also lay the groundwork for future opportunities for research and innovation in food policy and product development.

Authors and affiliations (presenter underlined): Camila Schultz Marcolla[1], Samantha Tapping[2], Kara Sampsell[3], Yi Fan[1], Carla Liria Sánchez-Lafuente, Raylene Reimer[3], Benjamin Willing[1], and Jeremy Burton[4]
[1] University of Alberta, Department of Agricultural, Food and Nutritional Science, Edmonton, AB T6G 2P5, Canada.
[2] Western University, London, ON N6A 3K7, Canada.
[3] University of Calgary, Faculty of Kinesiology, Calgary, AB T2N 1N4, Canada.
[4] Lawson Health Research Institute, London, AB N6C2R5, Canada. Canadian Fermented Food Initiative

**Poster 40**
**Bowel preparation reshapes the gut microbiota: consequences for probiotic engraftment and pathobiont invasion**

Bowel preparation is a highly common procedure performed before colonoscopies, requiring patients to undergo intense laxative cleansing of the intestine. Despite its prevalence, the impact of bowel preparation on the gut and associated microbiota – especially in patients with compromised gut health – is poorly understood. In this study we investigate the impact of high-osmolality bowel preparation with the laxative polyethylene glycol (PEG) on both conventional and mice colonized with human microbiota from healthy or ulcerative colitis patients, showing short-term damage to the mucosal epithelium and microbiome. Our findings demonstrate that during this period of damage the gut becomes susceptible to pathogen colonisation, both by *Salmonella* Typhimurium challenge and by gut pathobionts from a human ulcerative colitis microbiota. Moreover, we observed the translocation of these pathogens to extra-intestinal organs such as nearby lymph nodes, the liver, and spleen. These findings emphasise the need for thoughtful microbiome replenishment post-procedure to prevent pathogen colonisation following gastrointestinal perturbations in susceptible patients. Based on prior work identifying probiotic strains capable of surviving in high osmolality conditions, we present putative suitable post-colonoscopy probiotics that may fill ecological niches vacated by disrupted microbiota and enhance pathogen exclusion while the gut epithelium recovers.

Authors and affiliations (presenter underlined): Imogen Porter[1], Charlotte Clayton[2], Katharine M. Ng[2,3], Sagar Pannu[2], Brian Deng[2], Carolina Tropini[2,3,4]

[1]Genome Science & Technology, University of British Columbia, Vancouver, Canada
[2]Department of Microbiology and Immunology, University of British Columbia, Vancouver, Canada
[3]School of Biomedical Engineering, University of British Columbia, Vancouver, Canada
[4]Humans and the Microbiome Program, Canadian Institute for Advanced Research, Toronto, Canada

**Poster 41**
**Animal-Free Milk Proteins: Bovine Casein Expression in Pichia Pastoris**

As valuable ingredients in various applications (food, beverages, nutrition, pharmaceuticals), milk proteins are of major industrial interest. Yet, concerns about sustainability and animal welfare of traditional milk production are two important motivations for an increasing percentage of consumers to replace animal-based proteins with plant-based protein sources. Consequently, the demand for animal-free alternatives produced by precision fermentation is rising.
In this project, *Pichia pastoris* is used as a microbial host to express bovine milk protein, with a focus on casein. Four different types of caseins exist (αs1, α s2, β and κ-casein) are present in milk in different ratios. They are generally considered to be intrinsically disordered proteins, and they have post-translational modifications like phosphorylation and O-glycosylation. These play a role in the association and stabilization of casein in a micellar form in milk.

Caseins are notoriously difficult proteins to produce efficiently in microbial hosts. The aim of this research is to evaluate different expression strategies in *Pichia pastoris*, to evaluate the yield, and to characterize the products. These efforts involve developing casein expression and purification, studying micelle assembly, and comparing functional and nutritional aspects.

A significant advantage of recombinantly produced proteins is that they have, in contrast to plant-based proteins, similar or even an improved composition and structure compared to the original animal-based dairy proteins. Moreover, precision fermentation allows for customization of protein modifications, such as

phosphorylation or glycosylation, to enhance stability, solubility, or interaction with other food ingredients. These factors enable the formulation of microbial-based dairy alternatives with improved textural, emulsifying, and nutritional properties.

Authors and affiliations (presenter underlined): A. Thiel[1], L. Iaria[1,2], M. Werten[1,2], E. Bijl[1], K. Hettinga[1]
1. Dairy Science and Technology, Food Quality and Design group, Wageningen University, Bornse Weilanden 9, Wageningen, 6708 WG, the Netherlands
2. Food and Bio-Based Research, Wageningen University, Bornse Weilanden 9, Wageningen, 6708 WG, the Netherlands

**Poster 42**

**Responsiveness to 2'FL and GOS by infant gut microbiota differs by history of individual 2'FL consumption**

The microbiota strongly influence human gut homeostasis and health through their metabolism. The metabolic products of the infant microbiota are strongly influenced by human milk or formula feeding. Human milk contains oligosaccharides (HMOS) that are prebiotic, promoting gut colonization by mutualists. Most human milk contains 2'-fucosyllactose (2'FL) as its principal oligosaccharide, but its abundance varies. A secondary analysis was performed on fecal samples from a randomized, controlled trial (RCT) of 2'FL-supplemented and unsupplemented formula to investigate the relationship between dietary exposure to 2'FL and the subsequent ability of fecal microbiota to metabolize 2'FL and galacto-oligosaccharides (GOS) *ex vivo*. Microbial metabolic response was measured using *in vitro* anaerobic fermentation and metabolomics read-out, including short-chain fatty acids (SCFA). Microbial diversity was characterized using whole metagenome sequencing of raw stool. Exposure to 2'FL in the trial formula arm primed the growth and metabolism of the microbiota toward increased responsiveness to 2'FL ($p=0.005$), whereas responsiveness to GOS, a prebiotic to which the infants had no prior exposure, declined ($p=0.18$). Individuals with no dietary exposure to prebiotics resulted in their gut microbiota being less responsive to both 2'FL ($p=0.05$) and GOS ($p=0.05$). The response to 2'FL or GOS in fermentation analysis at baseline was associated with differences in microbial beta-diversity, suggesting that individual response to prebiotic may be predicted.

Authors and affiliations (presenter underlined): Alexander W. Thorman[1], Ardythe L. Morrow[1], Andre Groeneveld[2], Arjen Nauta[2], Ellen Looijesteijn[2], David S. Newburg[1]
[1]University of Cincinnati College of Medicine, Department of Environmental and Public Health Sciences, Cincinnati, OH, USA; [2]FrieslandCampina, Amersfoort, NL

**Poster 43**

**Capacity of fermented cabbage to protect against cytokine-induced damage to intestinal barrier integrity**

Fermented fruits and vegetables have garnered growing interest in their beneficial associations with human health. However, the mechanistic details underlying the outcomes of consuming these foods require further investigation. This study examined the capacity of soluble metabolites in laboratory-scale and commercial fermented cabbage (sauerkraut) to protect against disruption of polarized Caco-2 monolayers caused by IFN-γ and TNF-α. Laboratory-scale ferments (LSF) were prepared with and without adding probiotic *Lactiplantibacillus plantarum* NCIMB8826R (LP8826R) and sampled after 7- and 14-days of incubation. Trans-epithelial electrical resistance (TER) and paracellular permeability to fluorescein isothiocyanate-dextran (FITC) revealed that sauerkraut, but not raw cabbage or brine, protected against cytokine-induced damage to the Caco-2 monolayers. Metabolomic analyses performed using gas and liquid chromatography identified 149 and 333 metabolites, respectively, and revealed significant differences between raw and fermented cabbage. LSF metabolomes changed over time, and the profiles of LSF with LP8826R best resembled the commercial product. Overall, fermentation reduced carbohydrate concentrations and elevated levels of lactic acid, lipid, and amino acid derivatives (e.g., D-phenyl-lactate (D-PLA), indole-3-lactate (ILA), and γ-aminobutyric acid). Lactate, D-PLA, and ILA tested individually and combined only partially protected against cytokine-induced TER reductions and increases in paracellular permeability of Caco-2 monolayers. The findings show that intestinal barrier-protective compounds are consistently enriched during cabbage fermentations, irrespective of scale or microbial additions, and may contribute to the gut health-supporting activities of these foods.

Authors and affiliations (presenter underlined): Lei Wei, University of California - Davis, Maria L. Marco, University of California - Davis